

B2

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
19 April 2001 (19.04.2001)

PCT

(10) International Publication Number  
WO 01/27158 A2(51) International Patent Classification<sup>7</sup>: C07K 14/705Street, 75751 Rishon LeZion (IL). YANAI, Itai [US/US];  
55 Leicester Street, Brookline, MA 02146 (US).

(21) International Application Number: PCT/US00/27582

(22) International Filing Date: 6 October 2000 (06.10.2000)

(74) Agents: CERPA, Robert, K. et al.; Morrison & Foerster  
LLP, 755 Page Mill Road, Palo Alto, CA 94304-1018 (US).

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/158,615 8 October 1999 (08.10.1999) US  
60/184,809 24 February 2000 (24.02.2000) US(81) Designated States (national): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,  
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,  
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,  
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(71) Applicants (for all designated States except US): DIGIS-  
CENTS [US/US]; Suite 720, 1814 Franklin Street, Oak-  
land, CA 94612 (US). YEDA RESEARCH AND DE-  
VELOPMENT CO., LTD. [IL/IL]; Weizmann Institute of  
Science, P.O. Box 95, 76100 Rehovot (IL).(84) Designated States (regional): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,  
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (for US only): BELLENSON, Joel  
[US/US]; 244 Lakeside Drive, Apartment 15, Oakland,  
CA 94612 (US). SMITH, Dexter [US/US]; 868 Trestle  
Glen Road, Oakland, CA 94610 (US). LANCET, Doron  
[IL/IL]; 15 Weizmann Street, 76280 Rehovot (IL). GLUS-  
MAN, Gustavo [IL/IL]; 33/37 Ha'Alon Street, 79845  
Bnei Ayish (IL). FUCHS, Tania [IL/IL]; 12 Harav neria

Published:

— Without international search report and to be republished  
upon receipt of that report.For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

BEST AVAILABLE COPY

WO 01/27158 A2

(54) Title: OLFACTORY RECEPTOR SEQUENCES

(57) Abstract: The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensation. The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these polynucleotide sequences and host cells transfected with these polynucleotide sequences. The present invention further provides for functional variants and homologues of these polynucleotide sequences and the polypeptides encoded by these polynucleotides. Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of polypeptides in screening odorant molecules to determine the correspondence (scent representation, scent fingerprint or scent profile) between individual odorant receptors (the polypeptides) and particular odorant molecules. Also encompassed by the present invention is the use of the scent representation, scent fingerprint or scent profile to re-create and edit scents.



## **OLFACTORY RECEPTOR SEQUENCES**

### **CROSS-REFERENCE TO RELATED APPLICATIONS**

5        This application claims priority benefit of United States Provisional Patent Application Serial No. 60/158,615, filed on October 8, 1999, and United States Provisional Patent Application Serial No. 60/184,809, filed on February 24, 2000. The contents of those applications are hereby incorporated by reference herein in their entirety.

### **STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH**

Not applicable.

### **TECHNICAL FIELD**

15        The present invention is in the field of human olfactory receptors and their use in screening for olfactory agonists and antagonists. The present invention pertains to isolated nucleotide sequences which encode human olfactory receptors and also to the proteins  
20        encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of secondary scents and the identification of  
25        combinations of odor receptors which are encoded to detect such secondary scents.

## BACKGROUND ART

Our sense of smell plays an important role not only in our appreciation of our surroundings such as the smell of flowers or new mown grass, but also evolved as a survival skill. Numerous odorant molecules can be detected at extremely low concentrations, providing early warning of danger, such as the smell of smoke or contaminated food. Indeed, a potent example of this is that most pregnant women experience a heightened sense of smell, presumably to protect the fetus from the deleterious effects of food poisoning.

It is estimated that humans can detect millions of different molecular species; however, our nose can discriminate only a fraction of these different chemicals (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320), usually estimated at about 10,000 odorants (Axel, *Scientific American* 1995, October, 154-159). Odorants for terrestrial species such as humans, are volatile (air born) ligands which are detected by the olfactory system. Odorants have vastly different chemical structures and subtle differences can lead to pronounced changes in the perceived odor (Mombaerts, *supra*). For instance, when the hydroxyl group of octanol is replaced by a carboxyl group to give octanoic acid, its perceived odor changes from orange and rose-like to rancid and sweaty (Malnic *et al.*, *Cell* 1999 96, 713-723). The basis for these feats of sensory perception are just beginning to be understood at a cellular and molecular level.

The olfactory system contains millions of olfactory sensory neurons (OSNs) located in the olfactory epithelium of the nasal cavity. In humans, the olfactory epithelium occupies an area of approximately 5 cm<sup>2</sup>. The OSNs are bipolar with one end extending through the supporting cell into the mucosal layer, terminating in hairlike cilia. These cilia are the site of the olfactory receptors (OR) where the odorant ligands are thought to bind (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320, Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). The OSNs also have a single unbranched axon which leads to the olfactory bulb, a part of the brain containing approximately 2000 glomeruli where the axons terminate and initial processing of the sensory code takes place. OSNs expressing the same OR are randomly interspersed throughout the olfactory epithelium, but in both the nose and the bulb, information derived from different ORs is strictly segregated; each OSN in the nose and each glomerulus in the olfactory bulb appear to be dedicated to input from one or few OR type(s) (Malnic *et al.*, *Cell* 1999 96, 713-723). It also appears that the location of the glomeruli are conserved across individuals of a species, providing the first spatial processing of particular odorant patterns (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). The domains in the olfactory bulb for

different odors may overlap, but the overall patterns are distinct (Hildebrand *et al.*, *supra*), therefore, it should be possible to identify and reproduce the characteristic pattern of a given odorant. Output neurons project from the olfactory bulb to the primary olfactory cortex and from there to the higher cortical areas of the brain and to the limbic system (Malnic *et al.*,  
5 *supra*; Hildebrand *et al.*, *supra*, 20, 595-631).

Until the identification of a large family of genes encoding putative odorant receptors (Buck & Axel *Cell* 1991 65, 175-187), progress towards understanding the process of odor recognition was negligible. In recent years there has been an explosion in this field as more and more putative odor receptors are isolated and cloned. The odorant receptor gene products  
10 have thus far been characterized through homology as seven transmembrane domain G protein-coupled receptors (GPCR). It is estimated that there are probably 500-750 OR-like sequences in humans, while there are 500-1000 OR genes in rat and mouse (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). In mice, OR-like sequences make up approximately 1% of their genome, the largest known family in the mammalian genome, surpassing the complexity of  
15 even the immunoglobulin and T-cell antigen receptor gene families (Mombaerts, *supra*). The OR are concentrated on the surface of the OSN's mucus coated cilia and it is thought that odorant molecules bind to the OR in the olfactory epithelium and thereby initiate signal transduction. Current interpretation of recent experimental evidence favors the idea that each neuron expresses only one, or very few, ORs. Since mammals can detect at least 10,000 odors and  
20 there are approximately 1,000 or fewer ORs, each of the ORs must respond to several odorant molecules, and each odorant molecule must bind to several receptors. It is believed that various receptors respond to discrete parts of an odorant molecule's structure and that an odorant consists of several chemical groups each of which bind a characteristic receptor (Axel *Scientific American* 1995, October, 154-159; Malnic *et al.*, *Cell* 1999 96, 713-723).

25 The main signal transduction pathway mediated by OR homologues in vertebrate species involves G protein-mediated stimulation of adenylyl cyclase activity, resulting in cAMP elevation that opens cyclic-nucleotide gated channels with a non-specific cation selectivity (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). However, there are still numerous unanswered questions and recently it has come to light that 38-76% of the human  
30 gene OR sequences that are being reported may be pseudogenes and therefore incapable of expressing the proteins that encode the olfactory receptors. Some of the incidences may be due to the method of extracting the genomic DNA libraries (Mombaerts, *supra*). Few pseudogenes have been found in other vertebrates and their incidence in libraries from testicular DNA is also

rare (Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). cDNA should not contain pseudogenes. There are a number of examples of ORs which have been successfully expressed and reactions to certain odorant ligands have been determined (Malnic *et al.*, *Cell* 1999 96, 713-723; Mombaerts, *supra*; Zhao *et al.*, *Science* 1998 279, 237-242).

5        Some attempts to express the ORs in heterologous cell lines resulted in the formation of inclusion bodies rather than the insertion of the proteins into the membrane (Kiefer *et al.*, *infra*). However, purification of the receptors after expression in *E. coli* and their insertion into lipid vesicles facilitates the use of these receptors in odorant ligand screening using a combination of photoaffinity labeling and Trp fluorescence (Kiefer *et al.*, *Biochemistry* 1996 10 35, 16077-16084). In addition, a functional human OR receptor protein has been expressed in HEK-293 cells and oocytes and found to interact with odorant ligands (Wetzel *et al.*, *J. Neurosci.* 1999 19, 7426-7433). There have also been, a number of successful efforts of expressing cDNA in insect Sf9 cells using *baculovirus* vectors (Mombaerts *Annu. Rev. Neuorsci.* 1999) as well as assays with neuronal tissue (Malnic *et al.*, *Cell* 1999 96, 713-723; 15 Zhao *et al.*, 1998; Firestein *et al.*, WO 98/50081). In addition, recent work accomplished the expression of chimeric mouse olfactory receptor sequences in HEK-293 cells and showed their reactivity towards a panel of odorant ligands, some at micromolar concentrations (Krautwurst *et al.*, *Cell* 1998 95 917-926). The drawback to expression in heterologous cell systems is the lack of working signal transduction pathways which can be used to detect responses to odorant 20 ligands; these drawbacks can be overcome with methods known in the art (e. g. U.S. Pat. No. 5,798, 275). There are also methods of expressing and assaying functional neuronal receptors in neuronal cells, including methods for detecting particular odorant ligand specificity (Malnic *et al.*, *supra*; Zhao, *supra*; Firestein *et al.*, *supra*).

25        Other publications of interest are: *Chemical Senses* 6: 343-349 (1981); *Proc. Natl. Acad. Sci. USA* 79: 670-674 (1982); *Proc. Natl. Acad. Sci. USA* 81(6): 1859-1863 (1984); *Nature* 316: 255-258 (1985); *Brain Research* 368: 329-338 (1986); *J. Biol. Chem.* 261: 1299-1305 (1986); *Proc. Natl. Acad. Sci. USA* 83(13): 4947-4951 (1986); *J. Neurosci.* 6: 2146-2154 (1986); *J. Neurochem.* 47: 1527-1533 (1986); *Chemical Senses* 13: 191-204 30 (1988); *Biochem. J.* 260:121-126 (1989); *J. Biol. Chem.* 264: 6780-6785 (1989); *Biochim. Biophys. Acta* 1013: 68-72 (1989); *J. Biol. Chem.* 264: 18803-18807 (1989); *Biochemistry* 29: 7433-7440 (1990); *FEBS lett.* 270: 24-29 (1990); *Chemical Senses* 15: 529-536 (1990); *Eur. J. Biochem.* 196: 51-58 (1991); *Nature* 349: 790-793 (1991); *Neurosci. Lett.* 141: 115-

118 (1992); Developmental Brain Res. 73: 7-16 (1993); Proc. Natl. Acad. Sci., USA 90: 3715-3719 (1993); Human Mol. Genetics 3: 229-235 (1994); Eur. J. Biochem. 225: 1157-1168 (1994); European Journal of Biochemistry 238: 28-37 (1996); Receptors and Channels 4: 141-147 (1996); Genomics 37(2): 147-160 (1996); Protein Science 8: 969-977 (1999); Genomics 53: 56-68 (1998); Genomics 61:24-36 (1999); Genomics 63: 227-245 (2000); Trends in Neurosci. 7:35-36 (1984); Ann. Rev. Neurosci. 9:329-355 (1986); Trends Biochem. Sci. 12:63-66 (1987); Nature 351: 275-276 (1991); Nature 353: 799-800 (1991); Current Biol. 3(10): 668-674 (1993); Nature 372:321-322 (1994); Essays in Biochemistry. 33: 93-104 (1998); and Nature, 398 (6725): 285-287 (1999).

10           However, despite the forgoing, there has been relatively little work with human olfactory receptors, in particular in determining the sequences of large numbers of receptors, and less progress in determining the correspondence between particular human olfactory receptors and the scent(s) to which they respond.

15           All publications cited herein are hereby incorporated by reference in their entirety.

### **DISCLOSURE OF THE INVENTION**

20           An object of the invention is to determine the correspondence between ORs and the scent(s) to which they respond. Once this is accomplished, scents can be both analyzed and re-created for enhancing human experiences or eliciting particular responses. The present invention pertains to isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation. The present invention also pertains to the proteins encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the  
25           nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of receptor complex scent components and the identification of combinations of odor receptors which are encoded to detect such receptor complex scent  
30           components scents.

The invention provides isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation that are isolated from human olfactory epithelial tissue. The invention further provides expression vectors containing such nucleotide sequences. Also provided by the invention are purified polypeptides encoded by the nucleotide sequences. The invention further provides transformed cells which comprise a suitable host cell transfected with a suitable expression vector containing the nucleotide sequence encoding the receptor. The present invention also encompasses nucleotide sequences isolated from human olfactory epithelial tissue which encode receptors capable of binding odorant molecules. The invention further provides expression vectors containing such nucleotide sequences and homologues of both the polynucleotides and polypeptides. Further, the invention provides a means of using the nucleotide sequences of the invention in a method of screening odorant ligands to determine the specific binding of odorant molecules to a particular receptors, and further, determining the component odorant molecules of subjectively experienced smells, determining the combination odorant molecules and receptor stimulation or inhibition to re-create a particular scent. The binding of odorant molecules by the receptors encompassed in the present invention includes binding resulting in both the agonism (excitation/activation) and antagonism (inhibition/blocking) of receptor function(s) upon binding of the molecule.

Accordingly, the invention includes an isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence at least 95% homologous to said sequences. The invention also encompasses the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention. The invention further encompasses fragments of said polynucleotides which can be used as probes or primers to identify additional polynucleotide sequences through techniques known in the art, including those fragments depicted in SEQ ID NOs: 74-105.

The invention also includes additional isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides

encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:153 through SEQ ID NO: 1084, or a nucleotide sequence at least 95% homologous to said sequences. The invention also comprises the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing  
5 such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

10 The invention also encompasses an isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function. Host cells expressing such polypeptides and phages displaying such  
15 polypeptides are also encompassed by the invention. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

Scents can be captured, analyzed and recorded by a sensory device using various  
20 methods. Scent capture can be initiated by the user or by an automatic sensing system. A scent can be analyzed in terms of its interaction with olfactory neurons of a mammalian, preferably human, olfactory system, or by the expression of individual receptors under appropriate conditions and appropriate assay conditions in multiwell plates or in terms of its perception by a panel of mammalian, preferably human, subjects. The interaction with olfactory neurons can  
25 be determined experimentally, in vitro, by determining the interaction of an odorant with olfactory receptors of a given type. Alternatively, the interaction with olfactory receptor can be determined using a computer simulation which provides information regarding the interaction of an odorant with the olfactory receptors. A panel of subjects can be used to represent odors in terms of their perception. The data so generated can be used to represent a scent in a manner  
30 which can be recorded in digital or other format, stored in media such as computer memory, disks, or printed format, and transmitted over a data network. The representation of the scent can be used to re-create the scent at a local or remote site using an emitter module. The

representation of the scent allows for scent editing, where desirable aspects of an odor are enhanced or added and undesirable aspects are attenuated or eliminated.

Accordingly, the invention also embraces libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084, where the polynucleotides encode functional olfactory receptors; or functional fragments of the expression products. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

Also encompassed by the invention are libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, where the polypeptides are functional olfactory receptors; or functional fragments of the polypeptides. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

The invention also embraces methods for determining the binding pattern of a composition with olfactory receptors, involving exposing the composition to an olfactory receptor library, and determining whether the composition binds to each olfactory receptor, thereby determining the overall binding pattern of the composition. In additional embodiments, the method also involves determining the approximate binding constant with which the composition, or the various chemicals within the composition, bind to the receptors; determining whether a receptor or functional fragment thereof is activated; and determining the absolute amount of activation, or amount of activation relative to another receptor or a control substance. The composition can consist essentially of one compound or chemical, or can comprise at least two compounds or chemicals.

The invention also embraces DNA arrays or DNA chips comprising the DNA segments derived from any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084. The invention also embraces a method of determining differences among one or more individuals with respect to their olfactory faculties, comprising the steps of comparing the olfactory DNA of each individual against the array or chip.

The invention also embraces a method to determine single nucleotide polymorphisms in olfactory receptors, comprising the steps of uniquely amplifying olfactory receptor sequences from DNA obtained from one or more individuals, based on



primers designed according to the first 25 bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084, and determining the similarities and differences between said amplified DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

5

### **Brief Description of the Drawings**

Figure 1 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 1 - 73.

10

Figure 2 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 111 - 152.

### **Detailed Description of the Invention**

15

The present invention provides isolated polynucleotides comprising sequences that encode polypeptides which are involved in olfactory sensation and which can be used to screen odorant ligands, e.g., odorant receptor agonists and antagonists.

#### **Definitions**

20

The term "olfactory receptor" (OR) refers to a polypeptide involved in olfactory sensation. An "olfactory receptor polynucleotide" or "OR polynucleotide" is a polynucleotide encoding a polypeptide involved in olfactory sensation.

25

The term "odorant ligand" as employed herein refers to a molecule that has the potential to bind to an olfactory receptor. Equivalent terms employed herein include "odorant", "odorant molecule" and "odorant compound". The term "binding" or "interaction" as used herein with respect to odorant ligands refers to the interaction of ligands with the receptor polypeptide where the ligands may serve as either agonists and/or antagonists of a given receptor or receptor function. An odorant ligand may thus directly cause a perception of odor (an agonist), or may block the perception of odor (an antagonist). An odorant ligand may include, but is not limited to, molecules which interact with polypeptides involved in olfactory

30

sensation. Odorant ligands and molecules which interact with olfactory receptors are generally small, approximately 1000 Daltons, more preferably approximately 750 Daltons, more preferably approximately 500 Daltons, or even more preferably approximately 300 Daltons, hydrophobic molecules with a variety of functional groups. Small changes in structure can induce profound changes in odorant ligand binding and hence in the odor perceived by an individual.

A more detailed description of these sequences, as well as how these sequences were obtained, is provided below.

10

As used herein, a "polynucleotide" is a polymeric form of nucleotides of any length, which contain deoxyribonucleotides, ribonucleotides, and/or their analogs. The terms "polynucleotide", "nucleotide" and "nucleic acid" as used herein are used interchangeably. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The term "polynucleotide" includes double-, single-stranded, and triple-helical molecules. Unless otherwise specified or required, any embodiment of the invention described herein that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double stranded form. Not all linkages in a polynucleotide need be identical.

20

The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, primers, and adaptors. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. The use of uracil as a substitute for thymine in a deoxyribonucleic acid is also considered an analogous form of pyrimidine.

25

In the context of polynucleotides, a "linear sequence" or a "sequence" is an order of nucleotides in a polynucleotide in a 5' to 3' direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polynucleotide. A "partial sequence" is a linear sequence of part of a polynucleotide which is known to comprise additional residues in one or both directions.

30

If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by

conjugation with a labeling component. Other types of modifications included in this definition are, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g.,  $\alpha$ -anomeric nucleic acids, peptide nucleic acids, etc.), as well as unmodified forms of the polynucleotide(s).

Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH groups can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups.

Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, but not limited to, 2'-O-methyl-, 2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carboxycyclic sugar analogs,  $\alpha$ -anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs and abasic nucleoside analogs such as methyl riboside.

Although conventional sugars and bases will be used in applying the method of the invention, substitution of analogous forms of sugars, purines and pyrimidines can be advantageous in designing a final product, as can alternative backbone structures like a polyamide backbone such as those used in peptide nucleic acids (PNAs).

A polynucleotide or polynucleotide region has a certain percentage (for example, 75%, 80%, 85%, 90%, 95% or 99%) of "sequence identity" to another sequence means that, when aligned, that percentage of bases are the same in comparing the two sequences.

Homology, as described herein, means that the polypeptide sequences that are encoded by the nucleic acids demonstrate a certain relatedness (i.e., there exists regions of conserved amino acids), but not the same amino acid identity. There is complete or 100% homology at a particular amino acid residue when the amino acids of sequences being compared are the same (there is identity) or represent a conservative amino acid substitution (there is homology). A

“conservative amino acid substitution” occurs when a particular amino acid is substituted by an alternate amino acid of similar charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Ile). A “nonconservative amino acid substitution” occurs when a particular amino acid is substituted by an alternative amino acid of differing properties, that is, charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Tyr). The nucleic acid sequences within the scope of the present invention include those nucleic acids which differ in exact sequence from those listed in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152 but which encode identical or homologous polypeptide amino acid sequences.

10 A “primer” is a short polynucleotide, generally with a free 3’ -OH group, that binds to a target potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target.

15 An “adaptor” is a short, partially-duplexed polynucleotide that has a blunt, double-stranded end and a protruding, single-stranded end. It can be ligated, through its double-stranded end, to the double-stranded end of another polynucleotide. This provides known sequences at the ends of thus modified polynucleotides. Often adaptors contain specific sequences for primer binding and/or restriction endonuclease digestion.

20 A “probe” when used in the context of polynucleotide manipulation refers to a polynucleotide which is provided as a reagent to detect a target potentially present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and enzymes.

25 “Transformation” or “transfection” refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, lipofection, transduction, infection or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host cell genome.

30 A polynucleotide is said to “encode” a polypeptide if, in its native state or when manipulated by methods well known to those skilled in the art, it can be transcribed and/or translated to produce the polypeptide, a homologous polypeptide or a fragment thereof. For purposes of this invention, and to avoid cumbersome referrals to complementary strands, the anti-sense (or complementary) strand of such a polynucleotide is also said to encode the

sequence; that is, a polynucleotide sequence that "encodes" a polypeptide includes both the conventional coding strand and the complementary sequence (or strand).

The terms "polypeptide", "oligopeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, it may be interrupted by non-amino acids, and it may be assembled into a complex of more than one polypeptide chain. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), as well as other modifications known in the art.

In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an N-terminal to C-terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide. A "partial sequence" is a linear sequence of part of a polypeptide which is known to comprise additional residues in one or both directions.

"Recombinant," as applied to a polynucleotide or gene, means that the polynucleotide is the product of various combinations of cloning, restriction and/or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature.

A "vector" is a self-replicating nucleic acid molecule that can be used to transfer an inserted nucleic acid molecule into and/or between host cells. The term includes vectors that function primarily for insertion of a nucleic acid molecule into a cell, vectors that function primarily for the amplification of nucleic acid, and expression vectors that function for transcription and/or translation of the DNA or RNA. Also included are vectors that provide more than one of the above functions.

"Expression vectors" are defined as polynucleotides which, when introduced into an appropriate host cell, can be transcribed into a mRNA capable of being translated into a polypeptide(s). An expression vector also comprises control elements operatively linked to the coding region to enable and/or facilitate expression of the polypeptide in the target cell. These can include transcriptional, translational, posttranscriptional, and posttranslational control elements, as are known in the art. An "expression system" usually connotes a suitable host cell comprised of an expression vector that can function to yield a desired expression product.

A "host cell" includes an individual cell or cell culture which can be or has been a recipient for vector(s) or for incorporation of nucleic acid molecules and/or proteins. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell  
5 due to natural, accidental, or deliberate mutation. A host cell includes cells transfected in vivo with a polynucleotide(s) of this invention.

A "cell line" or "cell culture" denotes eukaryotic cells, derived from higher, multicellular organisms, grown or maintained in vitro. It is understood that the descendants of a cell may not be completely identical (either morphologically, genotypically, or phenotypically) to the parent cell.  
10 Cells described as "uncultured" are obtained directly from a living organism, and are generally maintained for a limited amount of time away from the organism (i.e., not long enough or under conditions for the cells to undergo substantial replication).

As used herein, "expression" includes transcription and/or translation.

"Heterologous" means derived from (i.e., obtained from) a genotypically distinct entity  
15 from the rest of the entity to which it is being compared. For example, a polynucleotide may be placed by genetic engineering techniques into a plasmid or vector derived from a different source, thus becoming a heterologous polynucleotide. A promoter which is linked to a coding sequence with which it is not naturally linked is a heterologous promoter.

An "isolated" or "purified" polynucleotide, polypeptide or cell is one that is  
20 substantially free of the materials with which it is associated in nature. By substantially free is meant at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90%, even more preferably at least 99%, and even more preferably at least 99.9% free of the materials with which it is associated in nature. As used herein, an "isolated" polynucleotide or polypeptide also refers to recombinant polynucleotides or polypeptides,  
25 which, by virtue of origin or manipulation: (1) are not associated with all or a portion of a polynucleotide or polypeptide with which they are associated in nature, (2) are linked to a polynucleotide or polypeptide other than that to which they are linked in nature, or (3) do not occur in nature, or (4) in the case of polypeptides, arise from expression of recombinant polynucleotides. Thus, for example, an isolated substance may be prepared by using a  
30 purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per volume of solution, by specific activity or it can be measured in relation to a second, potentially interfering substance present in the source mixture. Increasing enrichments of the embodiments of this invention are increasingly more preferred.

Thus, for example, a 2-fold enrichment is preferred, 10-fold enrichment is more preferred, 100-fold enrichment is more preferred, 1000-fold enrichment is even more preferred. A substance can also be provided in an isolated state by processes such as chemical synthesis or recombinant expression.

5       A "reagent" polynucleotide, polypeptide, or antibody, is a substance provided for a reaction, the substance having some known and desirable function in the reaction. A reaction mixture may also contain a "target", such as a polynucleotide, antibody, polypeptide, or assembly of polypeptides that the reagent is capable of reacting with. For example, in some types of diagnostic tests, the presence and/or amount of the target in a sample is determined by  
10       adding a reagent, allowing the reagent and target to react, and measuring the amount of reaction product (if any).

      "Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogsteen binding, or in any  
15       other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of an amplification reaction such as PCR, or the enzymatic cleavage of a polynucleotide by a ribozyme.

20       When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, those polynucleotides are described as "complementary". A double-stranded polynucleotide can be "complementary" to another polynucleotide if hybridization can occur between one of the strands of the first polynucleotide and the second. The degree to which one polynucleotide is complementary with another is quantifiable in terms of the proportion of bases in  
25       opposing strands that are expected to form hydrogen bonds with each other, according to generally accepted base-pairing rules of A-T, A-U and G-C.

      A "stable duplex" of polynucleotides, or a "stable complex" formed between any two or more components in a biochemical reaction, refers to a duplex or complex that is sufficiently long-lasting to persist between formation of the duplex or complex and subsequent detection,  
30       including any optional washing steps or other manipulation that may take place in the interim.

      A substance is said to be "selective" or "specific" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular cell or substance than it does with alternative cells or substances. An odorant ligand "specifically

binds" to a target if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds to other substances.

As used herein, "naturally occurring," "native," or "wild type" refers to endogenous polynucleotides and the protein(s) expressed thereby. These terms include full-length and  
5 processed polynucleotides and polypeptides. Processing can occur in one or more steps, and these terms encompass all stages of processing. For instance, polypeptides having or lacking a signal sequence are encompassed by the invention. "Non-naturally occurring", "non-native", or "non-wild type" refer to all other polynucleotides and polypeptides.

A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made  
10 of a target polynucleotide using one or more primers, and a catalyst of polymerization, such as a reverse transcriptase or a DNA polymerase, and particularly a thermally stable polymerase enzyme. Methods for PCR are taught in U.S. Patent Nos. 4,683,195 (Mullis) and 4,683,202 (Mullis et al.). All processes of producing replicate copies of the same polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "amplification."

According to this invention, a "genomic DNA library" is a clone library which contains  
15 representative nucleotide sequences from the DNA of a given genome. It is constructed using various techniques that are well known in the art, for instance, by enzymatically or mechanically fragmenting the DNA from an organism, organ, or tissue of interest, linking the fragments to a suitable vector, and introducing the vector into appropriate cells so as to  
20 establish the genomic library. A genomic library contains both transcribed DNA fragments as well as nontranscribed DNA fragments.

In comparison, a "cDNA library" is a clone library that differs from a genomic library in that it contains only transcribed DNA sequences and no nontranscribed DNA sequences. It is established using techniques that are well known in the art, i.e., selection of mRNA (e.g. by  
25 polyA) making single stranded DNA from a population of cytoplasmic mRNA molecules using the enzyme RNA-dependent DNA polymerase (i.e., reverse transcriptase), converting the single-stranded DNA into double-stranded DNA, cloning the resultant molecules into a vector, and introducing the vector into appropriate cells so as to establish the cDNA library.

Alternately, a cDNA library need not be cloned into a vector and/or established in cells, but can  
30 be screened using PCR with gene-specific primers, as is well known in the art.

An "individual" is a vertebrate, preferably a mammal, more preferably a human.

### General Techniques



The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as: "Molecular Cloning: A Laboratory Manual", second edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984); "Animal Cell Culture" (R.I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller & M.P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987 and annual updates); "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994); "Current Protocols in Immunology" (J.E. Coligan et al., eds., 1991).

***Basis for identification and description of the polynucleotides and polypeptides***

The polynucleotide sequences were identified using oligonucleotide primers which were complementary to OR membrane-spanning regions. A number of different primers were used to elicit a variety of nucleotide sequences which encode polypeptides involved in olfactory sensation. The identification and isolation of nucleotide sequences which encode polypeptides involved in olfactory sensation and the polypeptides that they encode is vital for determining the response of receptors to odorant molecules, the elucidation of scent representations, profiles, or fingerprints, the reproduction of scent representations, profiles, or fingerprints and the editing of scent representations, profiles, or fingerprints.

***Polynucleotides encoding polypeptides involved in olfactory sensation***

The present invention provides isolated polynucleotides encoding polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. These polynucleotides are isolated and/or produced by chemical and/or recombinant methods, or a combination of these methods. The present invention includes polynucleotides isolated from the human olfactory epithelium which encode polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. Unless specifically stated otherwise,

“polynucleotides” shall include all embodiments of the polynucleotides of this invention. These polynucleotides are useful as probes, primers, in expression systems, and, in a preferred embodiment, in screening methods as described herein. In one embodiment the polynucleotides of the present invention can be isolated by creating a cDNA library using  
5 template RNA from human olfactory epithelium tissue. A detailed example is related in Example 1, below.

The advantage of constructing a cDNA library for isolation of the desired nucleotide sequences is that the likelihood of obtaining pseudogenes is greatly reduced compared to using a genomic DNA library for the same purpose. cDNA libraries contain only mRNA expressed  
10 in the tissue used for the construction of the library, in this case, the human olfactory epithelium. The preferred olfactory epithelium tissue should express only those nucleotide sequences which are relevant for olfactory function, thereby excluding nonfunctioning pseudogenes and also GPCRs which may be similar in primary structure (amino acid sequence) but are not encoded in OSNs. As the number of GPCRs utilized in human signal transduction  
15 pathways is extremely wide and varied, cDNA libraries constructed using olfactory tissue are preferable for isolating nucleotide sequences that encode polypeptides which are involved in olfactory sensation, inasmuch as genomic libraries can contain abundant nucleotide sequences which encode for a variety of GPCRs performing numerous functions, and are likely to contain pseudogenes.

20 The isolation of polynucleotide sequences which encode polypeptides involved in olfactory sensation is described in Example 1. Accordingly, this invention provides isolated polynucleotides that contain sequences encoding polypeptides or portions thereof which are involved in olfactory sensation, wherein the polypeptide is at least 10 amino acids in length, and wherein the polynucleotide sequences are depicted in SEQ ID NOs:1-73 and SEQ ID  
25 NOs:111-152.

The invention includes modifications to said polynucleotides described above such as deletions, substitutions, additions, or changes in the nature of any nucleic acid moieties. A “modification” is any difference in nucleotide sequence as compared to a polynucleotide shown herein to encode a polypeptide involved in olfactory sensation, and/or any difference in  
30 the nucleic acid moieties of the polynucleotide(s), wherein such a modified polynucleotide encodes a polypeptide involved in olfactory sensation or a variant of said polypeptide that is useful in the practice of the invention. Such changes can be useful to facilitate cloning and modify expression of polynucleotides encoding polypeptides which are involved in olfactory

sensation. Such changes also can be useful for conferring desirable properties to the polynucleotide(s), such as stability. The definition of polynucleotide provided herein gives examples of these modifications. Hence, the invention also includes variants of the nucleic acid sequences disclosed herein, which include nucleic acid substitutions, additions, and/or deletions.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, including polynucleotides that are full-length, processed, coding, non-coding (including flanking region) or portions thereof, provided that these polynucleotides contain a region encoding at least a portion of a polypeptide involved in olfactory sensation. (That is, the region encodes a functional fragment of an olfactory receptor or other polypeptide involved in olfactory sensation.) Also embodied are the mRNA, cDNA and genomic DNA sequences and fragments thereof that include a polynucleotide sequence comprising a coding sequence for a portion of a polypeptide involved in olfactory sensation.

Genes encoding human olfactory receptors, and optionally including related genomic sequences such as regulatory sequences, can be obtained using olfactory receptor cDNAs as hybridization probes. Under high stringency hybridization conditions, an OR cDNA will hybridize to its cognate OR gene. Use of lower stringency hybridization conditions allows the isolation of OR genes that are related to, but not identical with, the gene corresponding to a particular OR cDNA.

Conditions for hybridization are well-known to those of skill in the art and can be varied within relatively wide limits. Hybridization stringency refers to the degree to which hybridization conditions disfavor the formation of hybrids containing mismatched nucleotides, thereby promoting the formation of perfectly matched hybrids or hybrids containing fewer mismatches; with higher stringency correlated with a lower tolerance for mismatched hybrids. Factors that affect the stringency of hybridization include, but are not limited to, temperature, pH, ionic strength, and concentration of organic solvents such as formamide and dimethylsulfoxide. As is well known to those of skill in the art, hybridization stringency is increased by higher temperatures and/or lower ionic strengths. See, for example, Ausubel et al., supra; Sambrook et al., supra; M.A. Innis et al. (eds.) PCR Protocols, Academic Press, San Diego, 1990; B.D. Hames et al. (eds.) Nucleic Acid Hybridisation: A Practical Approach, IRL Press, Oxford, 1985; and van Ness et al., (1991) Nucleic Acids Res. 19:5143-5151. The degree of stringency can be adjusted not only during a hybridization reaction, but also in post-hybridization washes, as is known to those of skill in the art.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, functionally equivalent variants and derivatives of full-length polypeptides involved in olfactory sensation and functionally equivalent fragments. For instance, changes in a DNA sequence that do not change the encoded amino acid sequence, as well as those that result in conservative substitutions of amino acid residues, non-deleterious non-conservative substitutions, one or a few amino acid deletions or additions, and substitution of amino acid residues by amino acid analogs, will not significantly affect properties of the encoded polypeptide. Polypeptides homologous to the polypeptides encoded by the polynucleotides described herein can also be identified using algorithms and methods well-known to those of skill in the art, such as those described in Ausubel, "Current Protocols in Molecular Biology," Chapter 19; see also Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649-656. A preferred method of determining homology is the BLAST set of similarity search programs (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410. Polypeptides which are 40% homologous, 50% homologous, 60% homologous, 70% homologous, 80% homologous, 90% homologous, 95% homologous, or 99% homologous to the polypeptides encoded by the polynucleotides described herein are encompassed by the invention.

Nucleotide substitutions that do not alter the amino acid residues encoded can be useful for optimizing gene expression in different systems. Suitable substitutions are known to those of skill in the art and are made, for instance, to reflect preferred codon usage in the particular expression systems. In another example, alternatively spliced polynucleotides can give rise to different functionally equivalent fragments or variants of an polypeptide involved in olfactory sensation. Alternatively processed polynucleotide sequence variants are defined as polynucleotide sequences corresponding to mRNAs that differ in sequence from one another but are derived from the same genomic region, for example, mRNAs that result from: 1) the

use of alternative promoters; 2) the use of alternative polyadenylation sites; and/or 3) the use of alternative splice sites.

***Preparation of polynucleotides involved in olfactory sensation***

5       The polynucleotides of this invention can be obtained using chemical synthesis, recombinant methods, or PCR.

Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to produce a desired DNA sequence.

10       For preparing polynucleotides which encode polypeptides involved in olfactory sensation using recombinant methods, a polynucleotide comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification. Polynucleotides may be inserted into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct  
15 uptake, endocytosis, transfection, F-mating, particle bombardment, liposome mediation, or electroporation. Once introduced, an exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. The polynucleotide encoding a polypeptide involved in olfactory sensation can be isolated from the host cell by methods well known within the art. See, e.g., Sambrook et al. (1989).

20       Alternatively, PCR allows amplification of DNA sequences. PCR technology is well known in the art and is described in U.S. Pat. Nos. 4,683,195, 4,800,159, 4,754,065 and 4,683,202, as well as *PCR: The Polymerase Chain Reaction*, Mullis et al. eds., Birkhausw Press, Boston (1994).

25       RNA can be obtained in a number of ways in an appropriate vector and the vector is transformed into a suitable host cell. When the inserted DNA is transcribed into RNA, the RNA can then be isolated using methods well known to those of skill in the art, as set forth in Sambrook et al., (1989), for example. RNA can also be obtained through in vitro reactions. For example, the polynucleotide, which encodes a polypeptide involved in olfactory sensation, can be inserted into a vector that contains appropriate transcription promoter sequences.

30       Commercially available RNA polymerases will specifically initiate transcription at their promoter sites and continue the transcription process through the adjoining DNA polynucleotides. Placing the polynucleotide sequences which encode polypeptides involved in

olfactory sensation between two such promoters allows the generation of sense or antisense strands of desired RNA.

5 ***Cloning and expression vectors comprising polynucleotide sequences encoding polypeptides involved in olfactory sensation***

The present invention further includes a variety of vectors containing polynucleotides encoding polypeptides involved in olfactory sensation. These vectors can be used for expression of recombinant polypeptides as well as a source of polynucleotides which encode polypeptides involved in olfactory sensation. Cloning vectors can be used to obtain replicate  
10 copies of the polynucleotides, which encode polypeptides involved in olfactory sensation, they contain, or as a means of storing the polynucleotides in a depository for future recovery. Expression vectors (and host cells containing these expression vectors) can be used to obtain polypeptides produced from the polynucleotides they contain. Suitable cloning and expression vectors include any known in the art, e.g., those for use in in vitro, bacterial, mammalian, yeast  
15 and insect expression systems. Specific vectors and suitable host cells are known in the art and need not be described in detail herein. For example, see Gacesa and Ramji, *Vectors*, John Wiley & Sons (1994).

Cloning and expression vectors typically contain a selectable marker (for example, a gene encoding a protein necessary for the survival or growth of a host cell transformed with the  
20 vector), although such a marker gene can be carried on another polynucleotide sequence co-introduced into the host cell. Only those host cells into which a selectable marker has been introduced will survive and/or grow under selective conditions. Typical selectable markers encode protein(s) that (a) confer resistance to antibiotics or other toxins substances, e.g., ampicillin, neomycin, methotrexate, etc.; (b) complement auxotrophic deficiencies; or (c)  
25 supply critical nutrients not available from complex media. The choice of the proper marker gene will depend on the host cell, and appropriate genes for different hosts are known in the art. Cloning and expression vectors also typically contain a replication system recognized by the host.

Suitable cloning vectors may be constructed according to standard techniques, or may  
30 be selected from a large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self-replicate in an appropriate host, may possess a single target for one or more particular restriction endonucleases, and/or may carry genes for a marker

that can be used in selecting clones containing the vector. Suitable examples include plasmids and bacterial viruses, e.g., pUC18, pUC19, m13mp18, m13mp19, pBR322, pMB9, ColE1, pCR1, RP4, phage DNAs, and shuttle vectors such as pSA3 and pAT28. These and many other cloning vectors are available from commercial vendors such as BioRad, Stratagene, and  
5 Invitrogen.

Expression vectors generally are replicatable polynucleotide constructs that contain a polynucleotide encoding a polypeptide involved in olfactory sensation of interest. The polynucleotide, which encodes a polypeptide involved in olfactory sensation, encoding the polypeptide is operatively linked to suitable transcriptional controlling elements, such as  
10 promoters, enhancers and terminators. For expression (i.e., translation), one or more translational controlling elements are also usually required, such as ribosome binding sites, translation initiation sites, and stop codons. These controlling elements (transcriptional and translational) may be derived from the gene encoding polypeptides involved in olfactory sensation, or they may be heterologous (i.e., derived from other genes and/or other organisms).  
15 A polynucleotide sequence encoding a signal peptide can also be included to allow a polypeptide involved in olfactory sensation to cross and/or lodge in cell membranes or be secreted from the cell. A number of expression vectors suitable for expression in eukaryotic cells including yeast, insect, avian, plant and mammalian cells are known in the art. Common vectors, such as YEp13 and the Sikorski series pRS303-306, 313-316, 423-426 can also be  
20 used. Vectors pDBV52 and pDBV53 are suitable for expression. Another example of an expression vector/host cell system is the baculovirus (e.g., nuclear polyhedrosis virus)/insect cell (e.g., sf9 cells) system.

Human olfactory receptor polypeptides are expressed from olfactory receptor cDNA by methods well-known to those of skill in the art. A cDNA or portion thereof is inserted in an  
25 expression vector using standard molecular cloning techniques. Coupled in vitro transcription and translation of such a vector results in expression of the OR protein encoded by the cDNA. In vivo expression of a OR polypeptide is accomplished by inserting an OR cDNA into a eucaryotic or procaryotic expression vector, of which many are known in the art, to generate an OR expression construct. The OR expression construct is introduced into an appropriate  
30 host cell in which the OR sequences are expressed (by transcription and translation) and optionally secreted, and the expressed OR polypeptide is obtained from the cell growth medium and/or from cell lysates.

A number of expression vectors are known in the art. Prokaryotic expression vectors include, but are not limited to, T7 RNA polymerase/T7 promoter-based vectors, bacteriophage  $\lambda$ -based vectors and various types of fusion vectors. Fusion vectors include, but are not limited to, lacZ and trpE fusion vectors, maltose binding protein fusion vectors, glutathione-S-transferase fusion vectors, and thioredoxin fusion vectors. Baculovirus-based vectors are used for expression in insect cell systems. Expression in mammalian cells (such as HEK, COS and CHO cells) utilizes vectors containing a mammalian origin of replication (such as, for example, a SV40 origin), an efficient promoter (optionally including one or more enhancer sequences), mRNA processing signals (e.g., splice sites and polyadenylation sites), one or more selectable markers, and optionally a prokaryotic replicon to allow propagation and manipulation of the construct in prokaryotic cells. Alternatively, expression in mammalian cells is achieved through the use of any of a number of mammalian viral vectors including, but not limited to, retroviruses, lentiviruses, Semliki Forest viruses, vaccinia viruses, adenoviruses and adeno-associated viruses.

Vectors containing the polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including electroporation, direct injection, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent, such as a virus). The choice of means of introducing vectors or polynucleotides encoding polypeptides involved in olfactory sensation will often depend on the host cell, as will be well known to those of skill in the art.

***Host cells transformed with polynucleotides encoding polypeptides involved in olfactory sensation***

Another embodiment of this invention are host cells transformed with (i.e., comprising) polynucleotides encoding polypeptides involved in olfactory sensation, and/or vectors having polynucleotide(s) sequences encoding polypeptides involved in olfactory sensation, as described above. Both prokaryotic and eukaryotic host cells may be used. Prokaryotic hosts include bacterial cells, for example *E. coli*, *B. subtilis*, and mycobacteria. Among eukaryotic hosts are yeast, insect, avian, plant and mammalian cells. Host systems are known in the art and need not be described in detail herein.

The host cells of this invention can be used, *inter alia*, as repositories of polynucleotides encoding polypeptides involved in olfactory sensation, and/or vehicles for



production of polynucleotides encoding polypeptides involved in olfactory sensation, and/or polypeptides involved in olfactory sensation . They may also be used as vehicles for *in vivo* delivery of polypeptides involved in olfactory sensation .

5 ***Uses for and methods using polynucleotides encoding polypeptides involved in olfactory sensation***

To determine whether a vector containing polynucleotides is capable of expressing in eukaryotic cells, cells such as, for example, COS-7 (primate origin), CHO (rodent origin), HEK-293 (human origin), or HeLa (human origin) cells can be transfected with the vector.

- 10 Expression of a polypeptide(s) encoded by the vector is then determined by, for example, RIA, ELISA, immunofluorescence of fixed cells, or western blotting of cell lysate using an antibody as a probe. Antibodies can be obtained using, as immunogen, peptide sequences synthesized from the protein sequences encoded by the known polynucleotide sequence. Polypeptides can be purified by, for example, phase partitioning, affinity methods, gel filtration and ion
- 15 exchange, as well as additional methods known by those skilled in the art. Further characterization of the expressed polypeptide can be achieved by purification of the polypeptide using techniques known in the art.

***Polypeptides involved in olfactory sensation***

- 20 The present invention encompasses polypeptides involved in olfactory sensation. Expression of said polypeptides is localized in the olfactory neurons located in the olfactory epithelium, as described earlier. The polypeptides may comprise any novel sequence encoded by a nucleotide sequence as depicted in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152.
- 25 The invention includes modifications to polypeptides involved in olfactory sensation including functionally equivalent fragments of the polypeptides involved in olfactory sensation which do not significantly affect their properties and variants which may have enhanced or decreased activity. Collectively, these modifications may be termed "analogs" of or a fragment of polypeptides involved in olfactory sensation. Modification of polypeptides is routine practice in
- 30 the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or use of chemical analogs. Amino acid residues which can be conservatively substituted for

one another include but are not limited to: glycine/alanine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; serine/threonine; lysine/arginine; and phenylalanine/tyrosine. Such conservative substitutions are known in the art, and preferably, the amino acid substitutions would be such that the substituted amino acid would possess

5 similar chemical properties as that of the original amino acid. These polypeptides also include glycosylated and non-glycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with different sugars, acetylation, and phosphorylation. Amino acid modifications can range from changing or modifying one or more amino acids to complete redesign of a region. Other methods of

10 modification include using coupling techniques known in the art, including, but not limited to, enzymatic means, oxidative substitution and chelation. Modified polypeptides involved in olfactory sensation are made using established procedures in the art.

The invention also encompasses fusion proteins comprising one or more polypeptides involved in olfactory sensation. For purposes of this invention, an fusion protein contains one

15 or more polypeptides involved in olfactory sensation and another amino acid sequence to which it is not attached in the native molecule, for example, a heterologous sequence or a homologous sequence from another region. Useful heterologous sequences include, but are not limited to, sequences that provide for secretion from a host cell, intracellular trafficking, and stability/degradation. Other useful heterologous sequences are ones which facilitate

20 purification. Examples of such sequences are known in the art and include those encoding epitopes such as Myc, HA (derived from influenza virus hemagglutinin), His-6, or FLAG. Other heterologous sequences that facilitate purification are derived from proteins such as glutathione S-transferase (GST), maltose-binding protein (MBP), or the Fc portion of immunoglobulin.

25

#### ***Preparation of polypeptides involved in olfactory sensation***

The polypeptides of this invention can be made by procedures known in the art. The polypeptides can be produced by recombinant methods (i.e., single or fusion polypeptides) or by chemical synthesis. Polypeptides, especially shorter polypeptides up to about 50 amino

30 acids, are conveniently made by chemical synthesis. Methods of chemical synthesis are known in the art and are commercially available. For example, a polypeptide can be produced by an automated polypeptide synthesizer employing the solid phase method. Polypeptides can also be made by chemical synthesis using techniques known in the art.

Polypeptides can also be made by expression systems, using recombinant methods. The availability of polynucleotides encoding polypeptides permits the construction of expression vectors encoding intact (i.e., native) polypeptide, functional equivalents and functional fragments thereof, modified forms or recombinant forms. A polynucleotide  
5 encoding the desired polypeptide, or a fusion protein, can be ligated into an expression vector suitable for any convenient host. Both eukaryotic and prokaryotic host systems can be used. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification or isolation of the polypeptides expressed in host systems can be accomplished by any method known in the art ( e.g. partitioning exclusion,  
10 ion exchange chromatograph, gel filtration, etc.). Other controlling transcription or translation segments, such as signal sequences that direct the polypeptide to a specific cell compartment (i.e., for secretion), can also be used. Examples of prokaryotic host cells are known in the art and include, for example, *E. coli* and *B. subtilis*. Examples of eukaryotic host cells are known in the art and include yeast, avian, insect, plant, and animal cells such as COS7, HeLa, CHO,  
15 HEK-293 and other mammalian cells.

Alternatively, in vitro expression systems may also be used to produce polypeptides involved in olfactory sensation. A plasmid containing a polynucleotide encoding polypeptides involved in olfactory sensation, under the control of an appropriate promoter, can be transcribed and the resultant RNA translated in vitro through the use of commercially  
20 available reagents. Such methods can be used to produce relatively pure samples of the polypeptide and are known in the art.

Preferably, the polypeptides are at least partially purified from other cellular constituents. In one embodiment, the polypeptides are at least 70%, more preferably at least 80%, even more preferably at least 90% or most preferably at least 95% pure. In this context,  
25 purity can be calculated as a weight percent of the total protein content of the preparation. More highly purified polypeptides may also be obtained and are encompassed by the present invention. Methods of protein purification are known in the art and are not described in detail herein. For membrane-bound proteins, the lipid content of the preparation, which is required to maintain the structure and function of the protein, is excluded from the purity calculation. That  
30 is, if a preparation weighing 10 mg has 5 mg lipid, 4 mg of desired protein, and 1 mg of undesired proteins, the purity is calculated as 80% (desired protein content divided by total protein content). Preparations of biological or synthetic molecules suitable for maintaining structure and function of membrane proteins are described in Etemadi AH (1985) *Adv Lipid*

- Res 1985;21:281-428; Villalobo A (1990) *Biochimica Et Biophysica Acta*, 1017(1):1-48; Montal M (1987) *Journal Of Membrane Biology* 98(2): 101-115; Scotto AW et al. (1987) *Biochemistry* 26(3): 833-839; Jain MK and Zakim D (1987) *Biochimica Et Biophysica Acta* 906(1): 33-68; Czerski L and Sanders CR (2000) *Anal Biochem* 284(2):327-33 (lipid-detergent mixtures or "bicelles"); Hrafnisdottir S and Menon AK (2000) *J Bacteriol* 182(15):4198-206 (proteoliposomes); Puu G et al. (2000) *Biosens Bioelectron* 15(1-2):31-41 (protein-lipid preparations on solid surfaces); Schafmeister CE et al. (1993) *Science* 262(5134):734-8 ("peptitergents").

#### 10 *Uses of polypeptides involved in olfactory sensation*

- The polypeptides of this invention have a variety of uses. They can be used, for example, to screen odorant ligands in order to determine the scent representations, scent profiles or scent fingerprints of particular odorant molecules and further to characterize the effect of functional groups and chemical characteristics on perceived smell. Methods for screening odorant compounds using odorant receptors in neuronal cells are known in the art (Firestein et al., WO 98/50081; Duchamp-Viret et al., *Science* 1999, 284 2171-2174; Sato et al., *J. Neurophys.* 1994 72 2980-2989; Malnic et al., *Cell* 1999 96 713-723; Zhao et al., *Science* 1998 279, 237-242). There are also methods which can be employed to screen odorant compounds which do not require neuronal cells and are known in the art (Kauvar et al., U. S. Pat. No. 5,798,275; Kiefer et al., *Biochemistry* 1996 35 16077-16084; Krautwurst et al., *Cell* 1998 95 917-926).

- Analysis of the scent can be performed in a number of ways. Various embodiments of the scent analysis system are presented. Examples of how these embodiments might operate are also presented, although it should be emphasized that the invention is not limited by any particular theory of olfactory perception or scent analysis.

#### Olfactory Space

- The sensory subsystem comprises a series of olfactory receptors, which selectively bind with the chemical component(s) making up the scent. The scent can be characterized in terms of which of the approximately 1,000 olfactory receptors the scent component(s) bind to, and the strength of the interaction of the component(s) with those receptors. Each olfactory receptor can be considered an orthogonal basis vector; the entire set of olfactory receptors can be considered a set of basis vectors spanning "olfactory space." This is analogous to vectors

pointing along the x, y, and z directions in three-dimensional space, where any point in space can be represented by a combination of the x, y, and z basis vectors (with each of the x, y, and z vectors multiplied by the appropriate scalar quantity). The intensity of interaction of a scent with an olfactory receptor determines the magnitude of the vector along that particular "axis" in olfactory space. Thus, every scent can be uniquely described by a vector representation in olfactory space.

A representation of a scent in such a manner that the scent can later be re-created is defined as scent profiling. The aforementioned vector representation is one example of a scent profile.

#### Primary Scents

For the purposes of this invention, a receptor primary scent component is defined as a chemical that interacts with one and only one scent receptor. A receptor complex scent component is defined as a chemical that interacts with more than one scent receptor; the receptor complex scent component can interact with each of the scent receptors to different degrees, to equal degrees, or can interact with some receptors to the same degree and others to different degrees.

Olfactory receptors are proteins which fall in the class of seven transmembrane domain G protein-coupled receptors, and are found in olfactory neurons *in vivo*. Binding of an odorant to an olfactory receptor causes second messenger systems to become activated or inhibited in the cell, leading to increased cellular production of second messenger molecules such as cyclic AMP. These second messenger systems in turn lead to the depolarization of the olfactory neuron, or other changes in the state of the neuron, which provides the signal to the nervous system that the odorant has been detected.

With a complete set of receptor primary scent components, any scent can be re-created with the knowledge to the degree to which it interacts with each olfactory receptor. The instant invention encompasses such complete sets of receptor primary scent components. Other embodiments of the invention encompass sets of receptor primary scent component chemicals which provide the ability to re-create a particularly desired subset of scents, but not necessarily all possible scents. Still more embodiments encompass sets of receptor primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

In some cases, a receptor complex scent will be an acceptable approximation to a receptor primary scent. That is, if a given receptor complex scent interacts with a first scent receptor strongly, but interacts with other scent receptors less strongly, it can be considered an approximation to a receptor primary scent component for the first receptor. Such a receptor complex scent component is described by the term receptor quasi-primary scent component. One embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating all scents. Another embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating a particularly desired subset of scents, but not necessarily all possible scents. Yet another embodiment encompasses sets of receptor quasi-primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

The identification of receptor primary or quasi-primary scent component chemicals provides the most conceptually straightforward method of re-creating scents. However, another embodiment of the invention encompasses the use of receptor complex scent components for re-creating scents. An example of such an embodiment would be re-creation of a scent that activates olfactory receptors designated OR1, OR2, OR3, OR4, OR5 and OR6 (for the sake of illustration, it is assumed that the olfactory receptors are stimulated to an equal extent). If one is in possession of two receptor complex scent component chemicals (RCSC's) where RCSC1 activates OR1 and OR5, and RCSC2 activates OR2, OR3, OR4, and OR6, then one can reproduce the original scent by mixing RCSC1 and RCSC2 to re-create the original olfactory receptor activation profile. In practice, the profiles of various receptor complex scent components will be much more complicated than the forgoing example, and components which inhibit olfactory activation as well as stimulate activation can be included in the sets. However, once receptor activation profiles of sufficient receptor complex scent components are known, computer algorithms can be utilized to create the appropriate combination of receptor complex scent components. Using vector representations of the olfactory receptor activation profiles for a set of receptor complex scent components, one can create linear combinations of such receptor complex scent components in order to represent a particular scent. For the example given above, such a vector representation would look like (1, 0, 0, 0, 1, 0) for the first receptor complex scent component and (0, 1, 1, 1, 0, 1) for the second receptor

complex scent component, while the vector representation of the scent to be re-created is (1, 1, 1, 1, 1, 1). If  $x_1$  and  $x_2$  are the relative proportions of the first receptor complex scent component and the second receptor complex scent component, respectively, to be combined to re-create the scent, then the problem can be represented as a series of linear equations:

$$1x_1 + 0x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

$$1x_1 + 0x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

and the solutions for  $x_1$  and  $x_2$  are  $x_1 = 1$ ,  $x_2 = 1$ . Solutions to systems of linear equations have been thoroughly studied and many algorithms are available for implementation on computers, including algorithms which evaluate the accuracy of an approximate solution when an exact solution cannot be determined. (See, e.g., Dettman, J.W., *Introduction to Linear Algebra and Differential Equations*, Dover Pubs., 1986; Press W.H. et al., *Numerical Recipes in C: The Art of Scientific Computing*, 2nd ed., Cambridge University Press, 1993; Vetterling (ed.) *Numerical Recipes in C: The Art of Scientific Computing/Disk V 2.02*, Cambridge University Press, 1997.) These methods can also be used to determine whether a set of receptor complex scent components is suitable for re-creating a given scent. For example, if the scent to be recreated is represented by the vector (1, 1, 1, 1, 1, 2), there will be no solution to the resulting system of linear equations using the two receptor complex scent components in the illustration above. In this instance, one or more additional receptor scent components will need to be identified in order to be able to re-create the scent in terms of the receptor primary scent components. Alternatively, the scent represented by (1, 1, 1, 1, 1, 1) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2). Integers are used in this example for clarity, but the vectors can contain any real number representing a measured intensity; for example, (1.1, 0.997, 1.08, 1.2, 0.88888..., 2.00001) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2).

It will be readily appreciated that the choice of a complete set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating all scents) versus a partial set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating, exactly or approximately, a subset of scents) depends on the application for which scent re-creation is desired.

A special category of receptor scent components are chemicals which bind to a receptor without activating it. If these non-activating chemicals prevent chemicals which do activate the receptors from binding, the non-activating chemicals act to "turn off" those receptors. These non-activating chemicals, or receptor binding antagonists, are particularly useful in editing scents, as they can be added to a scent to attenuate or eliminate particular aspects of the scent. In the vector example above, if a particular receptor antagonist blocks OR2, OR3, and OR4, but not OR1, OR5 or OR6, then it can be represented in vector format as (0, -1, -1, -1, 0, 0). In the reproduction of (1, 1, 1, 1, 1, 2) from the vectors (1, 0, 0, 0, 1, 0) and (0, 1, 1, 1, 0, 1), the following combination can be used:

$1 \times (1, 0, 0, 0, 1, 0) + 2 \times (0, 1, 1, 1, 0, 1) + 1 \times (0, -1, -1, -1, 0, 0)$  to yield the vector (1, 1, 1, 1, 1, 2). In some instances, enough of a particular receptor binding antagonist is used to eliminate any possibility of activation by a receptor scent component, in which case the vector entry for the receptor(s) which are blocked by that antagonist contains 0 in the vector position corresponding to that receptor(s).

Perceptive primary scents are defined as scents that give a single scent perception, for example, the scent "lemon" as perceived by a human. A perceptive primary scent can be composed of one or more receptor primary scent components, one or more receptor complex scent components, or a mixture of one or more receptor primary scent components and one or more receptor complex scent components. Since perceptive primary scents are to some extent subjective, identification of perceptive primary scents can be performed by using a panel of subjects who evaluate and describe scents. A perceptive complex scent is made up of more than one perceptive primary scent. The boundaries between a perceptive primary scent and a perceptive complex scent are also to some extent subjective; for example, one person may describe a scent as "pizza," while another person may describe the same scent as "sausage, cheese and tomato sauce." That is, one person may perceive a scent as a perceptive primary scent for "pizza," while another person may perceive the same scent as a perceptive complex scent made up of several individual perceptive primary scents. In order to standardize perceptive scents, a panel of five or more, preferably ten or more, more preferably fifty or



more, still more preferably one hundred or more, people can be surveyed to label various perceptive scents. When a plurality, preferably a majority, more preferably 66 2/3 % or greater, still more preferably 95 % or greater, even more preferably 99% or greater, of the panel identifies a scent as the same scent (e.g., of a panel of 100 people, 95 describe a scent as  
5 "pizza," while the other 5 describe the scent otherwise), the scent can be labeled as a perceptive scent (the perceptive scent can be primary or complex, depending on whether the panel identifies it as a single scent or a mixture of scents).

In fields where existing classification schemes already exist, the perceptive primary and complex scents can be indexed according to those schemes. For example, the SFP (Société  
10 Française des Parfumeurs) has drawn up a classification system based on 5 main groups, subdivided into classes. Such a classification can be used for selecting perceptive primary scents and used as guides for combining the scents.

#### Selecting Chemicals for Scent Re-creation

15 A scent which has been represented as a set of basis vectors in olfactory space can in principle be re-created simply by mixing the receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components needed to interact the olfactory receptors in the same pattern as the original scent. Such an approach requires 1) a method to generate a representation of the original scent in olfactory space, and 2) suitable  
20 receptor primary scent component chemicals which can be mixed in the appropriate manner.

Identification of receptor scent components can be performed by various methods. One such method assays the interaction of candidate components with each olfactory receptor. The receptors can be expressed *in vitro* and assays can be set up to monitor the interaction of various candidate components with each individual receptor. Chemicals which interact with  
25 one and only one olfactory receptor are receptor primary scent components, while chemicals which interact with more than one olfactory receptor are receptor complex scent components (and can possibly be receptor quasi-primary scent components, depending on the interaction profile it displays with the olfactory receptors). Such an approach can use methods known in the art, for example those of Breer *et al.*, Ann. N. Y. Acad. Sci. (1998) 855:175-81 or Malnic *et al.*,  
30 *Cell* (1999) 96(5):713-23. Breer *et al.* expressed olfactory receptors in Sf9 cells and evaluated the second-messenger response to various odorants. Malnic *et al.* isolated olfactory neurons from mice and utilized calcium imaging to study the response of the neurons to different odorants, while using RT-PCR to determine which olfactory receptor was expressed

in the neuron under study. U.S. Patent No. 5,798,275 describes a method for evaluating interaction of compounds with members of a reference panel of proteins. WO 98/50081 discloses methods for detecting particular odorant ligand specificity for particular odorant receptors in nasal epithelium tissue of mammals such as rats and mice.

5

Selection of Receptor Primary Scents by in silico Methods

An alternative method utilizes *in silico* screening techniques--that is, computer simulation methods--for selecting candidate components. Protein-ligand screening can be used to select compounds which bind to particular receptors in order to identify receptor primary  
10 scent components. Examples of such programs are DOCK, AutoDock, GOLD, FlexX, LUDI, GROWMOL, and HOOK. (See Wang, J., Kollman, P.A., Kuntz I.D., "Flexible ligand docking: a multistep strategy approach," *Proteins* 36(1):1-19 (1999) and references therein.) These programs function by taking a protein structure and either matching compounds of known structure to the protein structure to determine the protein-ligand interaction, or by  
15 "growing" a molecule in the active site or binding site of a protein to determine what molecule will best interact with the protein.

Olfactory receptor proteins are membrane proteins, and experimental determination of the three-dimensional structures of membrane proteins has lagged the corresponding structural determination of water-soluble proteins for various reasons. However, alternative methods for  
20 constructing the three-dimensional structures of proteins are available. The primary (amino acid) sequences of many olfactory receptors are known. This information can be used to model a three-dimensional structure of a receptor protein using various algorithms and computer programs known in the art. The resulting model structure can then be used as the basis for evaluating interaction of candidate components with the receptor.

25 Alternatively, given known chemical structures which give rise to a particular odor, analysis of the structures can indicate the particular portion of the chemical structure which is responsible for the odor. This is analogous to "pharmacore analysis" used in medicinal chemistry to determine the important portion of drugs.

Methods for developing compounds which bind to receptors and other proteins of  
30 known structure, and determining interactions between ligands and receptors, are described in various references. The DOCK program evaluates the fit of a ligand into a protein molecule of known structure (see Gschwend, D.A., Good, A.C. and Kuntz, I.D., "Molecular Docking Towards Drug Discovery", *J. Mol. Recognition* 9, 175-86 (1996); Kuntz, I.D., Meng, E.C., and

B.K. Shoichet, "Structure-Based Strategies For Drug Design and Discovery", *Acc. Chem. Res.* 27, 117-123 (1994); and Kuntz, I.D., "Structure-based strategies for drug design and discovery", *Science* 257, 1078-1082 (1992); see also

<http://www.cmpharm.ucsf.edu/kuntz/dock.html>). Using a known (or modeled) structure of an olfactory receptor, DOCK can be used to screen for compounds which bind to the receptor.

The program AMBER (see Cornell, WD, Cieplak P, Bayly CI, Gould IR, Merz KM Jr, Ferguson DM, Spellmeyer DC, Fox T, Caldwell JW and Kollman PA. "A second generation force field for the simulation of proteins and nucleic acids," *Journal of the American Chemical Society* 117, 5179-5197 (1995); Computer Simulation of Biomolecular Systems, A. Wilkinson,

P. Weiner, W. Van Gunsteren, eds. Volume 3, p. 83-96, P. Kollman, R. Dixon, W. Cornell, T. Fox, C. Chipot and A. Pohorille; Bayly CI, Cieplak P, Cornell WD and Kollman PA. "A well-behaved electrostatic potential based method using charge restraints for deriving atomic charges - the RESP model," *Journal of Physical Chemistry* 97(40), 10269-10280 (1993);

Cornell WD, Cieplak P, Bayly CI and Kollman PA. "Application of RESP charges to calculate conformational energies, hydrogen bond energies, and free energies of solvation," *Journal of the American Chemical Society* 115(21), 9620-9631 (1993); see also

<http://www.amber.ucsf.edu/amber/amber.html>) can be used to calculate more precise interaction energies between candidate ligands. Other examples of such methods are described in, for example, U.S. Patent No. 5,866,343, directed to determining the energetically favorable binding site between two molecules; U.S. Patent No. 5,854,992, a system and method for structure-based drug design which takes into account binding free energy as it "grows" candidate molecules into a receptor binding site; and U.S. Patent No. 5,495,423, which describes a method for ligand design (principally applicable to peptidic ligands).

The foregoing methods typically depend on a known three-dimensional structure for the receptor. When such a structure cannot or has not been determined experimentally, a structure can be modeled using computer algorithms. Blundell TL, Sibanda BL, Sternberg MJ, Thornton JM, "Knowledge-based prediction of protein structures and the design of novel molecules," *Nature* 326(6111):347-52 (1987); Shortle D, "Structure prediction: The state of the art," *Curr Biol* 9(6):R205-9 (1999), Morea V, Leplae R, Tramontano A, "Protein structure prediction and design," *Biotechnol Annu Rev* 4:177-214 (1998) and Onuchic JN, Luthey-Schulten Z, Wolynes PG, "Theory of protein folding: the energy landscape perspective," *Annu Rev Phys Chem* 48:545-600 (1997) address various methods of predicting protein structure from sequence data.

Various implementations for predicting protein structure from amino acid sequences are discussed in U.S. Patent Nos. 5,878,373 and 5,884,230.

If the structure, or even the identity, of the targeted receptor cannot be determined, alternative computational techniques can be used to generate information regarding possible  
5 ligands which will interact with the receptor. Quantitative structure-activity relationships (QSAR; see Green, S.M. and Marshall, G.R., "3-D QSAR: A current perspective," *Trends Pharmacol Sci* 16:285 (1995); and 3D QSAR in Drug Design: Theory, Methods and Applications, Kubinyi, H. Ed.; Escom, Leiden.), including QSAR refinements such as comparative molecular field analysis (ComFA) (Cramer, R. D. et al. "Comparative Molecular  
10 Field Analysis ComFA 1. Effect Of Shape On Binding Of Steroids To Carrier Proteins," *J. Am. Chem. Soc.* 110: 5959 (1988)); and pharmacophore mapping (Martin YC, Bures, MG, Danaher EA, DeLazzer J, Lico I, Pavlik PA, "A fast new approach to pharmacophore mapping and its application to dopaminergic and benzodiazepine agonists," *J Comput Aided Mol Des* 7(1):83-102 (1993)) have been used to design pharmacophores that can interact with the receptor. U.S.  
15 Patent No. 5,699,268 provides a method for producing computer-simulated receptors which functionally mimic biological receptors; the simulated receptors are essentially abstractions of structurally useful information from compounds which are known to interact with a receptor. U.S. Patent No. 5,901,069 describes a method of automatically refining a set of chemicals using structure/activity data. U.S. Patent No. 5,862,514 describes a method of simulating  
20 synthesis of compounds of desired biological activity and evaluating their activity via further simulations.

Application of structure-function relationships to classification of odors has been described by Chastrette M., Rallet E. "Structure-minty odour relationships: Suggestion of an interaction pattern," *Flavour and Fragrance Journal*, 13(1):5-18 (1998); Chastrette M., De  
25 Saint Laumer J.Y., Peyraud J.F., "Adapting the structure of a neural network to extract chemical information. Application to structure-odour relationships," *SAR QSAR Environ Res* 1 (2-3):221-231 (1993), Chastrette M., "Trends in structure-odor relationships," *SAR QSAR Environ Res* 6(3-4):215-254 (1997) and Jain et al., "A shape-based machine learning tool for drug design," *J Comput Aided Mol Des* 8(6):635-652 (1994). These methods can be useful in  
30 determining the "chemical distance" between odors. For example, isoamyl acetate is typically experienced as a banana-like odor, while octyl acetate is typically experienced as an orange-like odor, which gives a measure of how the chain length of the alkoxy portion of the ester influences perception.

Olfactory Receptors and Libraries of Olfactory Receptors

The olfactory receptors of the invention can be used to analyze and describe the interaction of scent odorant molecules with each receptor. This can be done individually, receptor-by-receptor and odorant molecule by odorant molecule. However, a combinatorial approach provides a much more powerful method of analyzing and describing the interaction of scent odorant molecules with olfactory receptors.

In one embodiment, the invention comprises libraries of olfactory receptors. These libraries are used to screen compositions for interaction with receptors. A composition can be a single compound (essentially a pure chemical), or a mixture of two or more compounds or chemicals. The compositions can be presented to the library in vapor form, or in solutions, typically aqueous solutions.

The method for determining the binding pattern of a composition with olfactory receptors comprises the steps of: exposing the composition to an olfactory receptor library; and determining whether the composition binds to each olfactory receptor of the library, thereby determining the overall binding pattern of the composition. While it is desirable to determine whether the composition binds to each of the olfactory receptors, in certain cases, determining the binding pattern to a subset of the receptors is suitable. Such a situation can arise if the complete pattern is not needed, or if the experiment cannot determine binding to a receptor for a particular reason. (Determining the binding to a subset is equivalent to reducing the olfactory receptor library to that subset of receptors.)

Typically, the libraries are prepared as arrays, where the position of each olfactory receptor is known on the array. The arrays can take the form of multiwell plates, solid substrates such as chips or wafers, or any other form allowing identification of the receptor location. The arrays can be prepared in order to simply assess binding, or can be prepared in order to assess degree of activation as described above, using, for example, the technique of Malnic *et al.*, *Cell* 1999 96, 713-723. Alternatively, an *in silico* array of structures can be prepared, using the known primary structure of the receptors and the modeling techniques described above.

The libraries contain at least two olfactory receptors. In increasing order of preference, the libraries contain at least 5, 10, 20, 30, 40, 50, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1500, 1600, 1800, or 2000 olfactory receptors. The

receptors are presented as ordered arrays. For example, a 96-well plate can contain 96 receptor preparations. Upon exposure to a composition, the plate can be scanned, and the response of each receptor in each well can be evaluated. This leads to a 96-element vector description of the composition in terms of those 96 olfactory receptors.

5           In one embodiment, binding to the olfactory receptors is assessed. In another embodiment, the approximate binding constant of the composition to the olfactory receptors is determined. In yet another embodiment, the degree of activation of the olfactory receptor by the composition is determined. For receptor antagonists, binding will occur, but no activation will occur; the invention embraces the identification of such  
10 antagonists.

          The compositions for use are varied. A set of all volatile compounds can be used. A standard set of perfumes or odorants can be used. A set of commercially used scents can be used. Sets of compounds particularly useful in the invention are disclosed in co-pending United States Patent Application Serial No. 09/620,753. However, it must be emphasized  
15 that the invention is not limited to any one set or classification of compounds.

          Preferred subsets of olfactory receptor polynucleotide sequences include:

SEQ ID NOS: 163, 331, 414, 425, 672, 762, 919, and 1027;

SEQ ID NOS: 809 and 1067;

SEQ ID NO: 744;

20           SEQ ID NOS: 207, 336, 441, and 615;

SEQ ID NOS: 157, 168, 197, 221, 250, 334, 340, 412, 413, 459, 491, 618, 690,  
694, 759, 760, 761, 767, 819, 860, 872, 873, 917, 936, 939, 940, 947, 952, 958, 959, 1023,  
1034, 1038, 1043, and 1044;

SEQ ID NOS: 783, 785, 882, 888, 922, and 925;

25           SEQ ID NOS: 707, 748, 752, 755, 756, 790, and 997;

SEQ ID NOS: 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075,  
1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, and 1084;

SEQ ID NOS: 163, 239, 331, 335, 368, 381, 385, 414, 425, 514, 572, 596, 603,  
628, 638, 642, 672, 674, 689, 744, 762, 809, 835, 885, 896, 919, 920, 938, 948, 972, 999,  
30 1007, 1014, and 1027;

SEQ ID NOS: 164, 173, 176, 180, 182, 184, 185, 188, 190, 194, 207, 210, 213, 214,  
215, 217, 219, 220, 223, 226, 227, 229, 230, 234, 235, 240, 249, 255, 265, 270, 273, 274,

276, 277, 279, 281, 289, 291, 293, 294, 298, 302, 307, 311, 318, 319, 321, 330, 336, 339,  
341, 342, 343, 348, 351, 356, 359, 361, 365, 366, 367, 368, 370, 372, 373, 374, 375, 376,  
378, 379, 380, 382, 383, 384, 385, 388, 391, 392, 393, 398, 400, 401, 403, 408, 420, 423,  
427, 428, 431, 434, 435, 438, 439, 440, 441, 447, 448, 450, 455, 458, 464, 465, 468, 471,  
5 473, 474, 475, 478, 479, 481, 482, 484, 485, 492, 494, 499, 502, 508, 511, 512, 513, 515,  
526, 532, 534, 541, 543, 545, 546, 550, 552, 553, 557, 558, 560, 563, 564, 568, 572, 576,  
582, 583, 584, 585, 586, 588, 599, 600, 605, 606, 607, 608, 609, 610, 615, 620, 621, 631,  
632, 636, 638, 640, 642, 645, 648, 650, 651, 652, 654, 656, 657, 661, 662, 664, 668, 679,  
680, 686, 687, 689, 691, 696, 699, 700, 702, 706, 713, 720, 721, 723, 729, 734, 738, 745,  
10 768, 772, 773, 775, 791, 798, 799, 823, 857, 898, 900, 901, 903, 914, 931, 933, 937, 941,  
945, 948, 956, 965, 969, 983, 992, 993, 994, 999, 1003, 1005, 1009, 1010, 1011, 1019,  
1028, 1035, 1037, 1052, 1061, 1062, and 1063

SEQ ID NOS: 157, 161, 163, 168, 197, 200, 205, 218, 221, 242, 250, 331, 334,  
340, 412, 413, 414, 419, 425, 452, 453, 454, 456, 459, 462, 491, 591, 618, 622, 663, 665,  
15 667, 670, 672, 690, 694, 695, 709, 759, 760, 761, 762, 767, 819, 820, 822, 826, 832, 846,  
847, 860, 872, 873, 877, 881, 887, 908, 911, 913, 917, 919, 921, 936, 939, 940, 942, 944,  
947, 951, 952, 955, 958, 959, 960, 964, 975, 977, 979, 986, 1023, 1027, 1034, 1038, 1043,  
1044, 1049, and 1051;

SEQ ID NOS: 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 164, 165, 166,  
20 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184,  
185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,  
203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220,  
221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238,  
240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257,  
25 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275,  
276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293,  
294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311,  
312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329,  
330, 332, 333, 334, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349,  
30 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367,  
369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 382, 383, 384, 386, 387, 388,  
389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406,

407, 408, 409, 410, 411, 412, 413, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 426,  
427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444,  
445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462,  
463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480,  
5 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498,  
499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 515, 516, 517,  
518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535,  
536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553,  
554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571,  
10 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590,  
591, 592, 593, 594, 595, 597, 598, 599, 600, 601, 602, 604, 605, 606, 607, 608, 609, 610,  
611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 629,  
630, 631, 632, 633, 634, 635, 636, 637, 639, 640, 641, 643, 644, 645, 646, 647, 648, 649,  
650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667,  
15 668, 669, 670, 671, 673, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687,  
688, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706,  
707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724,  
725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742,  
743, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761,  
20 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780,  
781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798,  
799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 810, 811, 812, 813, 814, 815, 816, 817,  
818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 836,  
837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854,  
25 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872,  
873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 886, 887, 888, 889, 890, 891,  
892, 893, 894, 895, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910,  
911, 912, 913, 914, 915, 916, 917, 918, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930,  
931, 932, 933, 934, 935, 936, 937, 939, 940, 941, 942, 943, 944, 945, 946, 947, 949, 950,  
30 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968,  
969, 970, 971, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987,  
988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 1000, 1001, 1002, 1003, 1004, 1005,



1006, 1008, 1009, 1010, 1011, 1012, 1013, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, and 1064;

5 and any and all combinations of the foregoing sets.

The polypeptide translation products of those polynucleotide sequences form sets of preferred olfactory receptor polypeptides, as well as any and all combinations of those polypeptide sets. The preferred sets of polypeptide translation products, and any and all combinations thereof, are also preferred sets for use as libraries of olfactory receptors for  
10 scent analysis.

#### Scent Fingerprinting

It will be appreciated that in many instances, analysis of a scent (whether in terms of  
15 receptor primary scent components, receptor quasi-primary scent components, receptor complex scent components, or other scent representations) is of great utility in and of itself, in addition to the utility of that analysis in scent re-creation. Thus, another embodiment of the invention encompasses "scent fingerprinting," which comprises analysis of a scent profile when re-creation of that scent may not be necessary or desirable. The distinction between scent  
20 profiling, as defined above, and scent fingerprinting, as defined here, is that scent profiling is a representation of a scent relative to a mammalian olfactory system in such a manner as to provide useful information about the interaction of the scent with that olfactory system, such as sufficient information to enable re-creation of the scent from receptor primary scent  
25 components. In contrast, scent fingerprinting can, but does not necessarily, provide such information.

Various applications and examples of scent fingerprinting can include, but are not limited to, the following illustrative situations. Natural gas is widely used as a heating and fuel supply, but is in itself odorless. Utility companies routinely add small amounts of odorants such as mercaptans to allow detection of natural gas leaks in households. Should a leak occur  
30 at an unattended site, however, potentially dangerous quantities of natural gas can accumulate. In such areas, a device which can recognize odorants would be useful.

Another use of scent fingerprinting is quality control of a manufacturing process. Many food items, such as freshly-baked bread and pastries, sauces, and cheeses, have distinct

odors. A manufacturer can record a scent fingerprint for a given food item, e.g. spaghetti sauce for packaging in jars. The quality of the product can then be monitored at various stages in manufacture and storage, and deviations from the established scent fingerprint can be used to alert the manufacturer to problems in manufacture or storage. Quality control scent fingerprints  
5 are not limited to food items, but can be used in any circumstance where a volatile component of an item of manufacture can be used as a quality control indicator, e.g., perfume, deodorants, solvent mixtures, etc.

While scent fingerprints need not be meaningful in terms of a mammalian olfactory system, it will be readily appreciated that a scent profile, which does represent a scent in a  
10 manner relevant to an olfactory system, is a special type of scent fingerprint. Additionally, the response of a device which yields a scent fingerprint of an odor (such as the "artificial nose" described in U.S. Pat. Nos. 5,571,401, 5,698,089, 5,788,833, 5,891,398 and 5,911,872) can be calibrated against the response of a mammalian olfactory system in order to transform the scent fingerprint generated by the device into a true scent profile which can be utilized to re-create an  
15 odor using receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components. The invention encompasses such data transformations.

#### Scent Editing

Representation of a scent as a scent profile provides the capability of editing the scent.  
20 A scent profile which represents a scent in terms of perceptive primary scent components is the most straightforward representation to edit. An example is the perceptive complex primary scent of "burned pizza" comprised of perceptive primary scent components of sausage, cheese, tomato sauce, and burned dough. In order to edit the scent to provide a more pleasant re-creation, the perceptive primary scent component of burned dough would simply be eliminated.

25 Other scent profiles can be edited using a knowledge of the perception of a particular components. Using our six-receptor example, suppose that the (1, 0, 0, 0, 1, 0) receptor complex scent component is known to provide an unpleasant aspect of the scent, while the (0, 1, 1, 1, 0, 1) component is known to provide the pleasant aspect of the scent. The first complex scent component can be omitted from the edited scent profile, leaving (0, 1, 1, 1, 0, 1)  
30 as the edited scent profile. (This would also alter the index values for scent re-creation, from 1 and 1, to 0 and 1.) More complex editing situations can be manipulated using computer algorithms as discussed above.

Individual scent components can be omitted, added, weakened, or intensified, and different scent components can be adjusted in different manners or degrees, depending on the desired result. The editing can be done interactively, with each edited scent emitted by the emitter module for evaluation by the user, or can be done automatically, with  
 5 removal/weakening or addition/intensifying of particular components specified in advance, on either an absolute scale or relative to other components.

The following examples are presented to illustrate, but not to limit, the invention.

### EXAMPLES

#### 10 **Example 1: Isolation of human olfactory receptor cDNAs**

Total RNA was extracted from human olfactory epithelium and polyA<sup>+</sup> RNA was obtained by oligo-dT selection. This RNA served as template for cDNA synthesis using reagents from the SMART cDNA Library construction kit (Clontech K1051-1; Palo Alto, CA). The Superscript II<sup>TM</sup> reverse transcriptase (Life Technologies, Gaithersburg, MD)  
 15 was used for first-strand synthesis.

Double-stranded cDNA was passed through a Chroma-Spin<sup>+</sup> STE-100 column (Clontech) to remove unreacted primers and cDNA fragments shorter than 100 nucleotides. The olfactory epithelial cDNA population was then subjected to amplification using primers homologous to conserved regions in GPCRs. The first primer set was homologous  
 20 to transmembrane segment 2 (TM2) and the second set was homologous to TM 7.5. The TM2 primer set contained 32 oligonucleotides, representing all possible nucleotide sequences capable of encoding the TM2 amino acid sequence motif P-M-Y-F/L-F/Y-F/L, and designed to be non-degenerate at their 3' ends. Sequences of the TM2 primers are as follows:

25

	CCN ATG TAY TTN CTC CTA	SEQ ID NO: 74
	CCN ATG TAY TTN CTC CTC	SEQ ID NO: 75
	CCN ATG TAY TTN CTC CTG	SEQ ID NO: 76
	CCN ATG TAY TTN CTC CTT	SEQ ID NO: 77
30	CCN ATG TAY TTN CTC TTA	SEQ ID NO: 78
	CCN ATG TAY TTN CTC TTC	SEQ ID NO: 79
	CCN ATG TAY TTN CTC TTG	SEQ ID NO: 80
	CCN ATG TAY TTN CTC TTT	SEQ ID NO: 81
	CCN ATG TAY TTN CTT CTA	SEQ ID NO: 82
35	CCN ATG TAY TTN CTT CTC	SEQ ID NO: 83
	CCN ATG TAY TTN CTT CTG	SEQ ID NO: 84

	CCN ATG TAY TTN CTT CTT	SEQ ID NO: 85
	CCN ATG TAY TTN CTT TTA	SEQ ID NO: 86
	CCN ATG TAY TTN CTT TTC	SEQ ID NO: 87
	CCN ATG TAY TTN CTT TTG	SEQ ID NO: 88
5	CCN ATG TAY TTN CTT TTT	SEQ ID NO: 89
	CCN ATG TAY TTN TTC CTA	SEQ ID NO: 90
	CCN ATG TAY TTN TTC CTC	SEQ ID NO: 91
	CCN ATG TAY TTN TTC CTG	SEQ ID NO: 92
	CCN ATG TAY TTN TTC CTT	SEQ ID NO: 93
10	CCN ATG TAY TTN TTC TTA	SEQ ID NO: 94
	CCN ATG TAY TTN TTC TTC	SEQ ID NO: 95
	CCN ATG TAY TTN TTC TTG	SEQ ID NO: 96
	CCN ATG TAY TTN TTC TTT	SEQ ID NO: 97
	CCN ATG TAY TTN TTT CTA	SEQ ID NO: 98
15	CCN ATG TAY TTN TTT CTC	SEQ ID NO: 99
	CCN ATG TAY TTN TTT CTG	SEQ ID NO: 100
	CCN ATG TAY TTN TTT CTT	SEQ ID NO: 101
	CCN ATG TAY TTN TTT TTA	SEQ ID NO: 102
	CCN ATG TAY TTN TTT TTC	SEQ ID NO: 103
20	CCN ATG TAY TTN TTT TTG	SEQ ID NO: 104
	CCN ATG TAY TTN TTT TTT	SEQ ID NO: 105

The TM7.5 primer set was designed to contain the reverse complement of all sequences capable of encoding the TM7.5 amino acid sequence motif P-F/L/I/V-I/V-F/Y-

25 S/T-L. The sequences of the TM7.5 primers are as follows:

	YYTNGTNYTNRYNCYGATANATNATNGGRTT	SEQ ID NO: 106
	YTRTTNCKNAGNWRTANATRAANGGRTT	SEQ ID NO: 107
	TCYTTRTTNCKNAGNGWRTANAYNASNGGRTT	SEQ ID NO: 108
30	TCNTSRTTNCKNARNSARTANATNATNGGRTT	SEQ ID NO: 109
	RTTNCKNARNSWRTANATRAANGGRTT	SEQ ID NO: 110

Reagents and enzymes for amplification were from the Advantage cDNA amplification kit (Clontech). A primary amplification reaction was constructed as follows:

35	5 µl olfactory epithelial cDNA (10-20 µg/ml)
	5 µl 10X PCR reaction buffer (Clontech)
	1 µl TM2 primer set (10 µM)
	1 µl TM7.5 primer set (10 µM)
	1 µl dNTP mix (10 mM each dATP, dCTP, dGTP, dTTP)
40	36 µl PCR-grade H <sub>2</sub> O
	1 µl Advantage polymerase mix (Clontech)

Amplification was conducted in a PE 480 thermal cycler, using 28 cycles of 95°C for 15 sec, 45°C for 45 sec and 72°C for 2 min. After cycling, the amplification mixture was treated for 1 hour at 37°C with 10 Units of BspEI and 10 Units of PstI restriction enzymes, to degrade non-specific amplification products.

5       The primary amplification products were size-fractionated by agarose gel electrophoresis, and amplification products having a length between 600 and 800 base pairs were selected for secondary amplification.

10       The secondary amplification reaction was conducted identically to the primary amplification reaction, except that the size-selected primary amplification product was used as template. Secondary amplification reactions containing products which generated a specific gel band of between 600 and 800 base pairs were extracted once with phenol/chloroform and once with chloroform, and nucleic acids were precipitated from the reactions by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and  
15       resuspended in 15 µl distilled water. After the precipitate dissolved, 3 µl loading dye was added, and the sample was subjected to electrophoresis on a 1.0% low-melting agarose gel containing ethidium bromide. Electrophoresis was conducted at 60V for approximately 40 min, with a 1 kb marker in adjoining lanes.

20       Following electrophoresis, the gel was illuminated with long-wavelength ultraviolet light, and the band was excised from the gel. The gel slice was placed in a 0.5 ml tube, and the tube was heated at 68°C for 15 min. The temperature of the tube was then equilibrated at 45°C. (This is conveniently accomplished in a thermal cycler.) AgarACE™ (Promega) was then added to the tubes, according to the manufacturer's instructions, and incubation at 45°C was continued for 15 min. As a general rule, 2 µl of enzyme per 50 µl of gel slice is  
25       adequate. Following AgarACE™ digestion, the digestion mixture was extracted with phenol/chloroform according to the manufacturer's instructions, and nucleic acids were precipitated by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and resuspended in 5 µl distilled water.

30       Gel-purified amplification products were cloned using the TOPO XL PCR Cloning Kit (Invitrogen) according to the manufacturer's instructions. After cloning, individual

colonies were selected at random for nucleotide sequence analysis of the inserts, using procedures for sequence determination that are well-known to those of skill in the art.

**Example 2: Use of olfactory receptor polypeptides for screening**

5        Components of a scent are identified by determining the interaction between one or more potential odorant molecules and one or more OR polypeptides. For example, if a known original scent involves binding to a particular set of ORs, any subsequent set of molecules which bind to that same set of ORs and stimulate or inhibit the response of the ORs to the same extent as the original scent is capable of re-creating that original scent. If  
10        each of the subsequent set of molecules interacts with one and only one OR, then the set of molecules is composed of receptor primary scent components. In similar fashion, scents which involve binding of multiple ORs can be recreated by identifying a molecule, or combination of molecules, which binds to that particular set of ORs.

      Binding of molecules to ORs is determined by a number of methods that are well-  
15        known in the art including, but not limited to, in vitro and in silico methods as described herein. Binding of molecules to ORs can also be determined or approximated by using quantitative structure-activity relationships as described herein.

**Example 3: Identification of agonists and antagonists of olfactory receptors**

20        Interaction of an odorant with a particular OR embedded in the membrane of an olfactory neuron will activate a signaling cascade within the neuron, ultimately resulting in the perception of a particular smell. A molecule, produced for example by combinatorial chemistry, which activates a similar or identical signaling cascade, will induce the perception of the same smell. Such a molecule would be considered a OR agonist. An OR  
25        agonist, once identified, can be used as a probe to identify additional agonists, as well as antagonists, of that particular OR.

      Assays for the activation and the end product(s) of signaling cascades are known in the art. For example, direct  $\text{Ca}^{++}$  imaging can be employed, using either dye -labeled  $\text{Ca}^{++}$  or dyes that are sensitive to  $\text{Ca}^{++}$  concentration. Such dyes, and techniques for their use,  
30        are available from, for example, Molecular Dynamics (Sunnyvale, CA) and Molecular Probes (Eugene, OR).

Because ORs are transmembrane proteins, identification of agonists and/or antagonists for a particular OR require that the OR is present either in a living cell or in a membrane preparation.

In one embodiment of a method for the determination of OR agonists or  
5 antagonists, a known OR agonist is labeled *in situ*, or is resynthesized with an attached label, and is bound to an OR. The effect of various test molecules on the binding of the labeled OR agonist is then determined. Labeling of an OR agonist is accomplished by any of a number of methods that are known to those of skill in the art including, but not limited to, various fluorescent labels (for example, chemical fluorochromes or green fluorescent  
10 protein). Binding of the OR agonist is measured by any of a number of competitive binding assays, as are known in the art. A test molecule that displaces the agonist from the OR (*i.e.*, reduces the binding of the agonist) is identified as a candidate agonist or antagonist of the particular OR. In a subsequent experiment, the candidate molecule is bound to the OR, and the effect on the signaling cascade induced by the original agonist is  
15 determined. A similar of higher level of activation is indicative of an agonist; while a reduced level of activation of the signaling cascade reflects the action of an antagonist.

In additional embodiments of the displacement assay, an unlabeled agonist is used, and its degree of binding is determined by mass spectrometry. *See*, for example, U.S. Patent No. 5,894,063; U.S. Patent No. 5,719,060; and Wei *et al.* (1999) *Nature* 399:243-  
20 246.

In another embodiment, fluorescent microparticles ("beads"), which can be separated by flow cytometry, are used to identify OR agonists and antagonists. Such beads are available, for example, from Luminex (Austin, TX). Multiple different ORs are attached to the beads, wherein each distinct color of bead is associated with a particular  
25 OR. The collection of beads, containing different ORs, is exposed to a test molecule or a collection of test molecules, such as can be synthesized by combinatorial chemistry, and binding of the test molecule(s) is determined, for example, by use of a labeled ligand of the test molecule(s). The beads are sorted according to their color by flow cytometry. Correlation of test molecule binding with bead color allows the determination of test  
30 molecules capable of binding to the OR. Agonist or antagonist function of an OR binding molecule is determined by methods described *supra*.

**Example 4: Summary of search parameters for homology searches**

Step 1: (masking) rempolyatmask raw sequence on -NONE- [?] with remAT\_moderate (15) . Continue to step 2.

5 Step 2: (masking) mask masked sequence from step 1 on RepBase [N] with mask\_moderate (85) . Continue to step 3.

Step 3: (masking) mask masked sequence from step 2 on VecBase [N] with mask\_moderate (85) . Continue to step 4.

Step 4: blastn masked sequence from step 3 on NR-Nuc [N] with blastn\_10\_hits (V=10 B=10) . If the P/Z score is  $> 1.0E-50$ , or no hits are found go to step 5. Otherwise, stop.

10 Step 5: blastx masked sequence from step 3 on NR-Pro [P] with blastx\_10\_hits (V=10 B=10) . If the P/Z score is  $> 1.0E-50$ , or no hits are found go to step 6. Otherwise, stop.

Step 6: blastn masked sequence from step 3 on GB\_CurAwareness-Nuc [N] with blastn\_10\_hits (V=10 B=10) . If the P/Z score is  $> 1.0E-50$ , or no hits are found go to step 7. Otherwise, stop.

15 Step 7: blastx masked sequence from step 3 on GB\_CurAwareness-Pro [P] with blastx\_10\_hits (V=10 B=10) . If the P/Z score is  $> 1.0E-50$ , or no hits are found go to step 8. Otherwise, stop.

Step 8: tblastx masked sequence from step 3 on NR-Nuc [N] with tblastx\_10\_hits (V=10 B=10) . If the P/Z score is  $> 1.0E-50$ , or no hits are found go to step 9. Otherwise, stop.

20 Step 9: blastn masked sequence from step 3 on EST [N] with blastn\_10\_hits (V=10 B=10) . If the P/Z score is  $> 1.0E-50$ , or no hits are found go to step 10. Otherwise, stop.

Step 10: blastn masked sequence from step 3 on STS [N] with blastn\_10\_hits (V=10 B=10) . Stop.

25



**Example 5: Summary of search results**

Step	Program	Databases	Score	Sequences By Best Hit's				No Hits	Run	Not Finished	Not Run	
			Score									
1	rempolyat mask	NONE-[P]	P/Z/ E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0	0
2	mask	RepBase[N]	P/Z/ E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0	0
3	mask	VecBase[N]	P/Z/ E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0	0
4	blastn	NR-Nuc[N]	P/Z/ E	46	< 1.0E-20 <=	28		0	74	0		0
5	blastx	NR-Pro[P]	P/Z/ E	16	< 1.0E-20 <=	34		0	50	0		24
6	blastn	GB_CurAwareness-Nuc[N]	P/Z/ E	17	< 1.0E-20 <=	31		0	48	0		26
7	blastx	GB_CurAwareness-Pro[P]	P/Z/ E	13	< 1.0E-20 <=	28		2	43	0		31
8	tblastx	NR-Nuc[N]	P/Z/ E	14	< 1.0E-20 <=	29		0	43	0		31
9	blastn	EST[N]	P/Z/ E	10	< 1.0E-20 <=	33		0	43	0		31
10	blastn	STS[N]	P/Z/ E	5	< 1.0E-20 <=	33		0	38			

5

**Example 6. Datamining and analysis from GenBank**

*Datamining.* A datamining pipeline was built to detect all available OR-like sequences in the public databases and to update the results as new database versions are released. tblastn (Altschul et al., 1997) was used to compare amino acid query sequences to the non-redundant version of GenBank (partitions nt, htg and est\_human, all updated to August 6th, 2000), with a non-stringent expectation value cutoff of 1e-4. The queries used included 96 curated OR sequences representing all known families (SEQ ID NO:2651 through SEQ ID NO:2747) and 249 additional HORDE entries (SEQ ID NO:2402 through SEQ ID NO:2650). In a second round 105 newly mined mouse genes (SEQ ID NO:2296 through SEQ ID NO:2401) and 344 newly mined human genes (SEQ ID NO:2009 through SEQ ID NO:2295) were used as additional queries (all datasets are available

electronically). All resulting database entries were catalogued by species and subdivided into four types: mRNA, EST, DNA and genomic, the latter including entries annotated with keyword HTGS\_PHASE1-3, or with length at least 10 kb. Low-pass genomic sampling sequences were ignored (keyword HTGS\_PHASE0). In addition, a set of 132 olfactory sequence tag (OST) sequences was used. All sequences used were split into contigs according to annotation or, where unavailable, according to runs of at least 50 Ns. All resulting contigs were analyzed for interspersed repeats using RepeatMasker (Smit and Green, 1997). Subcontigs were defined as segments between interspersed repeats, ignoring simple repeats and low-complexity regions.

10       *Localization of genomic clones.* The University of Santa Cruz (UCSC) Working Draft Sequence ("golden path", <http://genome.ucsc.edu>) presents a first tentative assembly of the finished and draft human genomic sequence based on the WUSTL clone map (<http://genome.wustl.edu/gsc>). The "golden path" data was used to assign a coordinate to each finished or unfinished genomic clone, in Mb from the p telomere. In parallel, the  
15       Unified DataBase (UDB) was used to assign similar Mb coordinates to the clones, based on their marker contents (Chalifa-Caspi et al., 1998). The two maps are largely colinear, and were integrated based on the coordinates of clones that could be localized in both. Clones for which no coordinate could be obtained by either method were assigned a chromosome according to UDB, by sequence similarity to another mapped clone, by annotation, or by e-  
20       PCR (Schuler, 1997).

*Detection of OR sequences.* Each subcontig was compared using FASTY (Pearson et al., 1997) to a curated set of OR protein sequences from several species, yielding a conceptual translation product. The possibility of a pseudogene being disrupted by the insertion of interspersed repeats was taken into account, with the two or more resulting  
25       parts being therefore located in different subcontigs. Such compatible candidate sequences were automatically joined into a combined reconstructed pseudogene. Whenever possible, all resulting sequences were trimmed or extended to use a suitable ATG codon for initiation and to end at a stop codon, but avoiding those stop codons that yield products shorter than 275 amino acids. The sequences were finally split into OR or non-OR by comparing them  
30       to previously recognized OR sequences and to a non-redundant database of non-OR GPCRs which we extracted from Swiss-Prot. To be automatically classified as an OR, a

new sequence has to be at least 40% identical over at least 100 amino acids to another OR. A more stringent cutoff (50%) was required for shorter sequences.

*Definition of OR genes.* A given gene could be represented in more than one overlapping genomic clone. Such redundancy was removed by considering two sequences  
5 as representing the same gene, if they are in the same chromosome, located in clones less than 300 kb apart and at least 99% identical at the nucleotide level. An exception to this rule is when two genes coappear in the same clone, in which case they were considered to be distinct genes. Sequences localized to a chromosome but without a coordinate were only compared to other sequences within that chromosome, and finally those sequences  
10 lacking a chromosomal assignment were compared to the rest, applying only the criterion of sequence similarity. For each resulting gene with more than one constituent sequence, a consensus nucleotide sequence was created after multiple alignment by ClustalW (Higgins et al., 1996) using the fast comparison parameter. This was followed by conceptual translation and end trimming to suitable start and stop codons, as above. Genes with length  
15 at least 275 amino acids without frame disruptions (frameshifts, in-frame stop codons or disrupting interspersed repeats) were considered to be full-length and apparently intact. For partial sequences without frame disruptions no statement could be made on their apparent functionality, except when the partial sequences were observed in the genome as such, in which case they were considered to be pseudogenes. Finally, each OR gene was  
20 assigned a family and subfamily by amino acid sequence similarity to previously classified OR genes.

The references cited in this example are: Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D. J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25: 3389-402; Chalifa-Caspi, V., Prilusky, J. and Lancet, D. (1998) The Unified Database. Weizmann Institute of Science, Bioinformatics Unit and Genome Center (Rehovot, Israel). World Wide Web URL: [bioinformatics.weizmann.ac.il/udb](http://bioinformatics.weizmann.ac.il/udb); Higgins, D. G., Thompson, J. D. and Gibson, T. J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol* 266: 383-402; Pearson, W. R., Wood, T., Zhang, Z. and Miller, W. (1997)  
30 Comparison of DNA sequences with protein sequences. *Genomics* 46: 24-36; Schuler, G. D. (1997) Sequence mapping by electronic PCR. *Genome Res* 7: 541-50; and Smit, A. F.

A. and Green, P. (1997) RepeatMasker at URL: [repeatmasker.genome.washington.edu/cgi-bin/RM2\\_req.pl](http://repeatmasker.genome.washington.edu/cgi-bin/RM2_req.pl).

5 Tables 1 and 2 contain additional information regarding SEQ ID NO. 153 to SEQ ID NO. 1085. The explanation of the entries in Tables 1 and 2 is as follows:

Symbol: The Human Genome Organization gene symbol, as allotted by a procedure to be published soon. OR = Olfactory Receptor, numeral to the immediate right - family designation, capital letters - subfamily designation, rightmost numeral - individual gene within subfamily, n appearing when such number is not assigned yet; P = Pseudogene.

10 All ORs within a family share at least 40% protein sequence identity.

All ORs within a subfamily share at least 60% protein sequence identity.

HORDE: The H serial number within the Human Olfactory Receptor Data Exploratorium (URL [bioinfo.weizmann.ac.il/HORDE](http://bioinfo.weizmann.ac.il/HORDE)). The numeral 38 represents the HORDE build (version), gxxx is the individual gene number.

15 Digi: Appearance of a DSnn serial number here means that the sequence has been PCR-amplified from human olfactory epithelial cDNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. See separate page for explanations on the analysis of the DS entries.

20 OST: OSTnnn is the serial number of the sequence in the Olfactory Sequence Tag collection in the Lancet laboratory (URL [bioinfo.weizmann.ac.il/HORDE](http://bioinfo.weizmann.ac.il/HORDE)). Appearance here means that the sequence has been PCR-amplified from human genomic DNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. There are a total of 112 OST sequences.

Trivial name: One or more aliases given to the same gene by different laboratories.  
25 Many of the trivial names are of the form ORnn-xx, whereby nn is a chromosome number and xx is an arbitrary numerical identifier.

Tran: (transcribed) Plus appears if the entry was sequenced from cDNA, or was found in the Expressed Sequence Tags (EST) databases. Plus also appears if in the public databases the gene was annotated as mRNA.

30 Int.: (intact) "Yes" indicates that the gene may be intact, as there are no obvious sequence frame disruptions. "Put" (putative) indicates the same, except that the known sequence is short, hence there may be disruptions in the unsequenced segments. "Pol"

indicates a polymorphism between intact and pseudogenic alleles. When no word appears, this indicates a pseudogene.

E: (Extent) FL indicates that the Full Length sequence is known (typically  $310 \pm 30$  amino acids).

5 D: The number of sequence disruptions in the known sequence of a pseudogene.

C: The human chromosomal location of the OR gene, assigned as described under Mb coord.

Mb coord: The location of the OR gene within a human chromosome, in megabase units, beginning at the p-telomere and ending at the q-telomere, computed based on  
10 integrating information from Unified Database (URL is [bioinfo.weizmann.ac.il/udb](http://bioinfo.weizmann.ac.il/udb)) and the University of California Santa Cruz (URL is [genome.ucsc.edu](http://genome.ucsc.edu)).

CDR: The 17 amino acids suggested to line the odorant ligand binding pocket, delineated by the extracellular 2/3 of transmembrane helices 3,4 and 5. The assignment is based on an algorithm at URL  
15 [bioinformatics.weizman.ac.il/HORDE/humanGenes/CDR.html](http://bioinformatics.weizman.ac.il/HORDE/humanGenes/CDR.html).

%: (% id) The percent protein identity between the human sequence in the current line and the known rodent (rat or mouse) OR sequence to which it bears the highest similarity.

S: (Species) Rat (R) or mouse (M).

20 Acc: The Genbank accession number of the clone that contains the rodent sequence.

Range: The positions x ... y of the first and last bases within the rodent which constitute the OR coding region. If  $x > y$  then the OR is on the reverse strand.

Table 1

25

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
153	OR10D3	H38g001			HSHTPCR09			
154	OR7EnP	H38g002						FL
155	OR1D5	H38g003		OST901	OR17-31	+	pol	FL
156	OR10NnP	H38g00						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
157	OR2F1	H38g005		OST902	OLF3;OR7-139;OR7-140	+	yes	FL
158	OR7EnP	H38g006						FL
159	OR8FnP	H38g007						FL
160	OR2Q1P	H38g008			DJ0669B10;OR7-2			FL
161	OR2W1	H38g009			AL035402-B;dJ88J8.1;hs6M1-15		yes	FL
162	OR7EnP	H38g010				+		FL
163	OR6B1	H38g011	DS119		OR7-3;WUGSC:H_DJ0669B10.3	+	yes	FL
164	OR10Kn	H38g012					yes	FL
165	ORnP	H38g013				+		FL
166	OR4F2P	H38g014			HS191N21;dJ191N21.4;hs6M1-11			FL
167	OR7EnP	H38g015						FL
168	OR1F2P	H38g016			OLFMF2	+	yes	FL
169	OR2P1P	H38g017			AL035402-A;dJ88J8.2;hs6M1-26			
170	OR7E43P	H38g018		OST903	OR4-116			FL
171	OR4F1	H38g019			HSDJ0609N19			FL
172	OR7E55P	H38g020		OST904	OR2DG;OR3.2			FL
173	OR13Dn	H38g021					yes	FL
174	OR4CnP	H38g022						FL
175	OR10D1P	H38g023		OST074	HSHTPCR03	+		FL
176	OR4Cn	H38g02					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
177	OR8GnP	H38g02 5						
178	OR13CnP	H38g02 6						FL
179	OR4CnP	H38g02 7						FL
180	OR13Cn	H38g02 8					yes	FL
181	OR4CnP	H38g02 9						
182	OR51Bn	H38g03 0					yes	FL
183	OR7E5P	H38g03 1		OST905	OR11-12			FL
184	OR13Cn	H38g03 2					yes	FL
185	OR4Sn	H38g03 3					yes	FL
186	OR51BnP	H38g03 4						FL
187	OR6JnP	H38g03 5						FL
188	OR51Bn	H38g03 6					yes	FL
189	OR7EnP	H38g03 7						FL
190	OR2An	H38g03 8					yes	FL
191	OR7E22P	H38g03 9			OR3.6;OR6DG			FL
192	OR7E4P	H38g04 0			OR11-11a			FL
193	OR7E66P	H38g04 1		OST906	OR3.3;OR3DG;hg630			FL
194	OR6Mn	H38g04 2					yes	FL
195	OR2ALnP	H38g04 3						
196	OR6MnP	H38g04 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
197	OR4D1	H38g04 5			AC005962-A;HSTPCR16	+	yes	FL
198	OR5D2P	H38g04 6		OST907	OR11-7a;OR912-91			FL
199	OR7E38P	H38g04 7		OST127	AC004967	+		FL
200	OR4D2	H38g04 8			AC005962-B		yes	FL
201	OR7E7P	H38g04 9			AC004967-A			FL
202	OR5AHnP	H38g05 0						
203	OR2U2P	H38g05 1			AL050339- B;dJ974I11.2;hs6M1- 23			FL
204	OR2U1P	H38g05 2			974I11;AL050339- C;dJ974I11.3;hs6M1- 24			FL
205	OR2H2	H38g05 3			AC006137- A;dJ271M21.2;hs6M1- 12		yes	FL
206	OR2H5P	H38g05 4		OST616	HS271M21;hs6M1-13			FL
207	OR2In	H38g05 5				+	yes	FL
208	OR11HnP	H38g05 6						FL
209	OR7EnP	H38g05 7				+		
210	OR9In	H38g05 8					yes	FL
211	OR2AFnP	H38g05 9						FL
212	OR13KnP	H38g06 1						FL
213	OR13Cn	H38g06 2					yes	FL
214	OR13Fn	H38g06 3					yes	FL
215	OR9Qn	H38g06 4					yes	FL



SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
216	OR2TnP	H38g06 5						FL
217	OR4Kn	H38g06 6					yes	FL
218	OR2B8P	H38g06 7			dJ313I6.4;hs6M1-29P		yes	FL
219	OR2Tn	H38g06 8					yes	FL
220	OR4Kn	H38g06 9					yes	FL
221	OR2A4	H38g07 0			WUGSC:H_DJ0988G15.2	+	yes	FL
222	OR7EnP	H38g07 1						FL
223	OR4Kn	H38g07 2					yes	FL
224	OR13InP	H38g07 3						FL
225	OR7EnP	H38g07 4						FL
226	OR6Jn	H38g07 5					yes	FL
227	OR4Mn	H38g07 6					yes	FL
228	OR4VnP	H38g07 7						FL
229	OR6Xn	H38g07 8					yes	FL
230	OR51Gn	H38g07 9					yes	FL
231	OR6EnP	H38g08 0						FL
232	OR4NnP	H38g08 1						FL
233	OR6MnP	H38g08 2						FL
234	OR4Nn	H38g08 3					yes	FL
235	OR4Cn	H38g08 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
236	OR4KnP	H38g08 5						FL
237	ORnP	H38g08 6						
238	OR5D3	H38g08 7		OST908	OR11-8b;OR11-8c			
239	OR2G1P	H38g08 8	DS13;D S16	OST619	dJ974I11.4;hs6M1-25	+		FL
240	OR4Kn	H38g08 9					yes	FL
241	OR8BnP	H38g09 0						FL
242	OR2B2	H38g09 1			OR6-1;dJ193B12.4		yes	FL
243	OR7EnP	H38g09 2						FL
244	OR4KnP	H38g09 3						FL
245	OR2AD1P	H38g09 4			dJ25J6.1;hs6M1-8P			FL
246	OR1AAnP	H38g09 5						FL
247	OR1E3P	H38g09 6			OR17-210			FL
248	OR8BnP	H38g09 7						FL
249	OR5Hn	H38g09 8					yes	FL
250	OR1G1	H38g09 9		OST909	OR17-130;OR17-209	+	yes	FL
251	OR5HnP	H38g10 0						FL
252	ORnP	H38g10 1						
253	ORnP	H38g10 2						
254	OR4PnP	H38g10 3						FL
255	OR13Hn	H38g10 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
256	OR7D1P	H38g10 5		OST910	CIT-B-440L2;OR19- 131;OR19-A			FL
257	OR4KnP	H38g10 6						FL
258	OR7E24	H38g10 7		OST911	CIT-B-440L2;OR19-8	+		FL
259	OR51NnP	H38g10 8						FL
260	OR7E18P	H38g10 9		OST912	OR19-14;TPCR26	+		FL
261	OR7E19P	H38g11 0		OST913	HSCIT-B-440L2;OR19- 7;TPCR110	+		FL
262	OR7E41P	H38g11 1		OST914	OR11-20;hg84			FL
263	OR2R1	H38g11 2		OST058				FL
264	OR10ACn P	H38g11 3						FL
265	OR51Ln	H38g11 4					yes	FL
266	OR52JnP	H38g11 5						FL
267	OR9LnP	H38g11 6						
268	OR51PnP	H38g11 7						FL
269	OR5HnP	H38g11 8						FL
270	OR51An	H38g11 9					yes	FL
271	OR5HnP	H38g12 0						FL
272	ORnP	H38g12 1						
273	OR52En	H38g12 2					yes	FL
274	OR5Hn	H38g12 3					yes	FL
275	OR4CnP	H38g12 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
276	OR52En	H38g12 5					yes	FL
277	OR10Dn	H38g12 6					yes	FL
278	OR5HnP	H38g12 7						FL
279	OR13An	H38g12 8					yes	FL
280	OR5HnP	H38g12 9						FL
281	OR5Kn	H38g13 0					yes	FL
282	OR7EnP	H38g13 1						FL
283	OR4DnP	H38g13 2						FL
284	OR2ARnP	H38g13 3						
285	OR7E29P	H38g13 4		OST032				FL
286	OR4CnP	H38g13 5						FL
287	OR5PnP	H38g13 6						FL
288	OR7EnP	H38g13 7						FL
289	OR56An	H38g13 8					yes	FL
290	OR56AnP	H38g13 9						
291	OR5Pn	H38g14 0					yes	FL
292	OR7E53P	H38g14 1		OST915	OR3-142;OR3-143			FL
293	OR5Pn	H38g14 2					yes	FL
294	OR52Ln	H38g14 3					yes	FL
295	OR5E1	H38g14 4			HSTPCR24	+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
296	OR56AnP	H38g14 5						
297	OR4KnP	H38g14 6						
298	OR52Ln	H38g14 7					yes	FL
299	OR7EnP	H38g14 8						
300	OR52XnP	H38g14 9						FL
301	ORnP	H38g15 0						
302	OR56An	H38g15 1					yes	FL
303	OR56AnP	H38g15 2						
304	OR1R1P	H38g15 3			OR17-1			FL
305	OR52EnP	H38g15 4						FL
306	OR51AnP	H38g15 5						FL
307	OR51An	H38g15 6					yes	FL
308	OR4CnP	H38g15 7						FL
309	OR52JnP	H38g15 8						FL
310	OR4RnP	H38g15 9						
311	OR52Jn	H38g16 0					yes	FL
312	OR4CnP	H38g16 1						FL
313	OR51AnP	H38g16 2						FL
314	OR7EnP	H38g16 3						FL
315	OR5MnP	H38g16 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
316	OR10ABn P	H38g16 5						FL
317	OR52SnP	H38g16 6						FL
318	OR5Mn	H38g16 7					yes	FL
319	OR10Sn	H38g16 8					yes	FL
320	OR5MnP	H38g16 9						FL
321	OR10Gn	H38g17 0					yes	FL
322	ORnP	H38g17 1						FL
323	OR5MnP	H38g17 2						FL
324	OR10GnP	H38g17 3						
325	OR10TnP	H38g17 4						FL
326	ORnP	H38g17 5						
327	OR10RnP	H38g17 6						FL
328	OR5MnP	H38g17 7						FL
329	OR7EnP	H38g17 8						FL
330	OR10Tn	H38g17 9					yes	FL
331	OR1E1	H38g18 0	DS37;D S43;DS 46	OST916	HGMP07I;OR17-2;OR17- 32	+	yes	FL
332	OR5BKnP	H38g18 1						
333	OR5MnP	H38g18 2						FL
334	OR3A3	H38g18 3		OST917	OR17-137;OR17- 16;OR17-201	+	yes	FL
335	OR10ADn P	H38g18 4	DS10			+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
336	OR10Rn	H38g18 5				+	yes	FL
337	OR5TnP	H38g18 6						FL
338	OR4GnP	H38g18 7						FL
339	OR6Yn	H38g18 8					yes	FL
340	OR1E2	H38g18 9		OST918	OR17-135;OR17-93	+	yes	FL
341	OR8Hn	H38g19 0					yes	FL
342	OR4Fn	H38g19 1					yes	FL
343	OR10Kn	H38g19 2					yes	FL
344	OR7LnP	H38g19 3						
345	OR8InP	H38g19 4						FL
346	OR10RnP	H38g19 5						
347	OR2AFnP	H38g19 6						FL
348	OR8Kn	H38g19 7					yes	FL
349	ORnP	H38g19 8						
350	OR8KnP	H38g19 9						FL
351	OR51Hn	H38g20 0					yes	FL
352	OR7EnP	H38g20 1						FL
353	ORnP	H38g20 2						
354	OR5BMnP	H38g20 3						FL
355	OR10GnP	H38g20 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
356	OR2Yn	H38g20 5					yes	FL
357	OR10DnP	H38g20 6						FL
358	OR3BnP	H38g20 7						FL
359	OR8Dn	H38g20 8					yes	FL
360	OR5RnP	H38g20 9						
361	OR10Gn	H38g21 0					yes	FL
362	OR5BDnP	H38g21 1						FL
363	OR5ALnP	H38g21 2						FL
364	OR52HnP	H38g21 3						
365	OR10Gn	H38g21 4					yes	FL
366	OR5Mn	H38g21 5					yes	FL
367	OR51Mn	H38g21 6					yes	FL
368	OR6Tn	H38g21 7	DS15;D S146;D S147			+	yes	FL
369	OR6DnP	H38g21 8						FL
370	OR4B1	H38g21 9		OST208			yes	FL
371	OR5ALnP	H38g22 0						FL
372	OR51Qn	H38g22 1					yes	FL
373	OR4Dn	H38g22 2					yes	FL
374	OR52Nn	H38g22 3					yes	FL
375	OR4Xn	H38g22 4					yes	FL



SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
376	OR8Jn	H38g22 5					yes	FL
377	OR51JnP	H38g22 6						FL
378	OR10Gn	H38g22 7					yes	FL
379	OR52En	H38g22 8					yes	FL
380	OR4Xn	H38g22 9					yes	FL
381	OR10A2	H38g23 0	DS5;DS 53;DS5 6	OST363		+		FL
382	OR5Mn	H38g23 1					yes	FL
383	OR52En	H38g23 2					yes	FL
384	OR8Kn	H38g23 3					yes	FL
385	OR10An	H38g23 4	DS55			+	yes	FL
386	OR8LnP	H38g23 5						FL
387	OR5BPnP	H38g23 6						
388	OR52Nn	H38g23 7					yes	FL
389	ORnP	H38g23 8						
390	OR8JnP	H38g23 9						FL
391	OR5Mn	H38g24 0					yes	FL
392	OR52En	H38g24 1					yes	FL
393	OR5Tn	H38g24 2					yes	FL
394	OR52NnP	H38g24 3						FL
395	OR4B2P	H38g24 4		OST919	hg449			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
396	OR51KnP	H38g24 5						FL
397	OR52QnP	H38g24 6						FL
398	OR4Fn	H38g24 7					yes	FL
399	OR11MnP	H38g24 8						
400	OR52Nn	H38g24 9					yes	FL
401	OR56An	H38g25 0					yes	FL
402	OR5AWnP	H38g25 1						FL
403	OR52Nn	H38g25 2					yes	FL
404	ORnP	H38g25 3						
405	OR52EnP	H38g25 4						FL
406	OR5BHnP	H38g25 5						FL
407	OR4QnP	H38g25 6						FL
408	OR51En	H38g25 7					yes	FL
409	OR11KnP	H38g25 8						FL
410	OR12D1P	H38g25 9			AC004174- B;dJ994E9.7;hs6M1-19			FL
411	OR4NnP	H38g26 0				+		FL
412	OR11A1	H38g26 1			AC004174- A;dJ994E9.6;hs6M1-18	+	yes	FL
413	OR10C1	H38g26 2			AC004174;dJ994E9.5;h s6M1-17	+	yes	FL
414	OR2H1	H38g26 3	DS114		OLFR42A-9004-14;OR6- 2;dJ994E9.4;hs6M1-16	+	yes	FL
415	OR9RnP	H38g26 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
416	OR4FnP	H38g26 5						
417	OR7D4	H38g26 6		OST920	OR19-B;hg105			FL
418	OR7E25P	H38g26 7		OST921	CIT-B-440L2;OR19-C			FL
419	OR2D2	H38g26 8			OR11-610		yes	FL
420	OR10An	H38g26 9					yes	FL
421	OR2WnP	H38g27 0				+		
422	OR7E16P	H38g27 1		OST922	CIT-B-440L2;OR19- 133;OR19-9			FL
423	OR52Pn	H38g27 2					yes	FL
424	OR6AnP	H38g27 3						FL
425	OR7D2	H38g27 4	DS70;D S73	OST923	HTPCRHO3;OR19-4	+	yes	FL
426	OR52UnP	H38g27 5						FL
427	OR2AGn	H38g27 6					yes	FL
428	OR7G3	H38g27 7		OST085			yes	FL
429	OR56BnP	H38g27 8						FL
430	OR2AGnP	H38g27 9						FL
431	OR56Bn	H38g28 0					yes	FL
432	OR6AnP	H38g28 1						FL
433	OR4FnP	H38g28 2						FL
434	OR6Wn	H38g28 3					yes	FL
435	OR4Mn	H38g28 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
436	OR52YnP	H38g28 5						
437	OR11HnP	H38g28 6						FL
438	OR9An	H38g28 7					yes	FL
439	OR5Mn	H38g28 8					yes	FL
440	OR6Vn	H38g28 9					yes	FL
441	OR4Nn	H38g29 0				+	yes	FL
442	OR51AnP	H38g29 1						FL
443	OR9PnP	H38g29 2						
444	OR4H6P	H38g29 3			OR15-71;OR15-82			FL
445	OR51FnP	H38g29 4						FL
446	OR7E1P	H38g29 5			AC004923			FL
447	OR51Tn	H38g29 6					yes	FL
448	OR2Vn	H38g29 7					yes	FL
449	OR51HnP	H38g29 8						FL
450	OR51An	H38g29 9					yes	FL
451	OR2AInP	H38g30 0						FL
452	OR2F2	H38g30 1			OR7- 1;WUGSC:H_DJ0669B10. 1		yes	FL
453	OR1F12	H38g30 2			dJ313I6.5;hs6M1-35P		yes	FL
454	OR7G1P	H38g30 3			OR19-15		yes	FL
455	OR7G2	H38g30 4		OST260			yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
456	OR1M1	H38g30 5		OST924	OR19-6		yes	FL
457	OR51UnP	H38g30 6						
458	OR52Hn	H38g30 7					yes	FL
459	OR1F1	H38g30 8		OST925	OLFMF;OR16-36;OR16- 37;OR16-88;OR16- 89;OR16-90	+	yes	FL
460	OR10PnP	H38g30 9						
461	OR4FnP	H38g31 0						FL
462	OR2T1	H38g31 1			OR1-25		yes	FL
463	OR7EnP	H38g31 2						FL
464	OR51Gn	H38g31 3					yes	FL
465	OR2Tn	H38g31 4					yes	FL
466	OR5BGnP	H38g31 5						
467	OR5WnP	H38g31 6						FL
468	OR51Sn	H38g31 7					yes	FL
469	OR5WnP	H38g31 8						
470	OR51AnP	H38g31 9						FL
471	OR5Dn	H38g32 0					yes	FL
472	OR7EnP	H38g32 1						FL
473	OR51Fn	H38g32 2					yes	FL
474	OR5Dn	H38g32 3					yes	FL
475	OR52Rn	H38g32 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
476	ORnP	H38g32 5						FL
477	OR7EnP	H38g32 6						FL
478	OR6Qn	H38g32 7					yes	FL
479	OR4Fn	H38g32 8					yes	FL
480	OR7EnP	H38g32 9						
481	OR7En	H38g33 0					yes	FL
482	OR4Nn	H38g33 1					yes	FL
483	OR2ASnP	H38g33 2						
484	OR11Hn	H38g33 3					yes	FL
485	OR2Tn	H38g33 4					yes	FL
486	OR2TnP	H38g33 5						
487	OR2AKnP	H38g33 6						FL
488	ORnP	H38g33 7						
489	OR5DnP	H38g33 8						FL
490	OR7EnP	H38g33 9						
491	OR5L2	H38g34 0			HSHTPCR16	+	yes	FL
492	OR5Dn	H38g34 1					yes	FL
493	ORnP	H38g34 2						
494	OR10Qn	H38g34 3					yes	FL
495	OR9MnP	H38g34 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
496	OR7E62P	H38g34 5		OST926	OR2-4;OR2-52;OR2- 53;OR2-75			FL
497	OR9LnP	H38g34 6						FL
498	OR7E46P	H38g34 7		OST379				FL
499	OR1S1	H38g34 8		OST034			yes	FL
500	OR5DnP	H38g34 9						
501	OR9InP	H38g35 0						FL
502	OR5Dn	H38g35 1					yes	FL
503	OR9QnP	H38g35 2						FL
504	OR51CnP	H38g35 3						
505	OR5WnP	H38g35 4						
506	OR9InP	H38g35 5						FL
507	OR51AnP	H38g35 6						FL
508	OR5L1	H38g35 7		OST262			yes	FL
509	OR7EnP	H38g35 8				+		
510	OR5BLnP	H38g35 9						
511	OR51En	H38g36 0					yes	FL
512	OR51Dn	H38g36 1					yes	FL
513	OR52In	H38g36 2					yes	FL
514	OR4KnP	H38g36 3	DS67			+		FL
515	OR52In	H38g36 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
516	OR4KnP	H38g36 5						FL
517	OR52MnP	H38g36 6						FL
518	ORnP	H38g36 7						
519	ORnP	H38g36 8						
520	ORnP	H38g36 9						FL
521	ORnP	H38g37 0						
522	ORnP	H38g37 1						
523	ORnP	H38g37 2						
524	ORnP	H38g37 3						
525	ORnP	H38g37 4						
526	OR6Pn	H38g37 5					yes	FL
527	OR7EnP	H38g37 6						FL
528	ORnP	H38g37 7						
529	OR7EnP	H38g37 8						FL
530	ORnP	H38g37 9						
531	OR10XnP	H38g38 0						FL
532	OR10Zn	H38g38 1					yes	FL
533	OR6KnP	H38g38 2						FL
534	OR6Kn	H38g38 3					yes	FL
535	OR1FnP	H38g38 4						



SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
536	OR1ABnP	H38g38 5						
537	OR52MnP	H38g38 6						FL
538	OR1XnP	H38g38 7						FL
539	OR4FnP	H38g38 8						
540	OR52MnP	H38g38 9						FL
541	OR2Vn	H38g39 0					yes	FL
542	OR2V1P	H38g39 1		OST265				FL
543	OR2Zn	H38g39 2					yes	FL
544	OR52KnP	H38g39 3				+		
545	OR10Hn	H38g39 4					yes	FL
546	OR2Dn	H38g39 5					yes	FL
547	OR7EnP	H38g39 6						
548	OR11GnP	H38g39 7						FL
549	ORnP	H38g39 8						
550	OR11Gn	H38g39 9					yes	FL
551	OR11HnP	H38g40 0						FL
552	OR6Kn	H38g40 1					yes	FL
553	OR11Hn	H38g40 2					yes	FL
554	OR6KnP	H38g40 3						
555	OR11HnP	H38g40 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
556	OR6KnP	H38g40 5						FL
557	OR6Kn	H38g40 6					yes	FL
558	OR2Ln	H38g40 7					yes	FL
559	OR4GnP	H38g40 8						
560	OR6Nn	H38g40 9					yes	FL
561	OR2LnP	H38g41 0						
562	OR9A1	H38g41 1			HSHTPCR06			
563	OR6Nn	H38g41 2					yes	FL
564	OR10Hn	H38g41 3					yes	FL
565	OR7EnP	H38g41 4						FL
566	OR2AQnP	H38g41 5						
567	OR2LnP	H38g41 6						FL
568	OR5ARn	H38g41 7					yes	FL
569	OR7EnP	H38g41 8						FL
570	OR10AAn P	H38g41 9						FL
571	OR10JnP	H38g42 0						FL
572	OR5A1P	H38g42 1	DS69;D S71;DS 128;DS 129	OST181		+	yes	FL
573	OR2AHnP	H38g42 2						FL
574	OR10JnP	H38g42 3						FL
575	OR56BnP	H38g42						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
576	OR5M1	H38g42 5		OST050			yes	FL
577	OR52WnP	H38g42 6						
578	OR5AMnP	H38g42 7						FL
579	OR52BnP	H38g42 8						FL
580	OR5MnP	H38g42 9						FL
581	OR5APnP	H38g43 0						FL
582	OR56Bn	H38g43 1					yes	FL
583	OR5APn	H38g43 2					yes	FL
584	OR52Bn	H38g43 3					yes	FL
585	OR9Gn	H38g43 4					yes	FL
586	OR52Kn	H38g43 5					yes	FL
587	OR5MnP	H38g43 6						FL
588	OR52Kn	H38g43 7					yes	FL
589	OR52KnP	H38g43 8				+		FL
590	OR52BnP	H38g43 9						FL
591	OR2B6P	H38g44 0			OR6-31		yes	FL
592	OR2WnP	H38g44 1						FL
593	OR2AnP	H38g44 2						FL
594	ORnP	H38g44 3						
595	OR2LnP	H38g44 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
596	OR2W2P	H38g44 5	DS148		dJ313I6.2;hs6M1-30P	+		FL
597	OR2LnP	H38g44 6						
598	OR2B7P	H38g44 7			dJ313I6.3;hs6M1-31P			FL
599	OR2Ln	H38g44 8					yes	FL
600	OR5BFn	H38g44 9					yes	FL
601	OR2LnP	H38g45 0						FL
602	OR7EnP	H38g45 1						
603	OR1H1	H38g45 2	DS122	OST26		+		FL
604	ORnP	H38g45 3						
605	OR4Dn	H38g45 4					yes	FL
606	OR1Ln	H38g45 5					yes	FL
607	OR5AXn	H38g45 6					yes	FL
608	OR5An	H38g45 7					yes	FL
609	OR5AYn	H38g45 8					yes	FL
610	OR13Gn	H38g45 9					yes	FL
611	OR5BBnP	H38g46 0						
612	OR9GnP	H38g46 1						FL
613	OR2TnP	H38g46 2						FL
614	ORnP	H38g46 3						FL
615	OR1Jn	H38g46 4				+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
616	OR2CnP	H38g46 5						FL
617	OR9GnP	H38g46 6						FL
618	OR2C1	H38g46 7			OLFmf3	+	yes	FL
619	OR51AnP	H38g46 8						
620	OR9Gn	H38g46 9					yes	FL
621	OR52Bn	H38g47 0					yes	FL
622	OR1K1	H38g47 1			hg99		yes	FL
623	OR51RnP	H38g47 2						FL
624	OR7EnP	H38g47 3						FL
625	OR52PnP	H38g47 4						FL
626	OR7EnP	H38g47 5						FL
627	OR7EnP	H38g47 6						
628	OR4KnP	H38g47 7	DS66		OR21-1	+		FL
629	OR4KnP	H38g47 8			OR21-2			FL
630	OR7EnP	H38g47 9						
631	OR51In	H38g48 0					yes	FL
632	OR51In	H38g48 1					yes	FL
633	OR2AnP	H38g48 2						
634	OR2A2	H38g48 3		OST008				FL
635	OR2AnP	H38g48 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
636	OR2Gn	H38g48 5					yes	FL
637	OR2AnP	H38g48 6						
638	OR6Fn	H38g48 7	DS20;D S21;DS 23;DS2 7;DS28 ;DS39; DS40;D S113;D S126;D S135;D S137;D S138;D S139;D S140;D S141;D S145			+	yes	FL
639	OR2AnP	H38g48 8						
640	OR2Gn	H38g48 9					yes	FL
641	OR7E37P	H38g49 0			hg533	+		FL
642	OR5AVn	H38g49 1	DS4;DS 6;DS11			+	yes	FL
643	OR2AJnP	H38g49 2						FL
644	OR13EnP	H38g49 3						FL
645	OR2Cn	H38g49 4					yes	FL
646	OR2TnP	H38g49 5						
647	OR2WnP	H38g49 6						
648	OR13Jn	H38g49 7					yes	FL
649	OR6RnP	H38g49 8						FL
650	OR5ATn	H38g49 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
651	OR2Zn	H38g50 0					yes	FL
652	OR4Ln	H38g50 1					yes	FL
653	OR4UnP	H38g50 2						FL
654	OR4Fn	H38g50 3					yes	FL
655	OR4FnP	H38g50 4						FL
656	OR4Fn	H38g50 5					yes	FL
657	OR4Fn	H38g50 6					yes	FL
658	OR4AnP	H38g50 7						FL
659	OR4LnP	H38g50 8						FL
660	OR7E33P	H38g50 9		OST927	hg688			FL
661	OR2Cn	H38g51 0					yes	FL
662	OR4Kn	H38g51 1					yes	FL
663	OR5U1	H38g51 2			ba150A6.4;hs6M1-28		yes	FL
664	OR4Kn	H38g51 3					yes	FL
665	OR5V1	H38g51 4			ba150A6.2;hs6M1-21		yes	FL
666	OR4QnP	H38g51 5						FL
667	OR12D3	H38g51 6			ba150A6.1;hs6M1-27		yes	FL
668	OR4Kn	H38g51 7					yes	FL
669	OR51CnP	H38g51 8						
670	OR1J2	H38g51 9		OST044	hg152		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
671	OR5BJnP	H38g52 0						
672	OR1J1	H38g52 1	DS130	OST928	hg32	+	yes	FL
673	OR13En	H38g52 2					put	
674	OR4KnP	H38g52 3	DS1			+		FL
675	OR1LnP	H38g52 4						
676	OR2CnP	H38g52 5						
677	OR4TnP	H38g52 6						FL
678	OR5BnP	H38g52 7						
679	OR4Kn	H38g52 8					yes	FL
680	OR11Ln	H38g52 9					yes	FL
681	OR7E68P	H38g53 0		OST929	OR912-108;OR912- 109;OR912-110;OR912- 46;hg523;hg674			FL
682	OR7EnP	H38g53 1						FL
683	OR7E31P	H38g53 2		OST016;O ST205				FL
684	OR7EnP	H38g53 3						FL
685	OR5AKnP	H38g53 4						FL
686	OR5AKn	H38g53 5					yes	FL
687	OR5AKn	H38g53 6					yes	FL
688	OR5BQnP	H38g53 7						
689	OR1Nn	H38g53 8	DS136; DS142			+	yes	FL
690	OR1J4	H38g53 9		OST930	HSHTPCR01	+	yes	FL



SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
691	OR1Nn	H38g54 0					yes	FL
692	OR2AnP	H38g54 1						FL
693	OR2ANnP	H38g54 2						
694	OR5K1	H38g54 3			HSHTPCR10	+	yes	FL
695	OR2K2	H38g54 4			HSHTPCR06		yes	FL
696	OR8Hn	H38g54 5					yes	FL
697	ORnP	H38g54 6						
698	OR4AnP	H38g54 7						
699	OR4An	H38g54 8					yes	FL
700	OR6Sn	H38g54 9					yes	FL
701	OR4RnP	H38g55 0						
702	OR13Cn	H38g55 1					yes	FL
703	OR13DnP	H38g55 2						FL
704	OR7EnP	H38g55 3						FL
705	OR10PnP	H38g55 4						FL
706	OR8In	H38g55 5					yes	FL
707	OR8G1	H38g55 6			HSTPCR25	+	put	
708	ORnP	H38g55 7						
709	OR5F1	H38g55 8			OR11-10		yes	FL
710	OR5FnP	H38g55 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
711	OR6BnP	H38g56 0						FL
712	OR2D1	H38g56 1			hg27		put	
713	OR5ASn	H38g56 2					yes	FL
714	OR5SnP	H38g56 3						FL
715	OR5AQnP	H38g56 4						
716	OR6BnP	H38g56 5						FL
717	OR5JnP	H38g56 6						FL
718	OR9AnP	H38g56 7						FL
719	OR5BEnP	H38g56 8						FL
720	OR9An	H38g56 9					yes	FL
721	OR8Hn	H38g57 0					yes	FL
722	OR5BNnP	H38g57 1						
723	OR8Jn	H38g57 2					yes	FL
724	OR9NnP	H38g57 3						
725	OR7EnP	H38g57 4						FL
726	OR7E9P	H38g57 5		OST289				FL
727	OR8KnP	H38g57 6						
728	OR2AnP	H38g57 7						
729	OR8Kn	H38g57 8					yes	FL
730	OR7E39P	H38g57 9		OST931	hg611			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
731	OR7E27P	H38g58 0		OST932	hg616			
732	OR2Hn	H38g58 1					put	
733	OR13CnP	H38g58 2						FL
734	OR13Cn	H38g58 3					yes	FL
735	OR2S1P	H38g58 4		OST611				FL
736	OR2AMnP	H38g58 5						
737	OR1N1	H38g58 6		OST933	OR1-26		put	
738	OR2S2	H38g58 7		OST715			yes	FL
739	OR7E26P	H38g58 8			OR1-51;OR1-72;OR1-73;OR912-95			
740	OR1F11	H38g58 9			hg91		put	
741	OR5ACnP	H38g59 0						FL
742	OR5B10P	H38g59 1			OR13-34;OR13-64;OR13-67			
743	OR2AnP	H38g59 2						FL
744	OR1E5	H38g59 3	DS117; DS143		OR13-66	+	put	
745	OR4Fn	H38g59 4					yes	FL
746	OR5CnP	H38g59 5						
747	OR2WnP	H38g59 6						
748	OR2L2	H38g59 7			HSHTPCRHO7	+	put	
749	OR4H8P	H38g59 8			OR14-58			
750	OR5D10P	H38g59 9			OR912-94			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
751	OR7A12P	H38g60 0			OR14-11;OR14-59			
752	OR2L1	H38g60 1			HSHTPCR02	+	put	
753	OR2F3P	H38g60 2			OR14-60		put	
754	OR4H10P	H38g60 3		OST934	OR15-69;OR15- 80;OR15-81			
755	OR5H1	H38g60 4			HSHTPCR14	+	put	
756	OR2K1	H38g60 5			HSHTPCR17	+	put	
757	OR7E11P	H38g60 6			OR11-2			
758	OR7A3P	H38g60 7		OST935	OR11-7b			
759	OR6A1	H38g60 8			OR11-55	+	yes	FL
760	OR5I1	H38g60 9			OLF1	+	yes	FL
761	OR2H3	H38g61 0			HUMORLMHC	+	yes	FL
762	OR10J1	H38g61 1	DS3;DS 14		HSHGMP07J	+	yes	FL
763	OR7E3P	H38g61 2			OR11-9			
764	OR1D6P	H38g61 3			OR11-13;OR11-22			
765	OR5D10P	H38g61 4			OR18-17;OR18- 42;OR18-43;OR18-44			
766	OR5D5P	H38g61 5			OR18-79;OR912-47			
767	OR52A1	H38g61 6			HPFH1OR	+	yes	FL
768	OR2AEn	H38g61 7					yes	FL
769	OR6LnP	H38g61 8						FL
770	OR6LnP	H38g61 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
771	OR7MnP	H38g62 0						
772	OR13Cn	H38g62 1					yes	FL
773	OR13Cn	H38g62 2					yes	FL
774	OR2InP	H38g62 3				+		
775	OR4An	H38g62 4					yes	FL
776	OR2InP	H38g62 5				+		
777	OR4AnP	H38g62 6						FL
778	OR4AnP	H38g62 7						FL
779	OR8C1P	H38g62 8			OR11-175			
780	OR4AnP	H38g62 9						FL
781	OR7E15P	H38g63 0			OR11-392			
782	OR10A1	H38g63 2			OR11-403		put	
783	OR2An	H38g63 3				+	put	
784	OR7EnP	H38g63 4				+		FL
785	OR7En	H38g63 5				+	put	
786	OR51A1P	H38g63 6			HPFH6OR	+		FL
787	OR7E47P	H38g63 7			HSORBPL41;bpl41-16	+		FL
788	OR5B5P	H38g63 8			OR3-144;OR912-92			
789	OR1F10	H38g63 9			OR3-145		put	
790	OR8G2	H38g64 0			HSTPCR120	+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
791	OR1Sn	H38g64 1					yes	FL
792	OR4AnP	H38g64 2						FL
793	OR4AnP	H38g64 3						FL
794	OR4AnP	H38g64 4						FL
795	OR4AnP	H38g64 5						FL
796	OR4AnP	H38g64 6						FL
797	OR4AnP	H38g64 7						FL
798	OR4An	H38g64 8					yes	FL
799	OR4An	H38g64 9					yes	FL
800	OR7E42P	H38g65 0		OST001				
801	OR2M3P	H38g65 1		OST003				
802	OR4H11P	H38g65 2			OR4-114;OR4-115;OR4- 119			
803	OR7E57P	H38g65 3		OST007				
804	OR2B1P	H38g65 4			OR5-40;OR5-41		put	
805	OR7E34P	H38g65 5		OST011				
806	OR7E56P	H38g65 6		OST013				
807	OR3AnP	H38g65 7						
808	OR4H5P	H38g65 8			OR5-39;OR5-84			
809	OR1En	H38g65 9	DS47;D S115;D S120;D S121;D S123;D			+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
			S125					
810	OR51CnP	H38g66 0						
811	OR2WnP	H38g66 1						FL
812	OR51B1P	H38g66 2			AF149710			FL
813	OR7E81P	H38g66 3		OST021				
814	OR7E44P	H38g66 4		OST022				
815	OR5B7P	H38g66 5			OR6-55;OR6-57			
816	OR7E36P	H38g66 6		OST024				
817	OR2A5	H38g66 7			OR7-138;OR7-141		put	
818	OR5B1P	H38g66 8		OST936	OR8-122;OR8-123			
819	OR8B8	H38g66 9			HSTPCR85	+	yes	FL
820	OR8B4P	H38g67 0			AC002556-D		yes	FL
821	ORnP	H38g67 1						FL
822	OR8B3	H38g67 2			AC002556-B		yes	FL
823	OR2Bn	H38g67 3					yes	FL
824	OR8B6P	H38g67 4			AC002556-G			FL
825	OR8B5P	H38g67 5			AC002556-A			FL
826	OR4E2	H38g67 6			AE000658-A		yes	FL
827	OR8B7P	H38g67 7			AC002556-F			FL
828	OR11JnP	H38g67 8						FL
829	OR4E1P	H38g67 9			AE000658			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
830	OR10DnP	H38g68 0						
831	ORnP	H38g68 1						
832	OR8D2	H38g68 2			AC002556-E		yes	FL
833	OR11InP	H38g68 3						FL
834	OR11JnP	H38g68 4						FL
835	OR10AnP	H38g68 5	DS12;D S65			+		FL
836	OR8C3P	H38g68 6			OR912-106;OR912- 45;pDJ9j14			FL
837	OR2DnP	H38g68 7						FL
838	OR4PnP	H38g68 8						
839	OR7E21P	H38g68 9		OST035	OR4DG			
840	OR2M1	H38g69 0		OST037			put	
841	OR7AnP	H38g69 1						
842	OR5D11P	H38g69 2			OR8-125;OR8-127			
843	OR7E50P	H38g69 3			OR8-126			
844	OR7E45P	H38g69 4		OST049				
845	OR7E77P	H38g69 5		OST060				
846	OR8B2	H38g69 6			AC002556-C		yes	FL
847	OR8D1	H38g69 7		OST004	pDJ9j14		yes	FL
848	OR8B1P	H38g69 8		OST937	OR11-561			FL
849	OR7A1P	H38g69 9		OST938	OLF4p;OR19-3;hg513			FL



SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
850	OR7E8P	H38g70 0			OR11-11a;pDJ392a17			FL
851	OR4DnP	H38g70 1						FL
852	OR7E80P	H38g70 2		OST939	pDJ392a17			FL
853	OR4DnP	H38g70 3						FL
854	OR7E10P	H38g70 4			AC000385-A			FL
855	OR10B1P	H38g70 5			AC003956-A;OR19-19			FL
856	OR2InP	H38g70 6				+		
857	OR4Dn	H38g70 7					yes	FL
858	OR5ACn	H38g70 8					put	
859	OR2I1	H38g70 9			AC004179-A;dJ271M21.7;hs6M1-14	+		
860	OR10H1	H38g71 0			AC004510	+	yes	FL
861	OR7E59P	H38g71 1		OST119				
862	OR7E28P	H38g71 2		OST128				
863	OR5B3	H38g71 3		OST129			put	
864	OR2A6	H38g71 4		OST182			put	
865	OR6Cn	H38g71 5					put	
866	OR7E54P	H38g71 6		OST185				
867	OR7E48P	H38g71 7		OST193				
868	OR67AnP	H38g71 8						FL
869	OR4DnP	H38g71 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
870	OR4CnP	H38g720						FL
871	OR4DnP	H38g721						FL
872	OR10H2	H38g722			AC004597-A	+	yes	FL
873	OR10H3	H38g723			AC004597-B	+	yes	FL
874	OR55CnP	H38g724						
875	OR55BnP	H38g725						
876	OR52VnP	H38g726						FL
877	OR2B3	H38g727			OR6-4;dJ80I19.1;hs6M1-1		yes	FL
878	OR52TnP	H38g728						FL
879	OR2J1P	H38g729			OR6-5;dJ80I19.2;hs6M1-4			FL
880	OR52HnP	H38g730						FL
881	OR2J3	H38g731			OR6-6;dJ80I19.7;hs6M1-3		yes	FL
882	OR52An	H38g732				+	put	
883	OR4Qn	H38g733					put	
884	OR52BnP	H38g734						FL
885	OR2N1P	H38g735	DS9		OR6-7;dJ80I19.3;hs6M1-2	+		FL
886	OR51EnP	H38g736				+		
887	OR2J2	H38g737			OR6-8;dJ80I19.4;hs6M1-6		yes	FL
888	OR2In	H38g738				+	put	
889	OR2J4P	H38g739			OR6-9;dJ80I19.5;hs6M1-5			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
890	OR7E40P	H38g74 0		OST215				
891	OR2H4P	H38g74 1			OR6- 3;dJ80I19.6;hs6M1-7			FL
892	OR7E52P	H38g74 2		OST245				
893	OR2InP	H38g74 3				+		
894	OR6C1	H38g74 4		OST267			put	
895	OR7E30P	H38g74 5		OST339				
896	OR5BAnP	H38g74 6	DS132			+		
897	OR7H1P	H38g74 7		OST940	CIT-B-440L2			FL
898	OR5B2	H38g74 8		OST073			yes	FL
899	OR5AZnP	H38g74 9						FL
900	OR5Bn	H38g75 0					yes	FL
901	OR52Bn	H38g75 1					yes	FL
902	OR5BnP	H38g75 2						FL
903	OR52Dn	H38g75 3					yes	FL
904	OR7A11	H38g75 4		OST527	CIT-HSP-87m17			FL
905	OR5BnP	H38g75 5						FL
906	OR51AnP	H38g75 6						FL
907	OR7A15P	H38g75 7		OST941	CIT-HSP-87m17;OR19- 1;OR19-134;OR19-146			FL
908	OR7C2	H38g75 8			CIT-HSP-87m17;OR19- 18		yes	FL
909	OR7E23P	H38g75 9		OST942	OR21-3			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
910	OR2E1	H38g760			HS29K1;HSNH0569I24;hs6M1-9			
911	OR1I1	H38g761			F20569;OR19-20		yes	FL
912	OR1RnP	H38g762						FL
913	OR4F3	H38g763			AC004908		yes	FL
914	OR2AEn	H38g764					yes	FL
915	OR2InP	H38g765				+		
916	OR52AnP	H38g766				+		
917	OR7C1	H38g767		OST943	CIT-HSP-146e8;OR19-5;TPCR86	+	yes	FL
918	OR2A3P	H38g768			AC004889-B			FL
919	OR7A5	H38g769	DS8;DS19;DS61;DS68;DS112	OST944	HTPCR2	+	yes	FL
920	OR2InP	H38g770	DS72			+		
921	OR7A10	H38g771		OST027	CIT-HSP-146e8		yes	FL
922	OR2An	H38g772				+	put	
923	OR2M2	H38g773		OST423			put	
924	OR7A8P	H38g774		OST042	OR19-11;hg83			FL
925	OR2An	H38g775				+	put	
926	OR7E20P	H38g776		OST516				
927	OR2AnP	H38g777				+		
928	OR5BHnP	H38g778				+		
929	OR1En	H38g77					put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
930	OR1EnP	H38g78 0						
931	OR5Bn	H38g78 1					yes	FL
932	OR8RnP	H38g78 2						
933	OR5ANn	H38g78 3					yes	FL
934	OR5ANnP	H38g78 4						FL
935	OR5BRnP	H38g78 5						FL
936	OR2A1	H38g78 6			AC004889-A	+	yes	FL
937	OR10An	H38g78 7					yes	FL
938	OR2A9	H38g78 8	DS149		HSDJ0798C17	+		FL
939	OR2A7	H38g78 9			HSDJ0798C17	+	yes	FL
940	OR10A3	H38g79 0			HSHTPCR12	+	yes	FL
941	OR10Cn	H38g79 1					yes	FL
942	OR7A2P	H38g79 2			OLF4p;OR19-18;hg1003		yes	FL
943	OR10WnP	H38g79 3						FL
944	OR7A17	H38g79 4			HSHTPCR19		yes	FL
945	OR5Bn	H38g79 5					yes	FL
946	OR5BnP	H38g79 6						FL
947	OR1Q1	H38g79 7		OST226	HSTPCR106;OR9-A;hRPK-465_F_21	+	yes	FL
948	OR2Hn	H38g79 8	DS133; DS144; DS150			+	yes	FL
949	OR7EnP	H38g79						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
950	OR7A14	H38g800		OST945	OR19-12			
951	OR1B1	H38g801			OR9-B;hrPK-465_F_21		yes	FL
952	OR12D2	H38g802			AC004171;dJ994E9.8;hs6M1-20	+	yes	FL
953	OR7EnP	H38g803						FL
954	OR8BnP	H38g804						FL
955	OR1L1	H38g805			OR9-C;hrPK-465_F_21;hg23		yes	FL
956	OR11An	H38g806					yes	FL
957	OR7AnP	H38g807						
958	OR1C1	H38g808			HSTPCR27	+	yes	FL
959	OR1D2	H38g809		OST946	OR17-4	+	yes	FL
960	OR1L3	H38g810			OR9-D;hrPK-465_F_21		yes	FL
961	OR12DnP	H38g811						FL
962	OR4G1P	H38g812			OLB			FL
963	OR2B4P	H38g813			AL050339-A;dJ974I11.1;hs6M1-22			
964	OR11H1	H38g814			OR22-1		yes	FL
965	OR4Fn	H38g815					yes	FL
966	OR56AnP	H38g816						FL
967	OR8NnP	H38g817						FL
968	OR7EnP	H38g818						
969	OR4Pn	H38g81					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
970	OR6Cn	H38g82 0					put	
971	OR5BCnP	H38g82 1						
972	OR10QnP	H38g82 2	DS64			+		FL
973	OR5BnP	H38g82 3						FL
974	OR10PnP	H38g82 4						FL
975	OR1L4	H38g82 5		OST046	OR9-E;hRPK-465_F_21		yes	FL
976	OR2APnP	H38g82 6						
977	OR1L6	H38g82 7		OST947	HShRPK-465_F_21;hg16		yes	FL
978	OR6UnP	H38g82 8						FL
979	OR5C1	H38g82 9			OR9-F;hRPK-465_F_21		yes	FL
980	OR11InP	H38g83 0						FL
981	OR4AnP	H38g83 1						FL
982	OR4GnP	H38g83 2						FL
983	OR10Vn	H38g83 3					yes	FL
984	OR4G2P	H38g83 4			HS14a-1-B			FL
985	OR10VnP	H38g83 5				+		
986	OR4F4	H38g83 6			HS14a-1-A		yes	FL
987	OR4G3P	H38g83 7			OLC-7501			FL
988	OR5AKnP	H38g83 8						FL
989	OR10YnP	H38g83 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
990	OR4GnP	H38g84 0						FL
991	ORnP	H38g84 1						
992	OR4Fn	H38g84 2					yes	FL
993	OR8A1	H38g84 3		OST025			yes	FL
994	OR8Bn	H38g84 4					yes	FL
995	OR6DnP	H38g84 5						
996	OR7E14P	H38g84 6		OST948	OR11-5	+		FL
997	OR2M4	H38g84 7		OST710	HSHTPCR18	+	put	
998	OR4WnP	H38g84 8						
999	OR4Fn	H38g84 9	DS36			+	yes	FL
1000	OR7EnP	H38g85 0						
1001	OR4GnP	H38g85 1						FL
1002	OR10JnP	H38g85 2						
1003	OR52En	H38g85 3					yes	FL
1004	OR4RnP	H38g85 4						FL
1005	OR4Cn	H38g85 5					yes	FL
1006	OR4AnP	H38g85 6						
1007	OR4AnP	H38g85 7	DS54			+		
1008	OR4AnP	H38g85 8						FL
1009	OR9Gn	H38g85 9					yes	FL



SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1010	OR10An	H38g86 0					yes	FL
1011	OR4Cn	H38g86 1					yes	FL
1012	OR10VnP	H38g86 2						
1013	OR10UnP	H38g86 3						FL
1014	OR7E2P	H38g86 4	DS127		OR11-6;hg94	+		FL
1015	OR7E35P	H38g86 5		OST018				FL
1016	OR9KnP	H38g86 6						
1017	OR7E13P	H38g86 7		OST949	OR11-4			FL
1018	OR7EnP	H38g86 8						FL
1019	OR9Kn	H38g86 9					yes	FL
1020	ORnP	H38g87 0						FL
1021	OR7EnP	H38g87 1		OST950	OR11-1;hg500	+		FL
1022	OR7EnP	H38g87 2						FL
1023	OR3A4P	H38g87 3		OST951	OR17-24;OR17-25	+	yes	FL
1024	OR8QnP	H38g87 4						
1025	OR7EnP	H38g87 5						FL
1026	OR7EnP	H38g87 6						FL
1027	OR3A1	H38g87 7	DS2		OLFRA03;OR17- 40;hg138	+	yes	FL
1028	OR5Gn	H38g87 8					yes	FL
1029	OR5MnP	H38g87 9						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1030	OR7EnP	H38g88 0						FL
1031	OR5G1P	H38g88 1		OST952	OR11- 104;OR93;OR93Hum			FL
1032	OR5PnP	H38g88 2						FL
1033	OR10AEn P	H38g88 3						
1034	OR3A2	H38g88 4		OST953	OR17-228	+	yes	FL
1035	OR10Jn	H38g88 5					yes	FL
1036	OR1D3P	H38g88 6		OST954	OR17-23			FL
1037	OR10Jn	H38g88 7					yes	FL
1038	OR1D4	H38g88 8			OR17-30	+	yes	FL
1039	OR5GnP	H38g88 9						FL
1040	OR4SnP	H38g89 0						FL
1041	OR5GnP	H38g89 1						FL
1042	OR9HnP	H38g89 2						FL
1043	OR1A1	H38g89 3			OR17-7	+	yes	FL
1044	OR1A2	H38g89 4			OR17-6	+	yes	FL
1045	OR8AnP	H38g89 5						FL
1046	OR1P1P	H38g89 6			OR17-208	+		FL
1047	OR7E12P	H38g89 7		OST955	AC000378-A;OR11- 3;hg1058	+		FL
1048	OR4A1P	H38g89 8			OR11-30			FL
1049	OR10G3	H38g89 9			AE000658-D		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1050	OR10G1P	H38g90 0			AE000658-C			FL
1051	OR10G2	H38g90 1			AE000658-B		yes	FL
1052	OR5Tn	H38g90 2					yes	FL
1053	OR7EnP	H38g90 3						FL
1054	OR7EnP	H38g90 4						FL
1055	OR4AnP	H38g90 5						FL
1056	OR4C1	H38g90 6			HSHTPCR11	+		FL
1057	OR1EnP	H38g90 7						
1058	OR7KnP	H38g90 8						FL
1059	OR4CnP	H38g90 9						FL
1060	OR1RnP	H38g91 0						FL
1061	OR5AUn	H38g91 1					yes	FL
1062	OR4Cn	H38g91 2					yes	FL
1063	OR4Cn	H38g91 3					yes	FL
1064	OR13DnP	H38g91 4						FL
1065	OR5n	H38g91 5	DSU116			+		
1066	OR2Hn	H38g91 6	DSU150			+		
1067	ORn	H38g91 7	DSU151			+	put	
1068	ORn	H38g91 8	DSU17			+		
1069	ORn	H38g91 9	DSU18			+		

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1070	ORn	H38g92 0	DSU35			+		
1071	OR6Fn	H38g92 1	DSU41			+		
1072	ORn	H38g92 2	DSU49			+		
1073	ORn	H38g92 3	DSU50			+		
1074	OR10An	H38g92 4	DSU57			+		
1075	ORn	H38g92 5	DSU58			+		
1076	OR2Ln	H38g92 6	DSU59			+		
1077	OR10Jn	H38g92 7	DSU60			+		
1078	OR1Kn	H38g92 8	DSU63			+		
1079	OR10Dn	H38g92 9	DSU7			+		
1080	ORn	H38g93 0	DSU32			+		
1081	OR2Ln	H38g93 1	DSU38			+		
1082	ORn	H38g93 2	DSU62			+		
1083	ORn	H38g93 3	DSU48			+		
1084	OR2n	H38g93 4	DSU111			+		

Table 2

5

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
153	OR10D3	0	11	137.96	.....SDVISV	69	M	AC074177.4	12106 ... 13038
154	OR7EnP	4	4	11.58	MVACGVLDLHIIDSFAL	53	R	AF091580.1	7 ... 663
155	OR1D5	0	17	3.75	LVVTNLLYLLLLTGIFT	49	M	AF073967.1	2 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
156	OR10Nn P	4	11	138.02	LQGSGVVHILFGNVLAT	82	M	AC074177.4	159287 ... 158526
157	OR2F1	0	7	148.62	LLGGFTSSVQIISSLLT	56	M	AF073974.1	41 ... 649
158	OR7EnP	7	4	11.58	MAGGELLDLHILPALGL	54	M	AF073989.1	547 ... 1515
159	OR8FnP	6	11	137.96	LLVICEMGAHCVCNIF	75	M	AC069561.1 0	51687 ... 50743
160	OR2Q1P	2	7	148.62	LLCGFSANMEIVSGVIL	49	M	AC020865.3	190954 ... 189954
161	OR2W1	0	6	33.74	LMGSCMINVLLVLGIVT	88	M	AF102516.1	52 ... 669
162	OR7EnP	7	4	11.58	MVACGVLDLHITHSFGL	53	R	AF091580.1	7 ... 663
163	OR6B1	0	7	148.62	LIMCCGIIAKFDLAIFF	61	M	NM_010983. 1	178 ... 975
164	OR10Kn	0	1	154.34	MLGSSACVVTILGALI	79	M	AC073778.1	168744 ... 167803
165	ORnP	13	11	138.02	VPYCIGGHLICLSLSS	33	M	AC074177.4	12106 ... 13038
166	OR4F2P	4	6	186.49	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
167	OR7EnP	3	4	11.58	MVACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
168	OR1F2P	0	16	6.15	MSADNGVNLHLIEAVTT	72	R	M64377.1	1 ... 939
169	OR2P1P	7	6	33.74	FGGSCMSNQSALVRXSV	48	M	NM_008762. 1	1 ... 936
170	OR7E43 P	5	4	5.57	MAGGELFDLHIMPAFGL	54	M	AF102536.1	22 ... 669
171	OR4F1	4	6	0.23	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
172	OR7E55 P	5	3	89.94	MAGDEFDLHILPAFGL	53	M	AF073989.1	547 ... 1515
173	OR13Dn	0	9	86.89	MLGSCWITLQLMTNSLI	61	M	AC023789.5	371264 ... 372220
174	OR4CnP	3	16		AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
175	OR10D1 P	1	11	137.96	LHGCGGFQFLGSMPS	83	M	AC074177.4	128803 ... 129726
176	OR4Cn	0	16		LHGGIVGHVQLVNSICL	86	M	AB030895.1	1 ... 924

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
177	OR8GnP	0	11	137.96	LSAICGLGIHFVLSNIM	73	M	AC074177.4	106297 ... 105361
178	OR13CnP	2	9	86.85	MFGACGGNLQLMASFLG	82	M	AJ251154.1	2703 ... 1747
179	OR4CnP	5	16		LHEAIVLHIQFINSCL	61	M	AF102522.1	40 ... 660
180	OR13Cn	0	9	86.81	MLGTCGINVQFMATFIT	69	M	AJ133425.1	61 ... 1014
181	OR4CnP	0	16		LHGGIMGHIQLVNSMCL	63	M	AB030895.1	1 ... 924
182	OR51Bn	0	11		AHSVSGRSPVRPLITIL	76	M	AF071080.2	15931 ... 16851
183	OR7E5P	2	11	51.76	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
184	OR13Cn	0	9	86.77	MFGSCVSNVQLMSNELL	71	M	AJ251154.1	2703 ... 1747
185	OR4Sn	0	16		LHGGIAAHLQLVNSISA	56	M	AB030895.1	1 ... 924
186	OR51BnP	4	11		VHYPEWRSPPPPLVIFL	72	M	AF071080.2	15931 ... 16851
187	OR6JnP	1	14	2.72	CFGTFFGSFPLDLSVIC	50	R	M64378.1	1 ... 933
188	OR51Bn	0	11		SHAISGRSPISPQTTVL	76	M	AF071080.2	26330 ... 27262
189	OR7EnP	2	11	71.8	MFACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
190	OR2An	0	6	144.32	TSVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
191	OR7E22P	3	3	89.94	MVACDVLDLHIIDSFGL	56	M	AF073989.1	547 ... 1515
192	OR7E4P	2	11	71.8	IVACDVLDLHIMHSFGL	55	M	AF102536.1	22 ... 669
193	OR7E66P	9	3	89.94	MAGGELLFLHIMPAFGL	55	M	AF073989.1	547 ... 1515
194	OR6Mn	0	11	138.18	TFGTFGGSFVNLSVIS	50	M	NM_010991.1	1 ... 939
195	OR2ALnP	11	11	112.69	ILGTCASNFDFFNHLLL	32	M	AL359352.1	85325 ... 86251
196	OR6MnP	2	11	138.18	TGGTFGGSCPVNLSILT	50	M	NM_010991.1	1 ... 939
197	OR4D1	0	17	60.7	IHGGVAGHVQLMNSLVI	90	M	AC019272.4	62255 ... 61317
198	OR5D2P	3	11	51.09	LCVVTWCTLFTSANES	48	M	AC073947.3	29192 ... 30115

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
199	OR7E38P	7	7	95.91	MAGGELFHLHIMPAFGL	55	R	AF091580.1	7 ... 663
200	OR4D2	0	17	60.7	IHGGVAGHVQLKNSLDV	89	M	AC019272.4	183633 ... 182701
201	OR7E7P	4	7	95.91	MIACGVLDLHIIDSFGL	56	R	AF091580.1	7 ... 663
202	OR5AHnP	0	19	68.97	.....RSGIMC	77	M	AC020957.2	48184 ... 49107
203	OR2U2P	5	6	33.53	LVYSCIVNIPYTMCIYV	49	M	AC044846.2	105668 ... 104736
204	OR2U1P	2	6	33.53	LVCTCMINILCCVVIFA	54	M	AF102516.1	52 ... 669
205	OR2H2	0	6	33.19	ILGTCVIEVQSVASILV	89	M	AL078630.1	41097 ... 40165
206	OR2H5P	7	6	33.19	FLGTCVIEVQSMASILV	84	M	AL078630.1	41097 ... 40165
207	OR2In	0	6	33.19	LLGSCASNAQLMARILL	74	M	AL078630.1	151152 ... 150391
208	OR11HnP	5	13		IFNTCLCWIPLCLSVIG	60	M	AF121972.1	171 ... 1109
209	OR7EnP	6			AAACDVIDLHITHSFGL	56	M	AF073964.1	41 ... 649
210	OR9In	0	11	54.06	FTAGCGCGLRCIFGVIA	50	R	AF091579.1	7 ... 663
211	OR2AFnP	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
212	OR13KnP	5	X	140.17	MFGMCVIIHIGIGTLL	43	R	L34074.1	73 ... 1011
213	OR13Cn	0	9	86.77	MFGSCVSNVQLLSNFL	68	M	AJ251154.1	2703 ... 1747
214	OR13Fn	0	9	86.77	MLGSCGTTVESMISLLM	55	M	AJ133428.1	61 ... 1017
215	OR9Qn	0	11	54.08	FTGSCGASVRSIFAVIA	47	M	AF146372.1	509 ... 1456
216	OR2TnP	1	1	254.77	ILIGFGDMLVMCCMLI	71	M	AF102527.1	22 ... 669
217	OR4Kn	0	14	0.08	IHVGMIVHSHFTNSISS	56	M	AF259072.1	104176 ... 105099
218	OR2B8P	0	6	31.6	LLGSCTINLQLLVSILV	62	R	L34074.1	73 ... 1011

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
219	OR2Tn	0	1	254.77	MLAGVALDLLITCCMLT	57	M	AF102527.1	22 ... 669
220	OR4Kn	0	14	0.08	IHTGIAMHSQFMTSIAS	53	M	AF259072.1	104176 ... 105099
221	OR2A4	0	6	144.76	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
222	OR7EnP	6	2	161.53	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
223	OR4Kn	0	14	0.08	MHGGILVHSQFMTSIAV	57	M	AF259072.1	104176 ... 105099
224	OR13InP	6	9	86.85	MYGSCVLNNVVIGKTLL	41	M	AJ251155.1	15491 ... 16423
225	OR7EnP	8	2	161.53	MVACDVLDLHIFFDFGL	54	M	AF073989.1	547 ... 1515
226	OR6Jn	0	14	2.72	CFGTFGGSFPLDLVIC	50	R	M64378.1	1 ... 933
227	OR4Mn	0	14	0.08	LHGAMLGHIQLMSSISV	54	M	AC019272.4	183633 ... 182701
228	OR4VnP	10	11	51.09	IHGIIVLHFQMVNSFAV	50	M	AB030896.1	1 ... 906
229	OR6Xn	0	11	138.36	AFGTFSVICQLGATVIG	46	M	AF106007.1	178 ... 975
230	OR51Gn	0	11	3.7	LHSSSSRLPLLGVVTVV	55	M	NM_013617.1	1 ... 921
231	OR6EnP	3	14	2.72	SFGTFCTLIPLGIASLG	82	M	NM_010991.1	1 ... 939
232	OR4NnP	2	14	0.08	LHGGGAGHIQLMNSMTL	54	M	AC019272.4	62255 ... 61317
233	OR6MnP	7	11	138.18	IFGTFGGARLVXSMTV	37	R	M64378.1	1 ... 933
234	OR4Nn	0	14	0.08	LHGGGAGHIQLMNSMTL	57	M	AC019272.4	62255 ... 61317
235	OR4Cn	0	11	51.09	LHGGIGGHIQFVNSMCA	65	M	AF102522.1	40 ... 660
236	OR4KnP	4	14	0.08	IHAGMGTHSQFMDSMGT	51	M	AF259072.1	104176 ... 105099
237	ORnP	8	11	137.59	AIAITVVVAHAAAGVVA	35	M	AC069559.8	73704 ... 74636
238	OR5D3	0	11	51.15	FCVVTAWCTYFISANES	46	R	U50948.1	34 ... 978
239	OR2G1P	6	6	33.53	LLGSCVSNIQVLASLLL	84	M	AL359352.1	85325 ... 86251



SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
240	OR4Kn	0	14	0.08	IHTGMIVHSQFINSLS	51	M	AF259072.1	104176 ... 105099
241	OR8BnP	2	11	137.59	LCVFSGMGAHNIVVGIV	68	M	AC069559.8	120212 ... 119283
242	OR2B2	0	6	31.47	LLGSCASNQWLISFLI	89	R	L34074.1	73 ... 1011
243	OR7EnP	3	2	73.87	MVACDVLRLIIDSFGL	54	M	AF073989.1	547 ... 1515
244	OR4KnP	3	14	0.08	IHTGIVVHSQFMTSIAI	57	M	AB030896.1	1 ... 906
245	OR2AD1P	6	6	33.87	FLGACTSSIVLVFGFLV	51	M	AL136158.1 4	162423 ... 161461
246	OR1AAnP	8	X	140.17	MIVDNTIVLHLIIGVII	48	M	AC068902.1 1	144125 ... 143193
247	OR1E3P	1	17	2.99	MLGVSLHLHLMMGILI	74	R	M64392.1	1 ... 942
248	OR8BnP	3	11	137.59	FCVFSGMGAHNIVVGIV	63	M	AC069561.1 0	96653 ... 95690
249	OR5Hn	0	3	104.18	FAGTCFGHIHLVLSIQF	55	R	AF091575.1	52 ... 663
250	OR1G1	0	17	2.99	LMVMAAMHLHLITGTGI	56	R	M64392.1	1 ... 942
251	OR5HnP	2	3	104.18	FAVTCGGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
252	ORnP	5	X	140.17	MLVTCSHHFLSFTGIWS	36	R	U50948.1	34 ... 978
253	ORnP	11	X	140.17	LIVTFAKITTTQDHHHH	29	M	AC069561.1 0	127636 ... 126698
254	OR4PnP	2	11	51.09	LHGDIAHSQLVNSISL	51	M	AB030895.1	1 ... 924
255	OR13Hn	0	X	140.17	TLATCTTVAMLITSTLL	47	M	AJ251154.1	35662 ... 36615
256	OR7D1P	5	19	11.38	VMAGTAIFVHLLATLGF	64	R	AF091580.1	7 ... 663
257	OR4KnP	2	18	47.77	IHNGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
258	OR7E24	1	19	11.38	MVACDLIDLHIIMGFGL	60	R	AF091580.1	7 ... 663
259	OR51NnP	2	11	3.6	LHGFSARSPSLGVLTV	49	R	AF079864.1	632 ... 1576
260	OR7E18P	6	19	11.38	VAGCOLLDLHIMLAFL	59	M	AF102536.1	22 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
261	OR7E19 P	2	19	11.38	MYVCDVLNLHIMDSFGL	58	M	AF073989.1	547 ... 1515
262	OR7E41 P	7	11	14.36	IVVCDMLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
263	OR2R1	3	7	148.69	LLGGFVVNMELISSVLV	77	M	AF073974.1	41 ... 649
264	OR10AC nP	7	7	148.69	MVGGCGRVGLLLACLLL	46	M	AC073778.1	168744 ... 167803
265	OR51Ln	0	11	3.79	LHTFSARVPTLGVVTLV	54	R	AF079864.1	632 ... 1576
266	OR52Jn P	3	11	3.79	MHTGSSRLPILGVALDA	57	M	AF121979.1	53 ... 1106
267	OR9LnP	9	8	45.22	TVVNNFFFFFFFIDLIA	37	M	AC069561.1 0	147203 ... 146274
268	OR51Pn P	4	11	3.79	MHSISARLPALGVVSML	48	M	AF071080.2	2641 ... 1697
269	OR5HnP	4	3	104.18	FAVTCLGHIHFFFSIQL	50	R	AF091575.1	52 ... 663
270	OR51An	0	11	3.79	EHSVSVKLPFTYFGCLV	48	R	AF079864.1	632 ... 1576
271	OR5HnP	6	3	104.18	FAVTCLGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
272	ORnP	11	17	17.43	LLPCILSIALLYYYYYY	27	M	AL359352.1	9138 ... 8177
273	OR52En	0	11	3.79	MHTGSARFPFFYCAILF	57	M	AF121979.1	53 ... 1106
274	OR5Hn	0	3	104.18	FVVTCLGHIHFVFAVQF	53	R	AF091575.1	52 ... 663
275	OR4CnP	3	11	50.21	VHRGVVGHIQFVNSICL	73	M	AF102522.1	40 ... 660
276	OR52En	0	11	3.79	MHTLSGRFPSLYCANLF	60	M	AF121979.1	53 ... 1106
277	OR10Dn	0	11	138	LHGCGGIHILLGNVLSI	86	M	AC074177.4	12106 ... 13038
278	OR5HnP	2	3	104.18	FVVTCLGHIHFVFAIQF	54	R	AF091575.1	52 ... 663
279	OR13An	0	10	47.91	LTASLALNIHLIADYGV	67	M	AF102520.1	16 ... 669
280	OR5HnP	2	3	104.18	FGGTCLGHIHILLSIQF	57	R	AF091575.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
281	OR5Kn	0	3	104.47	FCETCGAHIHLFSVQF	45	M	AC069559.8	36251 ... 35322
282	OR7EnP	9	21	17.99	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
283	OR4DnP	6	8	77.48	IHGGVAGHVQVMNSLVI	87	M	AC019272.4	62255 ... 61317
284	OR2ARn P	0	3	30.89	MLGSC.....	71	M	AJ251154.1	56533 ... 57369
285	OR7E29 P	4	3	136.03	MAGGELLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
286	OR4CnP	3	11	51.12	AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
287	OR5PnP	2	11	6.93	LVGTCVGNTFCPSSIIV	74	M	AF121977.1	262 ... 1197
288	OR7EnP	5	3	136.04	MVACGVLDLHIIGSFGL	52	R	AF091580.1	7 ... 663
289	OR56An	0	11	4.73	MNLPSFRLPILQAGLLS	41	M	AF121975.1	50 ... 1012
290	OR56An P	9	11	4.73	KNQAFFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
291	OR5Pn	0	11	6.89	LAATCVAISYSLSSIIV	63	M	AF121977.1	262 ... 1197
292	OR7E53 P	5	3	136.04	MAGGEFPDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
293	OR5Pn	0	11	6.89	LVGTCMGNTFCPSSIIA	83	M	AF121977.1	262 ... 1197
294	OR52Ln	0	11	4.73	MHSSSVRLPFLGMAVIL	59	M	AF121976.2	474 ... 1307
295	OR5E1	3	11	6.89	LGATXGYNIQLFSNLG	51	R	U50948.1	34 ... 978
296	OR56An P	3	11	4.73	MNLASFRMAILPPPPPP	39	M	AF121976.2	474 ... 1307
297	OR4KnP	2	8	88.25	IHTGMIVHSQFIDS...	57	M	AB030896.1	1 ... 906
298	OR52Ln	0	11	4.73	MHSSSVRLPFLGVAVVL	59	M	AF121976.2	474 ... 1307
299	OR7EnP	1	4	74.82	MVF.....	55	R	AF091580.1	7 ... 663
300	OR52Xn P	5	11	4.73	MHSASLXLSFLAVALGG	51	M	AF121976.2	474 ... 1307
301	ORnP	13	4	74.82	STGCKGRKXLKLVRFQ	24	R	M64386.1	130 ... 975
302	OR56An	0	11	4.73	MNLTSFRVPVLQAGLLS	84	M	AF121981.1	89 ... 475

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
303	OR56AnP	10	11	4.73	LI...GMMXNL...KKK	60	M	AF121981.1	89 ... 475
304	OR1R1P	5	17	3	MVGISAVHLHLIEGVVA	48	M	AF073967.1	2 ... 649
305	OR52EnP	2	11	3.79	MHTGSGRSPFLYGAILF	64	M	AF121979.1	53 ... 1106
306	OR51AnP	4	11	3.7	EHTVALKLPLLGAGSTL	46	R	AF079864.1	632 ... 1576
307	OR51An	0	11	3.7	EHSVSVKLPPTYFGCLV	48	R	AF079864.1	632 ... 1576
308	OR4CnP	1	11	51.12	VHGGVVGHVQFVNSICL	75	M	AF102522.1	40 ... 660
309	OR52JnP	9	11	3.79	MHTGACRFPI LGVVYLN	58	M	AF121979.1	53 ... 1106
310	OR4RnP	9	11	51.12	.....GGGVXSVNGNYL	66	M	AF102522.1	40 ... 660
311	OR52JnP	0	11	3.79	MHTGACRLPMLGVVFN	58	M	AF121976.2	474 ... 1307
312	OR4CnP	3	11	51.12	VHGGGVGHIQFINSICL	76	M	AF102522.1	40 ... 660
313	OR51AnP	2	11	3.79	EHSASAKLPPTYFVTGL	83	M	AF121985.1	2 ... 478
314	OR7EnP	15	12	93.55	IVVCDLLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
315	OR5MnP	2	11	52.17	CIVLHVYLMERMVASNQ	54	M	AF102528.1	52 ... 669
316	OR10ABnP	1	11	6.93	MLASCAVFCITILSVLG	47	M	AC073778.1	168744 ... 167803
317	OR52SnP	2	11	3.79	MHSTSARLPHLSVATGV	54	M	AF121976.2	474 ... 1307
318	OR5Mn	0	11	52.14	CIVHIFYTAAWMLANFY	49	R	AF091579.1	7 ... 663
319	OR10Sn	0	11	138.1	LHASCIIHIHLMSIVAG	61	M	AF259072.1	32953 ... 32000
320	OR5MnP	4	11	52.14	CIVHIFYTTAWMLANFY	48	R	AF091579.1	7 ... 663
321	OR10Gn	0	11	138.1	LHGSCGSHVQLIDIVAG	61	M	AF259072.1	55611 ... 54658
322	ORnP	20	11	29.15	ILGIYEGSAHYFIILFL	33	M	AL365337.1	192661 ... 191711
323	OR5MnP	2	11	52.19	CIVIIYGSMWVANLS	54	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
324	OR10GnP	10	11	138.1	LYGSCWGHLPYVIKFT	30	M	L14567.1	17 ... 667
325	OR10TnP	1	1	154.34	LVACCACTIVLILSVLV	57	M	X92969.1	8035 ... 8961
326	ORnP	16	11	52.17	LAAPLLLVFVLAASAAA	33	R	M64376.1	1 ... 999
327	OR10RnP	11	1	154.5	MLAVFTICVFLIGGALV	47	M	AC023611.2	108224 ... 107271
328	OR5MnP	2	11	52.16	CIVHLVYTMWMMVANFY	49	R	AF091579.1	7 ... 663
329	OR7EnP	4	8	6.68	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
330	OR10Tn	0	1	154.27	LLACCLTIVALLLSVIV	58	M	AC012302.5	54283 ... 55224
331	OR1E1	0	17	3.04	MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
332	OR5BKnP	4	12	42.11	STGGAIATMDFLSQWGL	46	M	AF073965.1	2 ... 643
333	OR5MnP	3	11	52.17	CIVHIVYTMWMMVANLF	48	R	AF091579.1	7 ... 663
334	OR3A3	0	17	3.06	LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
335	OR10ADnP	1	12	42.11	TFGVCTFNFLIIDAVIS	44	M	AF247657.1	1 ... 945
336	OR10Rn	0	1	154.5	MLAICAGATVLICGVLV	56	M	AC073778.1	168744 ... 167803
337	OR5TnP	4	11	51.94	MCGTCAAHIHAFFVIEV	51	M	AF121977.1	262 ... 1197
338	OR4GnP	15	7	0.23	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
339	OR6Yn	0	1	154.5	LVVCYGCTIKFDLAVII	61	M	NM_010983.1	178 ... 975
340	OR1E2	0	17	3.15	MLSDSLLHLHLIMGILI	80	R	Y07557.1	1 ... 942
341	OR8Hn	0	11	51.94	MVGACGINVNWILATLV	51	M	NM_013728.1	1 ... 948
342	OR4Fn	0	7	0.23	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
343	OR10Kn	0	1	154.27	MLGCSACVIIILCVLI	83	M	AC073778.1	168744 ... 167803
344	OR7LnP	11	X	140.17	MLGVCGHGTNLXFFFFI	32	M	AL133160.1	63932 ... 64759
345	OR8InP	7	11	51.94	MVCCMINVSVSLATLG	44	R	M64386.1	130 ... 975

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
346	OR10Rn P	0	1	154.5	MLAVCTSI VGFIFGV LV	54	M	AC073778.1	168744 ... 167803
347	OR2AFn P	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
348	OR8Kn	0	11	51.94	LEIILVYVFLKIFSNLF	55	M	AF102528.1	52 ... 669
349	ORnP	7	10	127.57	S.CCCLLTYYIIHHHHH	31	M	AC020958.1	164590 ... 163746
350	OR8KnP	10	11	51.94	MIIILYQMVKIFSNLF	35	M	AC073945.4	152209 ... 153150
351	OR51Hn	0	11	3.6	MHGISSRPVPLGVVTL	49	R	AF079864.1	632 ... 1576
352	OR7EnP	5	3	136.03	MVACGVLDLHIIDSFGL	51	M	AF073989.1	547 ... 1515
353	ORnP	8	3	56.17	LLLLFLIEQH.....I	32	R	M64376.1	1 ... 999
354	OR5BMn P	20	3	103.93	KXNKCTLSSSLMVFIQF	30	M	AF146372.1	509 ... 1456
355	OR10Gn P	0	11	138.1	LHGCCGGHFQFTDILAT	63	M	AF259072.1	55611 ... 54658
356	OR2Yn	0	5	209.23	LLGSCAANIQLMARVVV	74	M	AC044846.2	139468 ... 138536
357	OR10Dn P	1	11	138.1	LHGCCGGHVLLSNVVAM	66	M	AC074177.4	128803 ... 129726
358	OR3BnP	7	X	158.48	IHAPSILNTYLLSFVAA	37	M	AL136158.1 4	29455 ... 30402
359	OR8Dn	0	11	138.1	LCVICAVDIHCIIGNMA	62	R	X80671.1	203 ... 1129
360	OR5RnP	0	11	52.13	LLMICVYVFHIIFADMS	68	M	AF102528.1	52 ... 669
361	OR10Gn	0	11	138.1	LHGSCGSHVQLINIVAG	58	M	AF259072.1	55611 ... 54658
362	OR5BDn P	12	11	53.74	MTGTCVVIHRALSSITP	39	M	NM_013728. 1	1 ... 948
363	OR5ALn P	1	11	52.13	VIVVLSYVQALIANTC	52	M	AC073947.3	29192 ... 30115
364	OR52Hn P	3	11	4.15	LHFVSGRVPCLGVPVT	59	M	AF121975.1	50 ... 1012
365	OR10Gn	0	11	138.1	LHGCGSSHVQLITVVAG	56	M	AF259072.1	55611 ... 54658

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
366	OR5Mn	0	11	52.17	CIVHIVYTMEWMVANLF	52	M	AF146372.1	509 ... 1456
367	OR51Mn	0	11	4.15	MHSFSIRAPILGVVTVL	50	M	NM_013617.1	1 ... 921
368	OR6Tn	0	11	138.1	SFGTFAAWCPLALSVLG	52	M	NM_010991.1	1 ... 939
369	OR6DnP	5	10		SLGSFVVLGLKALVVLT	69	R	AF034903.1	85 ... 1053
370	OR4B1	0	11	45.36	IHGVIGGHIQVVSFSF	62	M	AF102522.1	40 ... 660
371	OR5ALnP	4	11	52.13	VISVVGMIQALIANVC	50	M	AF146372.1	509 ... 1456
372	OR51Qn	0	11	4.15	FHSFSACAPSLGLAIIV	49	M	NM_013617.1	1 ... 921
373	OR4Dn	0	11	138.1	LHGGIAGHVQLMNNVTM	63	M	AC019272.4	62255 ... 61317
374	OR52Nn	0	11	4.58	MHTGSLRLPSLGAIGF	52	M	NM_013619.1	118 ... 969
375	OR4Xn	0	11	45.36	MHGGAIHGQLINGISV	58	M	AB030896.1	1 ... 906
376	OR8Jn	0	11	52.03	LLIVVLYTVVYVSANVG	77	M	X89682.1	2 ... 472
377	OR51JnP	2	11	4.15	MHSMSIKLPLLGIVTFL	46	M	AF071080.2	15931 ... 16851
378	OR10Gn	0	11	138.1	LHGSCSSHVQLIDIVAG	60	M	AF259072.1	55611 ... 54658
379	OR52En	0	11	4.58	MHTGTVRLPFLGVIIID	66	M	AF121979.1	53 ... 1106
380	OR4Xn	0	11	45.36	LHGGIIGHAQLINGLSI	64	M	AB030895.1	1 ... 924
381	OR10A2	1	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
382	OR5Mn	0	11	52.14	CIVHVYVICWMIANFY	49	R	AF091579.1	7 ... 663
383	OR52En	0	11	4.58	MHTGSVRFPFLISVVGI	59	M	AF121979.1	53 ... 1106
384	OR8Kn	0	11	51.94	LLIGLIYILVKIFADLS	53	M	AF146372.1	509 ... 1456
385	OR10An	0	11	5.66	MFGACASVVQWAATFIF	89	M	AF247657.1	1 ... 945
386	OR8LnP	3	11	52.13	LIVMSYVLQLLANTF	51	M	AF102528.1	52 ... 669
387	OR5BPnP	8	11	52.82	VVVVVGSI VPPVGLHL	43	R	U50948.1	34 ... 978
388	OR52Nn	0	11	4.58	MHTGSARLPFLGAIGF	54	M	AF121976.2	474 ... 1307

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
389	ORnP	7	11	45.36	WWWIALLR.AAAAAK	28	M	X89686.1	32 ... 472
390	OR8JnP	1	11	51.94	LLIVILQTTVCVFSNLF	99	M	X89682.1	2 ... 472
391	OR5Mn	0	11	52.24	CIVIFVYNSQLMVATLS	50	R	AF091579.1	7 ... 663
392	OR52En	0	11	4.58	MHTVSIRMPLLGSILL	66	M	AF121979.1	53 ... 1106
393	OR5Tn	0	11	51.94	VCGTCAAHIALFVIEV	52	M	AF146372.1	509 ... 1456
394	OR52NnP	5	11	4.58	MHTGSVQLPFLGAAIGF	51	M	NM_013619.1	118 ... 969
395	OR4B2P	6	11	45.36	IFGIIGRHVQVVNSELS	53	M	AB030896.1	1 ... 906
396	OR51KnP	6	11	4.15	MHSCSGKLP LLGIVNFL	51	M	NM_013617.1	1 ... 921
397	OR52QnP	10	11	4.58	MYTGSVRFPFLFVAVGI	45	M	AF121979.1	53 ... 1106
398	OR4Fn	0	15	86.21	IHGGMIIHQFVNSISA	50	M	AF102522.1	40 ... 660
399	OR11MnP	1	12	41.92	FSAACGSSFTL.....	48	M	AL359381.1	175785 ... 176720
400	OR52Nn	0	11	4.44	MHTGSARLPFLGVAIGF	57	M	NM_013619.1	118 ... 969
401	OR56An	0	11	4.58	MNLASFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
402	OR5AwnP	14	X		LXADFTSNLPTTSSNVV	39	R	X80671.1	203 ... 1129
403	OR52Nn	0	11	4.51	MHTGSARLPFLGVAIGF	55	M	AF121976.2	474 ... 1307
404	ORnP	15	X		ISCIFELTLPLPSNVNV	31	M	AC073947.3	29192 ... 30115
405	OR52EnP	6	11	4.58	VHSVSVRMPILGNIILL	62	M	AF121979.1	53 ... 1106
406	OR5BHnP	9	X		MVASCGGKTVSLCGTLT	40	M	NM_013728.1	1 ... 948
407	OR4QnP	1	15	1.66	IHGAMAGHMQLMNSLSV	60	M	AC019272.4	62255 ... 61317
408	OR51En	0	11	3.04	MHSGSARLPFLGVIAIL	60	R	AF079864.1	632 ... 1576
409	OR11KnP	2	15	1.66	FSGYGFCITLLITFVFI	53	M	AF121972.1	171 ... 1109
410	OR12D1P	1	6	33.02	LHGSATIHLMSTGIAG	76	M	AL133159.4	16108 ... 15185



SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
411	OR4NnP	3	15	1.61	LHGGGAGHIQLMNSMTM	55	M	AC019272.4	62255 ... 61317
412	OR11A1	0	6	33.02	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
413	OR10C1	0	6	33.02	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
414	OR2H1	0	6	33.02	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
415	OR9RnP	8	12	59.71	LAVGGGCNIQFLLSITT	54	R	AF091579.1	7 ... 663
416	OR4FnP	0	7	0.53	.....VLHFQFVNSICG	50	M	AB030896.1	1 ... 906
417	OR7D4	3	19	11.31	VMAGTAIFVHLLATLGF	67	R	AF091580.1	7 ... 663
418	OR7E25 P	3	19	11.31	MIACSVLDLHIVIGFGL	61	R	AF091580.1	7 ... 663
419	OR2D2	0	11	5.69	LLGCCGSVVDFITGILI	65	M	AF073987.1	2 ... 649
420	OR10An	0	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
421	OR2WnP	3	1	254.49	LLGGCVCQGHVVLAVVS	54	R	L34074.1	73 ... 1011
422	OR7E16 P	8	19	11.31	IAGCDLLDLHIMLALGL	60	M	AF102536.1	22 ... 669
423	OR52Pn	0	11	4.44	MHCMSARLPCLGAAVIV	59	M	AF121976.2	474 ... 1307
424	OR6AnP	4	11	5.66	LLGCCGGIVKLDLAILG	94	R	M64386.1	130 ... 975
425	OR7D2	0	19	11.24	VMPITVITLHLIMTLGF	61	R	AF091580.1	7 ... 663
426	OR52Un P	3	11	4.44	LHSASVRFPMLGVAVAY	52	M	AF121976.2	474 ... 1307
427	OR2AGn	0	11	5.6	MLGGDTLSIYYVMGFLP	55	M	AF102527.1	22 ... 669
428	OR7G3	0	19	11.24	ILVGNLVDLHMVVT LGV	64	R	AF091580.1	7 ... 663
429	OR56Bn P	3	11	4.44	IHVGSFRFPVLQLAGMS	41	M	AF133300.1	25713 ... 26573
430	OR2AGn P	1	11	5.51	MLGSDTLIGHYITGFL	55	M	AF102527.1	22 ... 669
431	OR56Bn	0	11	4.44	MHVASFRCSVLQLALMS	39	M	NM_013619. 1	118 ... 969
432	OR6AnP	5	11	5.51	LLGCCGGIVKLDLAILG	93	R	M64386.1	130 ... 975
433	OR4FnP	4	19	63.23	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
434	OR6Wn	0	7	148.04	SFGSFAVSSPQDLSFVT	47	M	NM_010991.1	1 ... 939
435	OR4Mn	0	15	1.59	LHGAMLGHIQLMSSISV	52	M	AF259072.1	104176 ... 105099
436	OR52Yn P	13	11	3.6	VVVVVLQWPVMGMAVDF	29	M	AF133300.1	46551 ... 47498
437	OR11Hn P	2	15	1.78	FFGTCLCWIPCLSVIG	61	M	AF121972.1	171 ... 1109
438	OR9An	0	7	148.04	LSGTFVFSWPALMAILG	46	M	NM_010991.1	1 ... 939
439	OR5Mn	0	11	52.19	CILLFFYDFQLMSANLS	50	M	AC069563.9	129775 ... 130725
440	OR6Vn	0	7	148.04	FFGSFAAAPTSDMAFVS	45	M	NM_010991.1	1 ... 939
441	OR4Nn	0	15	1.61	LHGGGAGHIQLMNSMTL	53	M	AC019272.4	62255 ... 61317
442	OR51An P	4	11	3.6	EHTDSLILPFTGLACMS	43	M	NM_013617.1	1 ... 921
443	OR9PnP	10	7	148.04	FGSNSFEHLVFIHSLLM	39	M	NM_010983.1	178 ... 975
444	OR4H6P	3	15	1.66	MHGCILGHVQLVNSISG	59	M	AF259072.1	104176 ... 105099
445	OR51Fn P	2	11	3.6	MHTFSLRLPLLGLTTI	48	R	AF079864.1	632 ... 1576
446	OR7E1P	3	11	68.1	MVACGVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
447	OR51Tn	0	11	3.6	MHSLSVRFPLAGLQNT	44	R	AF079864.1	632 ... 1576
448	OR2Vn	0	13	104.15	IVVGGSFDIQVICMLF	84	M	AF102535.1	16 ... 669
449	OR51Hn P	7	11	3.6	MHGG SARAPVLGAVIIL	51	R	AF079864.1	632 ... 1576
450	OR51An	0	11	3.6	EHTVSIRLPFTGIAC TL	48	M	AF071080.2	26330 ... 27262
451	OR2AIn P	2	5	209.13	YLGSCLSNFHLMARILL	55	M	AC044846.2	112743 ... 113748
452	OR2F2	0	7	148.74	LLGGFTSNVQIISLLT	54	M	AF073974.1	41 ... 649
453	OR1F12	0	6	31.61	MMANNAINLHMVTVIFV	58	M	AC023167.7	60743 ... 61663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
454	OR7G1P	0	19	11.24	ILAGSLMDVQMIA SFGI	60	R	AF091580.1	7 ... 663
455	OR7G2	0	19	11.24	ILAGNLTNLLMIAAFGV	61	R	AF091580.1	7 ... 663
456	OR1M1	0	19	11.24	MHGISA FITHLIVAVIT	89	M	X89689.1	32 ... 472
457	OR51Un P	1	11	2.89	VTDDN.....	48	R	AF079864.1	632 ... 1576
458	OR52Hn	0	11	4.19	MHFVSGRIPDLGVPTVS	59	M	AF121975.1	50 ... 1012
459	OR1F1	0	16	6.15	MFVDNGVNLHLIEGVM T	75	R	M64377.1	1 ... 939
460	OR10Pn P	0	16	87.09	MIGICTTTTHLVATFII	48	M	AF247657.1	1 ... 945
461	OR4FnP	4	19	7.9	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906
462	OR2T1	0	1	254.77	HLVGFGD LLMCCMLI	92	M	AF102527.1	22 ... 669
463	OR7EnP	9	19	22.8	VAGCDLLDLHIMLAFGL	60	M	AF102536.1	22 ... 669
464	OR51Gn	0	11	3.6	LHSFSVRLPLMGVITVI	57	M	NM_013617.1	1 ... 921
465	OR2Tn	0	1	254.77	MVAGFGLDTFIMCCMLI	67	M	AF102527.1	22 ... 669
466	OR5BGn P	2	11	51.27	AAAAAGGSIHNLFAVEI	52	R	U50948.1	34 ... 978
467	OR5WnP	3	11	51.27	MGADCLVDIHC MFVVAC	51	M	AF146372.1	509 ... 1456
468	OR51Sn	0	11	3.6	MHSVSARLPLLLVLMGD	42	M	AF071080.2	26330 ... 27262
469	OR5WnP	1	11	51.27	.....LVFIES	55	M	AC074177.4	107189 ... 107708
470	OR51An P	3	11	3.6	EHTDSLILLPTGVAMMD	46	M	NM_013617.1	1 ... 921
471	OR5Dn	0	11	51.21	FCGVTGWCILFCIANES	46	M	AF146372.1	509 ... 1456
472	OR7EnP	4	4	5.55	MVACGVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
473	OR51Fn	0	11	3.6	MHTFSSRPVVF GALTTF	53	R	AF079864.1	632 ... 1576
474	OR5Dn	0	11	51.21	YCVVSGWGVLYLFANEC	48	M	NM_013728.1	1 ... 948
475	OR52Rn	0	11	3.6	VHSSSIRWPFMGVAVAF	58	M	AF121976.2	474 ... 1307
476	ORnP	27	11	51.21	FCFAAGQSPGFLCFFFF	23	M	AB030893.1	37 ... 930

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
477	OR7EnP	6	3	121.47	MVACDVLDLHIIDSFSL	57	M	AF073989.1	547 ... 1515
478	OR6Qn	0	11	54.04	LTGACAVTLPLDVSVLA	52	M	NM_010983.1	178 ... 975
479	OR4Fn	0	6	185.89	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
480	OR7EnP	3	13	40.31	FFSP.AAALHIMPAFGL	65	M	X89686.1	32 ... 472
481	OR7En	0	2	95.17	MVACDVLDLHIIDSFGL	57	M	AF073989.1	547 ... 1515
482	OR4Nn	0	14	0.27	LHGAMVGHVQLMNSLSL	58	M	AC019272.4	62255 ... 61317
483	OR2ASn P	7	1	254.77	.....GGGGMICGLLP	43	M	AF102535.1	16 ... 669
484	OR11Hn	0	14	0.33	FFGTCFIGIPYFSVLF	90	M	AF121972.1	171 ... 1109
485	OR2Tn	0	1	254.77	MLAGFGLDMLIMCCMLI	69	M	AF102527.1	22 ... 669
486	OR2TnP	1	1	254.77	CMMGFSGDLLIMCCMLI	77	M	AF102527.1	22 ... 669
487	OR2AKn P	3	1	254.55	TLGGACSNIHVSGILL	50	M	AF102533.1	16 ... 669
488	ORnP	16	12	4.38	VLKSKCWQLPFYMPLLM	25	R	Y07557.1	1 ... 942
489	OR5DnP	4	11	51.21	FCAVTGWSTLFCIANES	48	R	U50948.1	34 ... 978
490	OR7EnP	1	4	5.55	FVACDVLDLHIIDNFGFL	54	M	AF102536.1	22 ... 669
491	OR5L2	0	11	51.27	FCGVVCCCIHLLVANEV	53	M	AF146372.1	509 ... 1456
492	OR5Dn	0	11	51.27	FCVVLVWCTLSLVANES	48	M	NM_013728.1	1 ... 948
493	ORnP	4	9	81.99	..CCCLFFQSIASGTYYI	23	M	AL359381.1	82137 ... 81544
494	OR10Qn	0	11	54.08	MVGSCGLPQLLLVSVLI	50	M	AL365336.1	123248 ... 124093
495	OR9MnP	1	11	51.27	LCVDSGGSIHNLFAVEI	54	M	AC069559.8	73704 ... 74636
496	OR7E62 P	5	2	73.96	MAACDVLDLHTIDSFRL	56	M	AF073989.1	547 ... 1515
497	OR9LnP	13	11	54.06	MFVGCTLVAYGILTMIA	32	M	AC069561.1 0	147203 ... 146274

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
498	OR7E46P	10	2	73.96	MAGVEFCDLHIMPAFGL	54	M	AF102536.1	22 ... 669
499	OR1S1	0	11	54.08	MIVVNILITHLLVGVI	56	M	AC073769.1	133488 ... 132556
500	OR5DnP	0	11	51.21	FCVIMGWCTLSCISSEC	45	M	AC069563.9	111696 ... 112671
501	OR9InP	4	11	54.06	FTASCGGNICCSAVIT	46	R	AF091579.1	7 ... 663
502	OR5Dn	0	11	51.21	FCVVGWCELSLLANES	53	M	AF146372.1	509 ... 1456
503	OR9QnP	4	11	54.08	FTASCGASVRTIFAVMA	47	M	AL365337.1	192661 ... 191711
504	OR51CnP	0	11	3.04	MKTVSARMPMLGAMTVV	51	R	AF079864.1	632 ... 1576
505	OR5WnP	1	11	51.27	FCADCGVDIHL.....	53	M	AC069561.1 0	127636 ... 126698
506	OR9InP	2	11	54.06	FTAGCSCGLHCICAMFA	46	M	AC074177.4	106297 ... 105361
507	OR51AnP	4	11	3.04	MHSVSARVPVPGVVTGL	72	M	X89685.1	2 ... 481
508	OR5L1	0	11	51.21	FCVVVCCCIHLLVANEV	55	M	AF146372.1	509 ... 1456
509	OR7EnP	5	13	50.42	.....VVDLHIMPAFGL	66	M	X89686.1	32 ... 472
510	OR5BLnP	18	11	54.08	ILGNXLENQCIFAMIT	29	R	M64392.1	1 ... 942
511	OR51En	0	11	3.04	MHSASVRFPPLGAIVMV	95	R	AF079864.1	632 ... 1576
512	OR51Dn	0	11	3.04	MHSASSRFPLIGIIVMV	61	R	AF079864.1	632 ... 1576
513	OR52In	0	11	3.04	MHTATARFPLMSGSMVS	46	M	AF121975.1	50 ... 1012
514	OR4KnP	2	18	19.04	IHTGMIVHSQFIDSLSS	56	M	AB030896.1	1 ... 906
515	OR52In	0	11	2.99	MHTATARAPLMSGSMVS	47	M	AF121975.1	50 ... 1012
516	OR4KnP	2	18	19.04	IHNGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
517	OR52MnP	1	11	3.04	MHATSVRYLPIGIGVLL	51	R	AF079864.1	632 ... 1576

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
518	ORnP	7	6	31.58	FLVSCLLLLLLLEGIHW	30	M	AF073964.1	41 ... 649
519	ORnP	9	8	88.25	IXVVVLNIVNMTTIFL	24	M	AC074177.4	149899 ... 148964
520	ORnP	9	10	70.63	YSIVMFYHAHFICELN	26	M	AC068902.1 1	144125 ... 143193
521	ORnP	9	9	70.7	WWWWWSWYGNFDD SITX	26	R	AF091563.1	7 ... 669
522	ORnP	9	5	202.43	FFFFFF.PPPPP.....	27	R	AF034902.1	4197 ... 5177
523	ORnP	10	11	137.77	LLLLWSQFQFLAVVVV	29	R	M64376.1	1 ... 999
524	ORnP	3	11	16.31	NNNNNLLXMNILTLLAI	27	M	AL136158.1 4	29455 ... 30402
525	ORnP	17	11	55.6	LAGNNIYCYHM..LLLL	26	R	M64377.1	1 ... 939
526	OR6Pn	0	1	154.6	LIACCASSMKFDLAMIL	60	M	NM_010983. 1	178 ... 975
527	OR7EnP	3	14	33.48	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
528	ORnP	12	11	138.51	LMCHS.FFFFFFFMMMMM	29	R	AF091573.1	7 ... 663
529	OR7EnP	5	14	33.48	MAGGDFLDLYILPDFGL	55	M	AF073989.1	547 ... 1515
530	ORnP	7	10	127.4	S.CCCLLTYYIHHHHHH	31	M	AC020958.1	164590 ... 163746
531	OR10XnP	2	1	154.6	MLGGCSAITELIISGLG	49	M	AC073778.1	168744 ... 167803
532	OR10Zn	0	1	154.71	MAACCTTFGMVILSVLV	56	M	AC025913.3	108128 ... 109067
533	OR6KnP	2	1	154.73	MYGIVGCTPEWVVHEIT	40	R	M64386.1	130 ... 975
534	OR6Kn	0	1	154.73	MHGIVSCTPEWVIHEIT	44	M	AC027184.3	54955 ... 54017
535	OR1FnP	1	4	97.57	.....IEGVMT	73	R	M64377.1	1 ... 939
536	OR1ABnP	3	19	19.44	MIGISAFNTHLV.....	64	M	AC073769.1	133488 ... 132556
537	OR52MnP	1	11	2.89	MHATSARYLPIGIGVLL	49	M	AF121975.1	50 ... 1012
538	OR1XnP	6	5	202.43	MIANTLGIVHIFAALFA	71	M	AF102530.1	1 ... 666

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
539	OR4FnP	8	16	83.04	QQQQQVIHSQFVNSLTC	46	M	AC019272.4	62255 ... 61317
540	OR52Mn P	5	11	2.89	MHATSVRYLPIGIGVLM	45	R	AF079864.1	632 ... 1576
541	OR2Vn	0	5	209.61	IVVGGSFDIQVICMLF	83	M	AF102535.1	16 ... 669
542	OR2V1P	4	5	209.61	IVVGGSFDIQALCCMLL	90	M	AF102537.1	16 ... 669
543	OR2Zn	0	19	65.55	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
544	OR52Kn P	5	11	2.89	.....AMFIEL	52	M	AF121975.1	50 ... 1012
545	OR10Hn	0	19	19.7	MFGFSWGMVIGLVTAI	75	M	AC023604.2	214343 ... 213396
546	OR2Dn	0	11	5.77	ILGCCRSVVDIFIMGILA	85	M	AF073987.1	2 ... 649
547	OR7EnP	6	2	161.49	VVGCCSSDLHIMPAFGL	64	M	X89686.1	32 ... 472
548	OR11Gn P	4	14	0.27	FFGSCSLWIPVSLSLLI	68	M	AC027184.3	54955 ... 54017
549	ORn P	12	14	0.27	GSCGNSLHHYLMVNIIL	28	M	AF121972.1	171 ... 1109
550	OR11Gn	0	14	0.33	FFGSCNLWIPNFLSPVM	67	M	AF121972.1	171 ... 1109
551	OR11Hn P	5	14	0.33	FTGTAFSFSVSQFLSIIL	68	M	AF121972.1	171 ... 1109
552	OR6Kn	0	1	154.73	MHENGGFIPEDHATII	46	R	AF034897.1	354 ... 1199
553	OR11Hn	0	14	0.33	FFGTCVGCVPCLCFNIIG	71	M	AF121972.1	171 ... 1109
554	OR6KnP	0	1	154.73	MHGNGGFVPEWDHAAIF	46	M	AL365336.1	122764 ... 121784
555	OR11Hn P	2	14	0.33	FFGTCLIGISFFVSFIL	70	M	AF121972.1	171 ... 1109
556	OR6KnP	2	1	154.82	MHGVAGFMPECDRASIT	43	M	AC027184.3	54955 ... 54017
557	OR6Kn	0	1	154.84	MHGISGCLPEWVIHEIA	45	R	AF034900.1	1 ... 963
558	OR2Ln	0	1	254.55	SSGGAGINAHYVSTFLF	53	M	AF102527.1	22 ... 669
559	OR4GnP	8	16	83.04	ICRKMAVHSQFVNSISA	45	M	AB030892.1	1 ... 939

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
560	OR6Nn	0	1	154.84	IHGACGGGVELDINKIA	50	R	M64386.1	130 ... 975
561	OR2LnP	2	1	254.55	SLAVGGINAHY....W	52	M	AF102535.1	16 ... 669
562	OR9A1	0	7	146.91	LLGTLVLSWPALMAIIG	45	M	L14567.1	17 ... 667
563	OR6Nn	0	1	155.69	THGACACCSELDINIII	51	M	AL136158.1 4	29455 ... 30402
564	OR10Hn	0	19		MFGFSCGMVVAGLV TAL	86	M	AC023604.2	245345 ... 246298
565	OR7EnP	4	9	71.72	MVACDVLDLHIMNSFGL	57	M	AF073989.1	547 ... 1515
566	OR2AQn P	5	1	155.69	FCHSCLLLSLLPFFFF	31	M	AL359352.1	55588 ... 56546
567	OR2LnP	3	1	254.55	SMAGAGINAHYVSSFLF	50	M	AF102537.1	16 ... 669
568	OR5ARn	0	11	52.46	FVVDCGASAHLLLCIES	53	R	AF091579.1	7 ... 663
569	OR7EnP	4	9	71.79	TAGGETLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
570	OR10AA nP	2	1	155.69	THGMCAAAPLHV IATC	84	M	AC005992.1 5	9114 ... 8173
571	OR10Jn P	4	1	157.7	MIAICGVVVQSNVSVIV	72	M	X92969.1	8035 ... 8961
572	OR5A1P	0	11	55.81	FVGLCGSIQSNVVVGT	81	M	Y15525.1	1 ... 705
573	OR2AHn P	5	11	52.46	MLGSCISSVILVFSIVI	51	M	AF247657.1	1 ... 945
574	OR10Jn P	4	1	157.7	LLGICGIMVQSNVSVLL	68	M	X92969.1	8035 ... 8961
575	OR56Bn P	2	11	4.93	IHMCSSRLPVLQLVVVS	39	M	AF121975.1	50 ... 1012
576	OR5M1	0	11	52.35	CIVIFIYSSQLMVANLS	49	R	AF091579.1	7 ... 663
577	OR52Wn P	0	11	4.93	MHTASLLAVPLGLSISM	48	M	AF121976.2	474 ... 1307
578	OR5AMn P	5	11	52.35	FIVIIYAYNVQLMVANLC	35	M	AC068904.1 5	113793 ... 114719
579	OR52Bn P	3	11	4.93	MHFVSTQTPVLGVPSVV	89	M	AF121975.1	50 ... 1012
580	OR5MnP	1	11	52.35	CVLLYFWVMQLLSANLV	48	R	X80671.1	203 ... 1129



SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
581	OR5APn P	6	11	52.35	FGAGGALNIHFIFANES	55	R	X80671.1	203 ... 1129
582	OR56Bn	0	11	4.95	IHFCSFRLPVLQALVS	41	M	AF121975.1	50 ... 1012
583	OR5APn	0	11	52.35	FGLGCTANIHMIFSIVS	55	M	AF121977.1	262 ... 1197
584	OR52Bn	0	11	4.93	GHFVSARIPVLGVPMVL	73	M	AF121975.1	50 ... 1012
585	OR9Gn	0	11	52.5	FAAYCVGNIIKMLLNVC	45	M	AC074177.4	106297 ... 105361
586	OR52Kn	0	11	2.86	MHSISARLPLLGVASVL	53	M	NM_013619. 1	118 ... 969
587	OR5MnP	1	11	52.35	FIVIYAYNSQLMVANLC	51	M	AC074177.4	106297 ... 105361
588	OR52Kn	0	11	2.86	MHSISARLPLLGVAIVL	52	M	NM_013619. 1	118 ... 969
589	OR52Kn P	3	11	2.82	MHSISARLPLLGVAIGL	53	M	NM_013619. 1	118 ... 969
590	OR52Bn P	4	11	2.78	IHFISARVPDLGVLTVL	57	M	AF121975.1	50 ... 1012
591	OR2B6P	0	6	31.62	LLGAYATNWLLLVSFHI	79	R	L34074.1	73 ... 1011
592	OR2WnP	7	6	31.61	LLRGCASNVMLAFAIVL	58	M	AF102516.1	52 ... 669
593	OR2AnP	5	7	148.83	TMAHCTCLVHLISSILG	72	M	AF102521.1	22 ... 669
594	ORnP	16	6	31.61	FLVSCMDFMYIVLNNVI	39	M	AF102516.1	52 ... 669
595	OR2LnP	0	1	254.55	STAVAGINAHYVSAFLF	50	M	AF102527.1	22 ... 669
596	OR2W2P	5	6	31.61	LLGGCVCQSYWVLSIVM	55	R	L34074.1	73 ... 1011
597	OR2LnP	1	1	254.55	SLAGA.....	61	M	AF102535.1	16 ... 669
598	OR2B7P	1	6	31.61	LLGGCTTNIQLIVSFLV	59	M	AC044846.2	105668 ... 104736
599	OR2Ln	0	1	254.43	SLGGAGINAHYVSAFLF	53	M	AF102527.1	22 ... 669
600	OR5BFn	0	1	254.77	VVVYLASYMHSISAVGG	46	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
601	OR2LnP	4	1	254.55	SVAGMSMDAHYVSTFLF	47	M	AF102527.1	22 ... 669
602	OR7EnP	3	10	17.14	MVACCVLDLHI.....	51	R	AF091580.1	7 ... 663
603	OR1H1	2	9	106.04	LGADNVIHVHLLVALLA	57	M	AC073769.1	133488 ... 132556
604	ORnP	14	1	254.49	TTTKKSERIYIVSSFLI	24	M	AF102527.1	22 ... 669
605	OR4Dn	0	11	55.81	IHGGIASHIQLMNNVTL	64	M	AC019272.4	183633 ... 182701
606	OR1Ln	0	9	106.04	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
607	OR5AXn	0	1	254.2	L TSAIVIFAYGGVGLSS	47	M	AL136158.1 4	154973 ... 155908
608	OR5An	0	11	55.77	YCGLCGSIIESTVSVGV	64	M	Y15525.1	1 ... 705
609	OR5AYn	0	1	254.2	LVAGILNLLYGSIGYAS	50	M	AL359352.1	126933 ... 127889
610	OR13Gn	0	1	255.42	LTLGMMINVHLVADLAG	59	M	AF102540.1	16 ... 669
611	OR5BBn P	0	11	55.77	YASLCGGSVHPLEAVGG	54	M	Y15525.1	1 ... 705
612	OR9GnP	6	11	52.49	FVXNCAGNIIELMLNIT	47	M	AF121977.1	262 ... 1197
613	OR2TnP	4	1	254.77	HLAGFAGNLLVMCCMLI	75	M	AF102527.1	22 ... 669
614	ORnP	7	1	255.42	PVAGKGAF LHSVESLGS	38	M	AL365337.1	192661 ... 191711
615	OR1Jn	0	9	95.9	MITDSVLSSHLMVG VIL	66	M	AF102524.1	52 ... 669
616	OR2CnP	1	16	6.47	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
617	OR9GnP	2	11	52.49	FAAYCYGNILNLLLNVS	49	M	AL365337.1	192661 ... 191711
618	OR2C1	0	16	6.4	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
619	OR51An P	2	11	4.22	.....	52	M	AF071080.2	26330 ... 27262
620	OR9Gn	0	11	52.49	LCAYCGGNAHNLVVTVS	53	M	AC068904.1 5	165039 ... 165965

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
621	OR52Bn	0	11	2.78	LHFISTRTPILGILTVL	61	M	AF121975.1	50 ... 1012
622	OR1K1	0	9	105.89	MFGVSMVHLYLIEGVVT	58	R	M64377.1	1 ... 939
623	OR51Rn P	3	11	2.78	MHTYSARLPGLGSISLL	47	R	AF079864.1	632 ... 1576
624	OR7EnP	2	13	54.83	MVACDVLDLHILDSFGL	57	M	AF073989.1	547 ... 1515
625	OR52Pn P	3	11	2.82	MHSASARLPPLGAAVVT	55	M	AF121975.1	50 ... 1012
626	OR7EnP	5	9	70.7	MVACDVQYVHSMDSFGL	48	M	AF102536.1	22 ... 669
627	OR7EnP	5	9	70.7	TAGGD.CCCCC.....	43	M	AF073989.1	547 ... 1515
628	OR4KnP	1	21	8.12	IHTGMIVHSQFIDSLSS	57	M	AF259072.1	104176 ... 105099
629	OR4KnP	2	21	8.12	IHNGIVVHSQFMTSTAT	54	M	AB030896.1	1 ... 906
630	OR7EnP	6	9	70.7	.....VFLVHVPFAFGL	58	M	X89686.1	32 ... 472
631	OR51In	0	11	4.15	MHSFSGKTPFVGIVITYM	51	R	AF079864.1	632 ... 1576
632	OR51In	0	11	4.15	MHSMSGRTPLLGVLTFM	56	R	AF079864.1	632 ... 1576
633	OR2AnP	1	7	148.83	TLAICTFL.....	63	M	AF102521.1	22 ... 669
634	OR2A2	2	7	148.83	TLAVCTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
635	OR2AnP	8	7	148.83	TFAACTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
636	OR2Gn	0	1	256.63	LHGSCMSTVQLLASFLV	59	M	NM_008762.1	1 ... 936
637	OR2AnP	0	7	148.83	TLAHCAFFFFL.....	57	M	AF102521.1	22 ... 669
638	OR6Fn	0	1	254.2	MFGCYGCAVPLAIAVIS	71	R	M64378.1	1 ... 933
639	OR2AnP	4	7	148.83	TLAHCAFLVHLISCILG	68	M	AF102521.1	22 ... 669
640	OR2Gn	0	1	256.02	LLGSCISSIHFLVSEVI	63	M	M84005.1	1 ... 936
641	OR7E37 P	5	13	26.5	MAGGEFLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
642	OR5AVn	0	1	256.02	AMATVMSCMHA VFGLVI	51	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
643	OR2AJn P	7	1	254.43	VLLGCGINVHYVSAFLI	55	M	AF102527.1	22 ... 669
644	OR13En P	1	9	39.89	MLGSCLTNLQLLATLTA	79	M	AJ251155.1	15491 ... 16423
645	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
646	OR2TnP	0	1	254.43	IPGGCSLDLQAMCCMLV	59	M	AF102537.1	16 ... 669
647	OR2WnP	2			LMGSCVCNIMQTLGLLV	56	M	M84005.1	1 ... 936
648	OR13Jn	0	9	39.89	MLGSCALKTEILGSLLV	82	M	AJ251155.1	6062 ... 6997
649	OR6RnP	2	1	254.39	SFGCFLGLPSLDSSLIS	45	M	NM_010983. 1	178 ... 975
650	OR5ATn	0	1	254.39	VLASLVYIMHGLINLDC	50	M	AL359352.1	111313 ... 112242
651	OR2Zn	0	19	10.64	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
652	OR4Ln	0	14	0.08	MHGGMLIHSQVLDSLST	53	M	AB030893.1	37 ... 930
653	OR4UnP	14	14	0.15	RHSGMAMHSQVLDSLST	46	M	AB030895.1	1 ... 924
654	OR4Fn	0	6	185.98	IHGGMIIHIQFVNSISA	50	M	AF102522.1	40 ... 660
655	OR4FnP	2	6	185.98	IHGGMAIHVQFVNSISS	50	M	AB030896.1	1 ... 906
656	OR4Fn	0	6	185.98	IHGGMATHVQFVNSISG	50	M	AB030896.1	1 ... 906
657	OR4Fn	0	6	185.98	IHGGMTIHVQFVNSISG	50	M	AB030896.1	1 ... 906
658	OR4AnP	5	11	50.28	IHGGILGHVQFVNDICV	65	M	AF102522.1	40 ... 660
659	OR4LnP	1	14	0.21	KHGSMLIHSQVLDSLST	53	M	AB030893.1	37 ... 930
660	OR7E33 P	6	13	54.79	MAGGEFLDLRILPAFGL	56	M	AF073989.1	547 ... 1515
661	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
662	OR4Kn	0	14	0.15	MHGGMSVHSQFVDSLST	53	M	AF259072.1	104176 ... 105099
663	OR5U1	0	6	33.45	VIASVAASMHILFTAAI	84	M	AL359352.1	111313 ... 112242
664	OR4Kn	0	14	0.08	IHGGMAVHSQFMDLSS	58	M	AF259072.1	104176 ... 105099

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
665	OR5V1	0	6	33.45	LVVGCSANVHLLTGIGT	84	M	AL365337.1	192661 ... 191711
666	OR4QnP	1	14	0.08	LHGAMAGHVQLMNSISI	62	M	AF259072.1	104176 ... 105099
667	OR12D3	0	6	33.45	LHGSAAIYMHMLVTISG	70	M	AL359381.1	128169 ... 127234
668	OR4Kn	0	14	0.08	IHTGMIVHSQFIDSLSS	59	M	AF259072.1	104176 ... 105099
669	OR51CnP	3			MKTVSARMPMLGAMTVV	53	R	AF079864.1	632 ... 1576
670	OR1J2	0	9	105.94	MITDSVLSSHLMVGVL	66	M	AF102524.1	52 ... 669
671	OR5BJnP	3			SIGSAAVNTKFPSC LGV	46	M	AF073965.1	2 ... 643
672	OR1J1	0	9	105.82	TIADSGICLHLIAAAIL	63	M	AF102524.1	52 ... 669
673	OR13En	0			MLGSCLTNLQLLATLTA	83	M	AJ251155.1	15491 ... 16423
674	OR4KnP	5	14	0.08	IHGGMVIHTEFVNSLSM	53	M	AB030893.1	37 ... 930
675	OR1LnP	5	9	105.84	MYGNSFFHLHLQEAULT	54	M	AC023167.7	60743 ... 61663
676	OR2CnP	2			FHGACAGTVGLMASFVL	59	M	M84005.1	1 ... 936
677	OR4TnP	9	14	0.21	MLSELLSHSQFVKSLSI	47	M	AC019272.4	62255 ... 61317
678	OR5BnP	1			FVITSGCNIHNIVVND	51	M	AF121977.1	262 ... 1197
679	OR4Kn	0	14	0.21	IHGGM TLHFQFINSISS	53	M	AB030896.1	1 ... 906
680	OR11Ln	0	1	254.43	LVGACVTTLHMILSVLI	50	M	AF121972.1	171 ... 1109
681	OR7E68P	5	10	17.21	MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
682	OR7EnP	2	10	17.21	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
683	OR7E31P	6	9	70.71	TAGGELLDLHIMPAFGL	55	M	AF073989.1	547 ... 1515
684	OR7EnP	3	9	70.71	MVACDVLDLHIMDSFGL	58	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
685	OR5AKn P	3	11	52.82	LAATCGMNVHFLFVNLF	79	R	U50948.1	34 ... 978
686	OR5AKn	0	11	52.83	FAATCGMNVQFLFVNLF	79	R	U50948.1	34 ... 978
687	OR5AKn	0	11	52.83	FAATCGINVHFDFVDLF	79	R	U50948.1	34 ... 978
688	OR5BQn P	9	11	52.82	TTTTTLLLLMLTFFFF	42	R	U50948.1	34 ... 978
689	OR1Nn	0	9	105.94	LLGGNVLPMLHMGFLV	56	R	AF091566.1	1 ... 663
690	OR1J4	0	9	105.94	MITDNVLNSHLIVGVIL	69	M	AF102524.1	52 ... 669
691	OR1Nn	0	9	105.94	MLGDSLLVTHLVGLV	85	R	AB038167.1	1 ... 933
692	OR2AnP	4	3	94.41	TLAVCTIMVHHLGSIVG	65	M	AF102521.1	22 ... 669
693	OR2ANn P	17	9	93.78	.....VVVLEFMVNLLI	23	M	AC074177.4	128803 ... 129726
694	OR5K1	0	3	104.47	FCETCGAHIHLLFSVQF	51	R	AF091575.1	52 ... 663
695	OR2K2	0	9	93.78	MLGSCVTTLEFMVSLLI	60	M	AJ251154.1	35662 ... 36615
696	OR8Hn	0	11	51.76	MAGTCGIDVNSIIVTLV	51	M	AC069559.8	36251 ... 35322
697	ORnP	15	11	51.76	LIFKNLFSPLXXHYIL	28	M	X89682.1	2 ... 472
698	OR4AnP	14	11	50.28	FGRRVVGHIQLYGHNYV	38	M	AB030895.1	1 ... 924
699	OR4An	0	11	50.28	LHGGVVGQFQIVNGSCI	59	M	AB030895.1	1 ... 924
700	OR6Sn	0	14	0.58	FFGAFAGPGPADLAVIS	50	R	M64378.1	1 ... 933
701	OR4RnP	16	11	50.28	NLGAIMEHVXSVNGNYL	52	M	AF102522.1	40 ... 660
702	OR13Cn	0	9	86.77	MLGTCGINVQFLTTFLT	65	M	AJ133425.1	61 ... 1014
703	OR13Dn P	4	9	86.77	MYGSCVLNTELIGNFLS	64	M	AC023789.5	371264 ... 372220
704	OR7EnP	3	11	2.13	MIACGVLDLHIINSEGL	54	R	AF091580.1	7 ... 663
705	OR10Pn P	1	12	59.88	MIGICTTTTHLVATFII	49	M	AF247657.1	1 ... 945
706	OR8In	0	11	51.76	MVVCCMISISVSLATLS	50	M	AC069559.8	137090 ... 138039
707	OR8G1	0			..IIIGICVHCIVGNIV	75	R	AF091576.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
708	ORnP	7	12	59.88	CFPGEAFFTLL.....	34	M	AL359352.1	145887 ... 145042
709	OR5F1	0	11	51.76	MIATCGANVNHSLANIG	50	M	Y15525.1	1 ... 705
710	OR5FnP	1	11	51.76	MIATCGANVNYFFANKG	52	M	Y15525.1	1 ... 705
711	OR6BnP	6	2	251.7	LSVCCFSIIKFDLAILF	70	M	L14567.1	17 ... 667
712	OR2D1	0			LLGCCASVDFITGILI	64	M	AF073987.1	2 ... 649
713	OR5ASn	0	11	51.76	MAADCLSTVHLLLCIQS	52	M	AC068904.1 5	165039 ... 165965
714	OR5SnP	8	2	251.7	FSSTTGRSVQLKLCMMN	64	R	AF091579.1	7 ... 663
715	OR5AQn P	0	11	51.76	SAVTDAGNTHGPFSAIF	51	R	X80671.1	203 ... 1129
716	OR6BnP	3	2	251.7	LSVCCFSIIKFDLAILF	67	M	L14567.1	17 ... 667
717	OR5JnP	2	11	51.76	YVLTGGGNTHGLFSIAL	52	R	X80671.1	203 ... 1129
718	OR9AnP	4	7	146.91	QLGTLVFFWPALMAIIG	44	M	NM_010991. 1	1 ... 939
719	OR5BEn P	2	11	51.76	YSLTCVLNTHSFLSTST	45	R	AF091564.1	7 ... 663
720	OR9An	0	7	146.91	LLGTFVFFWPVLMVAVLG	47	M	NM_010991. 1	1 ... 939
721	OR8Hn	0	11	51.76	MVGTCGIDVNSIIATLV	51	M	AC069559.8	36251 ... 35322
722	OR5BNn P	14	11	51.76	LLMTCAVMSHS.....P	54	M	AF102528.1	52 ... 669
723	OR8Jn	0	11	51.76	LLIVVLYTVVCVSANLF	80	M	X89682.1	2 ... 472
724	OR9NnP	9	7	146.91	LFGTFIIIIIL.AAAAA	36	M	NM_010991. 1	1 ... 939
725	OR7EnP	4	7		MVACGMLDLHITHSFAL	51	R	AF091580.1	7 ... 663
726	OR7E9P	3	7		MVACDVLDLHVIDSFGL	51	M	AF073989.1	547 ... 1515
727	OR8KnP	8	11	51.76	MMITLICQIIDILTNP	36	M	AC069563.9	28460 ... 29383
728	OR2AnP	1	7	148.97	ILAHC.....	44	M	AF102521.1	22 ... 669
729	OR8Kn	0	11	51.76	LLIIFIYQMFKSFSNLS	56	M	AF102528.1	52 ... 669
730	OR7E39 P	4			MVGGEFLFHLHIMPAFGL	55	R	AF091580.1	7 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
731	OR7E27 P	3			MAGGELLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
732	OR2Hn	0	6		FLGTCVMEVQSLASILV	81	M	AL078630.1	41097 ... 40165
733	OR13Cn P	2	9	40.16	MLGACGATVQLMANFLV	87	M	AJ133428.1	61 ... 1017
734	OR13Cn	0	9	40.16	MFGACGAAVQLMTNFLV	89	M	AJ133424.1	61 ... 1017
735	OR2S1P	4	9	40.16	MFGACGANVQLMTNELL	89	M	AJ251154.1	2703 ... 1747
736	OR2AMn P	1	9	40.16	.....RRRRRV.MMMM	63	M	AJ251154.1	2703 ... 1747
737	OR1N1	0	1		MLGDSLLVTHLVGLV	85	R	AB038167.1	1 ... 933
738	OR2S2	0	9	40.13	MFAGCSIAVHLMTNFLV	83	M	AJ251154.1	2703 ... 1747
739	OR7E26 P	4	1		MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
740	OR1F11	0			LAGNNGVNLHLIEGVM	99	R	M64377.1	1 ... 939
741	OR5ACn P	3	3	103.97	FGATCIIHILFSIQF	66	R	AF091575.1	52 ... 663
742	OR5B10 P	2	13		MVATNGCNLRDLMSNV	46	M	AF102528.1	52 ... 669
743	OR2AnP	1	12	85.7	TLAVCAFLVHLIACILG	76	M	AF102521.1	22 ... 669
744	OR1E5	0	13		MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
745	OR4Fn	0	6	185.71	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
746	OR5CnP	0	9	40.53	MAADC.....	47	M	Y15525.1	1 ... 705
747	OR2WnP	0	6	31.62	LLGGCVSNIMQALAI	64	M	AF102516.1	52 ... 669
748	OR2L2	0			..IIIGINAHYVSSFL	48	M	AF102537.1	16 ... 669
749	OR4H8P	2	14		MHGCILGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
750	OR5D10 P	5			LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
751	OR7A12 P	1	14		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
752	OR2L1	0			..IIIGINAHYVSTFLF	48	M	AF102527.1	22 ... 669
753	OR2F3P	0	14		LLGGFTSSVQIISSLLT	55	M	AF073974.1	41 ... 649



SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
754	OR4H10P	2	15		MHGCILGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
755	OR5H1	0			..IIILGHIHFVFSIQF	56	R	AF091575.1	52 ... 663
756	OR2K1	0			..IIIIITTLVCMVSLLI	58	M	AJ133428.1	61 ... 1017
757	OR7E11P	7	11		MAGGEFLDLHILPAFGL	52	M	AF073989.1	547 ... 1515
758	OR7A3P	1	11		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
759	OR6A1	0	11		LLGCCGGIVKLDLAILG	91	R	M64386.1	130 ... 975
760	OR5I1	0	11		FCADSLGSHVFLYGVFI	52	M	Y15525.1	1 ... 705
761	OR2H3	0	6		ILGTCVIGVQSVASILV	86	M	AL078630.1	41097 ... 40165
762	OR10J1	0			MVGICGIVTQSTISVLV	73	M	X92969.1	8035 ... 8961
763	OR7E3P	3	11		MFACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
764	OR1D6P	1	11		LVVANLFYIHLTGIFI	48	R	Y07557.1	1 ... 942
765	OR5D10P	2	18		LCVVTWCTLTFSASES	45	R	U50948.1	34 ... 978
766	OR5D5P	2	18		LCVVTWCTLTFSANES	46	M	AC073947.3	29192 ... 30115
767	OR52A1	0	11		MHQGSMAVCLIGVAVAF	72	M	NM_013620.1	1 ... 945
768	OR2AEn	0	7	98.36	HLGGCMGNIHIVSSLLL	48	M	AC073769.1	143294 ... 142353
769	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	40	M	NM_010983.1	178 ... 975
770	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	41	M	NM_010983.1	178 ... 975
771	OR7MnP	7	10	149.44	.....NVYVSL.....	29	M	AC073947.3	43325 ... 42733
772	OR13Cn	0	9	86.77	MFGACGTDVQFMSNVLI	69	M	AJ133428.1	61 ... 1017
773	OR13Cn	0	9	86.85	MLGTCGANVQFMATFTM	71	M	AJ133425.1	61 ... 1014
774	OR2InP	6			LLGSC.....	79	M	AL078630.1	151152 ... 150391

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
775	OR4An	0	11	50.28	LHGGVVGHFQVVSICV	58	M	AB030895.1	1 ... 924
776	OR2InP	3			.....RRRRRMARILL	77	M	AL078630.1	151152 ... 150391
777	OR4AnP	4	11	50.28	LHGGVVGSHFQVVGICV	53	M	AB030896.1	1 ... 906
778	OR4AnP	7	11	50.28	PHGGAVAHFQVVGICV	57	M	AB030896.1	1 ... 906
779	OR8C1P	2	11		LCVHCGMGVHCMIVVVV	72	M	AC068905.1 2	76922 ... 75948
780	OR4AnP	1	11	50.28	LHGDVVGHFQVVGICV	56	M	AB030896.1	1 ... 906
781	OR7E15 P	5	11		MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
782	OR10A1	0	11		MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
783	OR2An	0			TSAVCTCLVHLI.....	70	M	AF102521.1	22 ... 669
784	OR7EnP	6			MAGGELFHLHIMPAFGL	57	M	AF073989.1	547 ... 1515
785	OR7En	0			MAGGDFLDLHIVPAFVL	54	R	AF091580.1	7 ... 663
786	OR51A1 P	5	11		MHTLSARLPLLAVITFL	43	R	AF079864.1	632 ... 1576
787	OR7E47 P	4			KAGTNLLDLYIMPTFGL	56	M	AF073989.1	547 ... 1515
788	OR5B5P	2	3		MAATNICNIHELVANIS	48	M	AF146372.1	509 ... 1456
789	OR1F10	0	3		MFVDNGVNLHLIEGVM	72	R	M64377.1	1 ... 939
790	OR8G2	0			...IIIGLGIHFVLSNIT	75	M	AF102518.1	52 ... 669
791	OR1Sn	0	11	54.08	MIVVNILITHLLVGIVF	55	M	AC073769.1	133488 ... 132556
792	OR4AnP	3	11	50.73	LHGGAVGHFQVVSGLCV	56	M	AB030896.1	1 ... 906
793	OR4AnP	7	11	50.76	LHGGILGHFQVVGMCV	58	M	AB030896.1	1 ... 906
794	OR4AnP	5	11	50.66	LHGGVLGHFQVVGMRV	56	M	AB030896.1	1 ... 906
795	OR4AnP	7	11	50.73	PHGGVVGGRFQVVKICV	54	M	AB030896.1	1 ... 906
796	OR4AnP	1	11	50.81	LHGGIVGHFQVVGMCV	60	M	AB030896.1	1 ... 906
797	OR4AnP	10	11	50.81	LHGGVVGNFQVVGICV	55	M	AF102522.1	40 ... 660
798	OR4An	0	11	50.73	LHAGVAGHVQFMNGICV	62	M	AB030895.1	1 ... 924
799	OR4An	0	11	50.73	LHGGVVGHVQFVNGICV	57	M	AB030896.1	1 ... 906
800	OR7E42 P	4			MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
801	OR2M3P	2			ITLGCFLDIDALCCMIF	55	M	AF102537.1	16 ... 669
802	OR4H11P	2	4		MHGCI LGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
803	OR7E57P	5			MAXGEFLDLHILPAFGL	51	M	AF102536.1	22 ... 669
804	OR2B1P	0	5		LLGAYATNWLLLVSFHI	78	R	L34074.1	73 ... 1011
805	OR7E34P	2			MAGGDSLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
806	OR7E56P	4			MAGDEFFLHILPAFGL	52	M	AF073989.1	547 ... 1515
807	OR3AnP	1	5		LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
808	OR4H5P	2	5		MHGCI LGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
809	OR1En	0	5		MLGDSLLHLHILMIGILI	82	R	Y07557.1	1 ... 942
810	OR51CnP	2	11		3MKTVSYYYIXQ.....	48	M	AF121975.1	50 ... 1012
811	OR2WnP	2	6	30.51	LLGGCVSNIMQALAIIA	64	M	AF102516.1	52 ... 669
812	OR51B1P	5	11		AHSVSGRSPVRPLITIL	68	M	AF071080.2	15931 ... 16851
813	OR7E81P	3			MAGGEFFSLHIMPAFGL	54	M	AF102536.1	22 ... 669
814	OR7E44P	1			MAGGELFDLHIMLAFL	53	M	AF073989.1	547 ... 1515
815	OR5B7P	2	6		MAATNICNIHEL VANIS	47	M	NM_013728.1	1 ... 948
816	OR7E36P	4			MAGGELFFLHIMPAFGL	58	M	AF073989.1	547 ... 1515
817	OR2A5	0	7		TMAHCTCLVHLIASILG	74	M	AF102521.1	22 ... 669
818	OR5B1P	2	8		MAATNICNIHEL VANIS	47	M	AF146372.1	509 ... 1456
819	OR8B8	0	11	137.68	LLVSGMGAHCVVVDIV	72	M	AC069559.8	120212 ... 119283
820	OR8B4P	0	11	137.71	LCVNCGVGAHSFVVITL	87	M	AC068910.2 1	133103 ... 132162

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
821	ORnP	15	11	137.77	LCVENRRTATHCKSHII	35	M	AC069563.9	60295 ... 59327
822	OR8B3	0	11	137.77	LLVICAMGAHCVVVNIV	85	M	AC069563.9	129775 ... 130725
823	OR2Bn	0	6	30.51	LLGSCASNQWLISFLI	89	R	L34074.1	73 ... 1011
824	OR8B6P	6	11	137.77	LAFFCGLSAHCVAAAVI	73	M	AC069559.8	96224 ... 95292
825	OR8B5P	6	11	137.77	LFFFFXGLGAHCVVANTV	73	M	AC069559.8	96224 ... 95292
826	OR4E2	0	14	1.7	LHACIAGHGQLINSISS	90	M	AF259072.1	104176 ... 105099
827	OR8B7P	4	11	137.77	FCVICGWAHCVA AIFV	71	M	AC069559.8	96224 ... 95292
828	OR11Jn P	3	15	1.82	FSCAGFGSMPLCVSIII	56	M	AF121972.1	171 ... 1109
829	OR4E1P	3	14	1.7	MHACIAGHALLINSISV	92	M	AB030893.1	37 ... 930
830	OR10Dn P	7	11	137.96	.....HHHILLGNVLSI	85	M	AC074177.4	12106 ... 13038
831	ORnP	10	14	1.7	VFRGGFHKFFF.....	23	M	AF102536.1	22 ... 669
832	OR8D2	0	11	137.77	LLVIGVLWVHRLIGNTA	70	M	AC073947.3	29192 ... 30115
833	OR11In P	1	1	126.31	FGAACGCLITLATSVTI	51	M	AL359381.1	175785 ... 176720
834	OR11Jn P	1	15	1.82	FSCACFGWTPLCISIIL	56	M	AF121972.1	171 ... 1109
835	OR10An P	3	11	5.64	MFGVCTPVVQWAGTVVI	74	M	AF247657.1	1 ... 945
836	OR8C3P	5	11	137.77	LCVHCGMGVHCMIVVVV	73	M	AC068905.1 2	76922 ... 75948
837	OR2DnP	6	11	5.64	LLGCCGSVVDFITGILI	62	M	AF073987.1	2 ... 649
838	OR4PnP	0	11	51.03	LHGGIVGHSQ.....	59	M	AB030895.1	1 ... 924
839	OR7E21 P	5			MAGGEFIDLHIMPAFGL	50	M	AF073989.1	547 ... 1515
840	OR2M1	0			IVLGCFLDIYAICSMLE	55	M	AF102537.1	16 ... 669
841	OR7AnP	4	19		NLAGVVMNLQM.....	63	M	AF073970.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
842	OR5D11 P	1	8		LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
843	OR7E50 P	7	8		IVVCDMLDLHVFLDIFL	57	M	AF102536.1	22 ... 669
844	OR7E45 P	3			MAGGELFDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
845	OR7E77 P	6			MAGGEFLDLHIMPAFGL	51	M	AF073989.1	547 ... 1515
846	OR8B2	0	11	137.77	LLVICAMGAHCVVVNIV	84	M	AC069563.9	129775 ... 130725
847	OR8D1	0	11	137.77	LVVVGALSTHALIANTV	87	M	AC073947.3	29192 ... 30115
848	OR8B1P	4	11	137.77	LLLVCGMGAHCVVVNIV	84	M	AC069559.8	96224 ... 95292
849	OR7A1P	2	19		MIVVSVVYLQMMTSLGG	72	R	M64376.1	1 ... 999
850	OR7E8P	4	8	13.72	MVACGVLDLHIIDSFGL	53	M	AF102536.1	22 ... 669
851	OR4DnP	7	11	55.86	MHGGVAGHVQLMNNISL	58	M	AC019272.4	183633 ... 182701
852	OR7E80 P	7	8	13.72	MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
853	OR4DnP	5	11	55.86	MHGGGAAGHVQLMNNLTL	62	M	AC019272.4	183633 ... 182701
854	OR7E10 P	8	8	13.72	IVACDLLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
855	OR10B1 P	3	19	17.91	MLGCCLSVIEMILSVVM	85	M	AC012302.5	54283 ... 55224
856	OR2InP	3			..... LLLLMARILL	75	M	AL078630.1	151152 ... 150391
857	OR4Dn	0	11	55.86	MHGGVGGAQLMNNVSF	65	M	AC019272.4	183633 ... 182701
858	OR5ACn	0			.VVVVIIHVHLIFGIQP	65	R	AF091575.1	52 ... 663
859	OR2I1	0	6	33.63	LLGSCASNAQLMARILL	79	M	AL078630.1	151152 ... 150391
860	OR10H1	0	19	19.86	MFGFSCGMVVAGLVTAL	88	M	AC023604.2	245345 ... 246298

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
861	OR7E59 P	5			CPEARVFLHIMPAFGL	53	M	AF102536.1	22 ... 669
862	OR7E28 P	4			MAGGELLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
863	OR5B3	0			MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978
864	OR2A6	0			TLAHCAFLVPLIACILG	75	M	AF102521.1	22 ... 669
865	OR6Cn	0			.VVVVCAIPPLVMAALI	47	M	NM_010991.1	1 ... 939
866	OR7E54 P	5			MAGGEFLDLHIMPAFGL	52	M	AF073989.1	547 ... 1515
867	OR7E48 P	3			MAGGEFLDLHIMPAFGL	57	R	AF091580.1	7 ... 663
868	OR67An P	3	11	76.42	MHSCAGTLPAQGIIVSL	83	R	AF091561.1	52 ... 663
869	OR4Dn P	1	11	55.86	MHGGVAGHVQLMNNLTL	63	M	AC019272.4	183633 ... 182701
870	OR4Cn P	1	11	50.91	VHGCILGHAQLNSICS	57	M	AB030896.1	1 ... 906
871	OR4Dn P	2	11	55.86	IHGGIAGHVQLMNNVTL	65	M	AC019272.4	183633 ... 182701
872	OR10H2	0	19	19.94	MFGFSCGMVVAGLVMAL	85	M	AC023604.2	245345 ... 246298
873	OR10H3	0	19	19.94	MFGFSWGMVMGLVTAI	75	M	AC023604.2	214343 ... 213396
874	OR55Cn P	2	11	2.65	VYLLYLQPGGG.....	45	M	AF121980.1	160 ... 1053
875	OR55Bn P	3	11	2.65	.VVVVLQVPLGMCTVS	53	M	AF121980.1	160 ... 1053
876	OR52Vn P	4	11	4.19	LHNHIMVYXFLGTTSP	48	M	NM_013619.1	118 ... 969
877	OR2B3	0	6	33.64	LLGACFINLQLFSILI	75	R	L34074.1	73 ... 1011
878	OR52Tn P	6	11	4.22	FGHFLIFLDFLDILTIS	45	M	AF121975.1	50 ... 1012
879	OR2J1P	5	6	33.64	LLGTCASTLHFLMSFVI	57	R	L34074.1	73 ... 1011
880	OR52Hn P	3	11	4.19	LHFVSGRPCLGVPTVT	60	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
881	OR2J3	0	6	33.64	LLGTCASNLHFLTSFVI	58	R	L34074.1	73 ... 1011
882	OR52An	0			FHSVS.....VVRLFS	75	R	AF079864.1	632 ... 1576
883	OR4Qn	0			.VVVVAGHMQLVNSLSV	56	M	AB030893.1	37 ... 930
884	OR52Bn P	2	11	4.22	LHFVSVRTSILGVPSVL	60	M	AF121975.1	50 ... 1012
885	OR2N1P	9	6	33.64	LHGGCPIYSEALVCM LV	81	M	AJ132195.1	79 ... 906
886	OR51En P	1			FHSASVRFP LLGAIAMV	90	R	AF079864.1	632 ... 1576
887	OR2J2	0	6	33.64	LLGICAIILHFLMSFVI	57	R	L34074.1	73 ... 1011
888	OR2In	0			.....RRRRRRMARILR	77	M	AL078630.1	151152 ... 150391
889	OR2J4P	5	6	33.64	LLGTCASNLHFLTSFVL	56	R	L34074.1	73 ... 1011
890	OR7E40 P	4			MAGGDILDLYILPDFGL	55	M	AF073989.1	547 ... 1515
891	OR2H4P	3	6	33.64	LLGAYLTQIQAMASLLM	63	M	AL078630.1	41097 ... 40165
892	OR7E52 P	5			IVVCDVLDLHVCDIFGL	61	M	AF073989.1	547 ... 1515
893	OR2InP	9			LLGSC.....	80	M	AL078630.1	151152 ... 150391
894	OR6C1	0			LIGVFTVIPALGCATLF	52	M	NM_010991.1	1 ... 939
895	OR7E30 P	3			MAGGEFLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
896	OR5BAn P	0	11	53.69	LVVTSVENIQNLFSVTL	51	R	AF091579.1	7 ... 663
897	OR7H1P	3	19	11.38	MMGGTVLYIQLLVALDV	74	M	AF073989.1	547 ... 1515
898	OR5B2	0	11	54.45	MVATNGCNFHLTSNIF	47	R	U50948.1	34 ... 978
899	OR5AZn P	1	11	53.69	MIGTCTVNLLCILCLIF	48	R	AF091579.1	7 ... 663
900	OR5Bn	0	11	54.45	MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
901	OR52Bn	0	11	4.22	KILFSARIPSLGAASTL	64	M	NM_013619.1	118 ... 969
902	OR5BnP	2	11	54.45	MAATNICNIHELVANIS	49	R	U50948.1	34 ... 978
903	OR52Dn	0	11	4.19	MHYASVRIPFLGVAAML	66	M	AF121976.2	474 ... 1307
904	OR7A11	1	19	17.72	MVEASAIIDLHMAVLGV	67	M	AF283558.1	1 ... 927
905	OR5BnP	9	11	54.45	MAATSALTVDLLQFFL	41	M	NM_013728.1	1 ... 948
906	OR51AnP	5	11	4.19	THSWFSRMPLLGIVAFV	50	R	AF079864.1	632 ... 1576
907	OR7A15P	4	19	17.72	MIVGSVTHLHMAALGG	74	R	M64376.1	1 ... 999
908	OR7C2	0	19	17.72	IIGCNGIGLETMTVLGF	98	R	AF091580.1	7 ... 663
909	OR7E23P	7	21	20.89	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
910	OR2E1	8	6	32.05	AHACCTINLQI.RRRRR	43	M	AL078630.1	106872 ... 105934
911	OR1I1	0	19	17.87	MHGTSIAIQIHLIFGVGS	57	R	AF091566.1	1 ... 663
912	OR1RnP	3	17	3.12	MVGISAVHLHLIEGVVA	45	R	M64377.1	1 ... 939
913	OR4F3	0	8	0.07	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
914	OR2AEn	0	7	98.7	HLGGCMGNIHIVSSLLL	49	M	AC073769.1	143294 ... 142353
915	OR2InP	7			.....TTTTMARILL	72	M	AL078630.1	151152 ... 150391
916	OR52AnP	2			IHSASVRFP LLGXPPPP	94	R	AF079864.1	632 ... 1576
917	OR7C1	0	19		ITGCNGIGLETIATLGI	81	R	AF091580.1	7 ... 663
918	OR2A3P	2	7	149.11	MLAACTCLINLVGGVLG	63	M	AF102521.1	22 ... 669
919	OR7A5	0	19		MIAGNAMYLMITVLGG	74	M	AF283558.1	1 ... 927
920	OR2InP	3			.....MARILL	67	M	AL078630.1	151152 ... 150391
921	OR7A10	0	19		MLVGNAMNLQMMAVLGG	76	R	M64376.1	1 ... 999
922	OR2An	0			.....	81	M	AF102521.1	22 ... 669
923	OR2M2	0			IISGCFDIDAICMLF	57	M	AF102537.1	16 ... 669



SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
924	OR7A8P	2	19		MLAVSSLNLQMIATLGG	71	M	AF283558.1	1 ... 927
925	OR2An	0			TSVCTTTLIHL.....	78	M	L14566.1	62 ... 667
926	OR7E20P	4			MAGGELLFLHIMPAFGL	56	M	AF073989.1	547 ... 1515
927	OR2AnP	3			TLAHCTCLVHL.....	65	M	AF102521.1	22 ... 669
928	OR5Bn P	7			MVASCCKGKTVS.....	34	M	Y15525.1	1 ... 705
929	OR1En	0			LMGDSLLHLHLIMGISI	92	M	AC068902.1 1	196434 ... 195499
930	OR1EnP	1			MLGDSLLHLHLIIGVVL	98	M	AF073976.1	32 ... 649
931	OR5Bn	0	11	54.45	FVITSGCNIHNIVVND	51	R	U50948.1	34 ... 978
932	OR8RnP	12	11	73.74	LFLSYGGGAHH.....	52	M	AC069561.1 0	7848 ... 8783
933	OR5ANn	0	11	55.69	YSGLSGTAFQATLTFGA	55	R	AF091564.1	7 ... 663
934	OR5ANn P	1	11	55.69	YSGLCGTGIQATLTFT	59	M	Y15525.1	1 ... 705
935	OR5BRn P	8	11	55.69	MSNVCGTVIQATLTFT	33	M	Y15525.1	1 ... 705
936	OR2A1	0	7	149.18	TLGHCTCLAHLIACFLG	77	M	AF102521.1	22 ... 669
937	OR10An	0	11	6.81	MLGGCFLVQWAGTIIV	54	M	AF247657.1	1 ... 945
938	OR2A9	3	7	149.18	TLAHCTCLVHLIACILG	78	M	AF102521.1	22 ... 669
939	OR2A7	0	7	149.18	TSVCTTTLIHLVAGLG	81	M	L14566.1	62 ... 667
940	OR10A3	0	11	6.81	MLGGCFVQWAGTIVV	58	M	AF247657.1	1 ... 945
941	OR10Cn	0	6	33.36	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
942	OR7A2P	0	19		MVIVSVMNLQVMAALDG	73	M	AF283558.1	1 ... 927
943	OR10Wn P	2	11	54.3	MIGSCASLQLFVAAAIV	47	M	AC012302.5	54283 ... 55224
944	OR7A17	0	19		MVGGSAINSOMMAALAG	76	M	AF283558.1	1 ... 927
945	OR5Bn	0	11	54.3	MAATNGINIQLDISNVF	47	M	AF102528.1	52 ... 669
946	OR5BnP	5	11	54.3	MVATNGCNLRDLMSNVL	47	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
947	OR1Q1	0	9	106.13	TIAVNMLHLHLIEGVIG	54	M	AF073967.1	2 ... 649
948	OR2Hn	0	6	33.33	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
949	OR7EnP	5	3	90.04	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
950	OR7A14	0	19	17.72	MVIVSAMNI.....	71	M	AC073772.1	227187 ... 226252
951	OR1B1	0	9	106.13	FYGVTLVHLRLIEGLMG	49	M	AC068902.1 1	83719 ... 84647
952	OR12D2	0	6	33.23	LHGSSTIHLHMLVTIAG	81	M	AL359381.1	105330 ... 104407
953	OR7EnP	4	3	11.92	MVACDVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
954	OR8BnP	5	15	74.31	LXVVEGMAHCVVVNIV	82	M	AC069559.8	96224 ... 95292
955	OR1L1	0	9	106.13	MLGNSLIHLHLVEGVIT	57	M	AC023167.7	60743 ... 61663
956	OR11An	0	6	33.36	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
957	OR7AnP	4	12	44.29	....HLLDCYIRTTLSG	55	M	AF102534.1	52 ... 669
958	OR1C1	0	1	254.35	LVVNSGVHLHLIVGLAT	56	M	AC073769.1	133488 ... 132556
959	OR1D2	0	17	2.99	LVVANLLYIHLLTGIFI	50	M	AF073967.1	2 ... 649
960	OR1L3	0	9	106.13	MLGNSFFHLHLAEGSVA	53	M	AC023167.7	14677 ... 15636
961	OR12DnP	1	6	33.36	LHGSATIHLHMSTGIAG	76	M	AL359381.1	105330 ... 104407
962	OR4G1P	4	16	83.04	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
963	OR2B4P	1	6	33.53	LLGSCGSNVQLLLGLLM	90	M	AL359352.1	95024 ... 95965
964	OR11H1	0	22		FFGTCLCWIPLCLSVIG	61	M	AC027184.3	54955 ... 54017
965	OR4Fn	0	16	83.04	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
966	OR56AnP	5	11	4.73	MNLPSFQLPVLQAGFLS	38	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
967	OR8NnP	7	4	164.13	REIIRVDAFLKKTANMI	34	M	AF102528.1	52 ... 669
968	OR7EnP	5			MVACDVLDLHIFDFGL	54	R	AF091580.1	7 ... 663
969	OR4Pn	0	11	50.95	LHGGIVGHSQLVNSIAV	56	M	AB030895.1	1 ... 924
970	OR6Cn	0			LIGVFCSTPPLGFATLF	51	M	NM_010991.1	1 ... 939
971	OR5BCnP	2	11	54.3	.....GCQIHFLLANIF	41	M	AC069561.10	51687 ... 50743
972	OR10QnP	4	11	54.3	MLGGCGLLQLLVSVLV	48	M	AC012302.5	54283 ... 55224
973	OR5BnP	6	11	54.3	TDASNGGNIHELVTNIF	45	R	U50948.1	34 ... 978
974	OR10PnP	2	12	115.61	MIGICTTTTHLVATFII	46	M	AF247657.1	1 ... 945
975	OR1L4	0	9	106.22	MMGNSGIHFLVETVIT	62	M	AF073967.1	2 ... 649
976	OR2APnP	3	12	115.61	YMGAFLLLLLL.....	49	M	AF073987.1	2 ... 649
977	OR1L6	0	9	106.22	MMGNSGIHFLVETVIT	63	M	AF073967.1	2 ... 649
978	OR6UnP	6	12	115.61	DIGAFTLFMPLDLAALG	52	M	NM_010991.1	1 ... 939
979	OR5C1	0	9	106.06	MAADCAGSVHLLICIQA	50	R	X80671.1	203 ... 1129
980	OR11InP	1	15	70.72	FGAACGLITLATSVTI	51	M	AL359381.1	175785 ... 176720
981	OR4AnP	6	11	50.78	LYGGVVGHFQVNVGVCV	57	M	AB030896.1	1 ... 906
982	OR4GnP	14	2	114.45	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
983	OR10Vn	0	11	56.15	MVGCGLLPLLLISVLI	48	M	AL136158.14	29455 ... 30402
984	OR4G2P	2	2	114.45	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906
985	OR10VnP	3	11	56.15	MIGRCGLLQLLMVSFLV	45	M	X92969.1	8035 ... 8961
986	OR4F4	0	2	114.45	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
987	OR4G3P	14	19	63.51	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
988	OR5AKnP	4	11	52.82	LGATCSMNINFLFVNLC	65	R	U50948.1	34 ... 978
989	OR10YnP	14	11	56.15	MIRGCGLLFLLLCGHHL	43	M	AF247657.1	1 ... 945
990	OR4GnP	2	19	63.51	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
991	ORnP	9	5	111.92	IMCSRTTYVXQLHGFFT	23	M	AF073989.1	547 ... 1515
992	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
993	OR8A1	0	11	137.56	LLVICVIGIELVSANIV	61	M	AC069559.8	96224 ... 95292
994	OR8Bn	0	11	137.56	LCVVSGMGAHSVVDVM	66	M	AC069559.8	120212 ... 119283
995	OR6DnP	3	10	47.91	AYVSSLLLRTH.....	55	R	AF034901.1	2110 ... 3078
996	OR7E14 P	7	11	16.31	MAGGELDLHIMPAFGL	58	R	AF091580.1	7 ... 663
997	OR2M4	0			IVLGCALDIVALCCMLF	57	M	AF102537.1	16 ... 669
998	OR4WnP	3	X		LLLLL.....LLFFII	36	M	AC069559.8	73704 ... 74636
999	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
1000	OR7EnP	3			MAGGESLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
1001	OR4GnP	4	19	63.51	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
1002	OR10Jn P	1			LLGVCGITIQTISVLL	60	M	X92969.1	8035 ... 8961
1003	OR52En	0	11	4.58	MHTASIRMPLLGNILL	71	M	AF121979.1	53 ... 1106
1004	OR4RnP	24	11		VHGAIMGHVXSFANNCL	54	M	AF102522.1	40 ... 660
1005	OR4Cn	0	11		AHGAIVGHIQFVNSICL	75	M	AF102522.1	40 ... 660
1006	OR4AnP	10	11		GLGGIVGHIQL.....	44	M	AF102522.1	40 ... 660
1007	OR4AnP	4	11		LHGGVAGHFQVVGCCI	55	M	AB030895.1	1 ... 924
1008	OR4AnP	8	11		LHGGVAGHSHSVNGICV	54	M	AF102522.1	40 ... 660
1009	OR9Gn	0	11	52.54	FAAYCVGNIIKMLLNVC	46	M	AC074177.4	106297 ... 105361
1010	OR10An	0	12	59.65	MFGSCGSVLQWASTFIF	64	M	AF247657.1	1 ... 945
1011	OR4Cn	0	11		VHRGVVGHIQFINSICL	73	M	AF102522.1	40 ... 660

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1012	OR10Vn P	8	11	56.15	.FFFFIIXNEXSVVVLV	37	M	AC073945.4	110931 ... 111893
1013	OR10Un P	3	12	59.65	MAGLCATVAQLMLSFIS	56	R	AF034898.1	1 ... 981
1014	OR7E2P	3	11	90.37	MVACDVLDLHICDIFGL	59	M	AF073989.1	547 ... 1515
1015	OR7E35 P	6	4	11.87	MAGGEFLDLHIVPAFVL	53	M	AF102536.1	22 ... 669
1016	OR9KnP	0	12	59.71	LAIVGGCSLQVSLSIIP	49	R	AF091579.1	7 ... 663
1017	OR7E13 P	5	11	90.37	MAGGEFLDLHIMLAFGL	54	R	AF091580.1	7 ... 663
1018	OR7EnP	4	8	6.5	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
1019	OR9Kn	0	12	59.71	LAIVGGCSIQMSLSIIP	49	M	NM_013728. 1	1 ... 948
1020	ORnP	13	11	137.56	PCVIYIGIDVHSLXEPAY	34	M	AC069559.8	36251 ... 35322
1021	OR7EnP	8	11	72.11	MAGGNLFFSLLMPAFGL	54	M	AF073989.1	547 ... 1515
1022	OR7EnP	5	3	140.64	MAGGKFLDLHIMPAFGL	53	M	AF073989.1	547 ... 1515
1023	OR3A4P	0	17	3.12	LHAGCMFNTQALAAMGA	44	M	AC073769.1	133488 ... 132556
1024	OR8QnP	9	11	137.56	LSIIIVETEFVFTXIVT	33	M	AC069559.8	137090 ... 138039
1025	OR7EnP	2	11	72.11	ILACGVLDLHIMHNFG	55	M	AF073989.1	547 ... 1515
1026	OR7EnP	3	3	140.64	MVACGVLDLHIHSFGL	56	M	AF073989.1	547 ... 1515
1027	OR3A1	0	17	3.07	LHVGCACNTHALVGMAT	50	M	AF073967.1	2 ... 649
1028	OR5Gn	0	11	52.52	MGEACGMSTHFLAIGL	69	M	AF146372.1	509 ... 1456
1029	OR5MnP	7	4	42.45	LIIIVYVNAQRIIIMLE	39	M	AF073987.1	2 ... 649
1030	OR7EnP	1	3	136.02	MVACDVLDLHIIDNFG	54	M	AF073989.1	547 ... 1515
1031	OR5G1P	2	11	52.51	QGVACGINTHNVVAVGF	68	M	AF146372.1	509 ... 1456
1032	OR5PnP	3	11	6.93	LVGTCAGNSEFCPSSVLS	70	M	AF121977.1	262 ... 1197

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1033	OR10AEnP	8	1	157.36	IIIIIGIMVIVQIHCVV	40	M	X92969.1	8035 ... 8961
1034	OR3A2	0	17	3.07	LHAGCACNTHALVGMAT	50	M	AC073769.1	133488 ... 132556
1035	OR10Jn	0	1	157.4	MVATCGIMLHANVSVIV	88	M	X92969.1	8035 ... 8961
1036	OR1D3P	2	17	2.94	LVVANLFYIHLTLTGIFI	50	R	Y07557.1	1 ... 942
1037	OR10Jn	0	1	157.36	TVAICGIMVQSNVRVIV	72	M	X92969.1	8035 ... 8961
1038	OR1D4	0	17	2.99	LVVTNLLYLLLTGIFT	49	R	Y07557.1	1 ... 942
1039	OR5GnP	8	11	52.51	QGVVYVANTHAVVAVLV	55	M	NM_013728.1	1 ... 948
1040	OR4SnP	1	11	50.99	LHGCIGGHIQLVNSIAG	61	M	AB030895.1	1 ... 924
1041	OR5GnP	4	11	52.51	LGVVCGVSTHFLVLGL	75	M	AF146372.1	509 ... 1456
1042	OR9HnP	2	1	254.35	FSGIAGWNAQMLLCIIS	59	R	AF091579.1	7 ... 663
1043	OR1A1	0	17	2.99	MIGNSGINPHLMGVIFV	86	M	AF073966.1	41 ... 643
1044	OR1A2	0	17	2.99	MIAKSGISPHMLGVFL	80	M	AF073966.1	41 ... 643
1045	OR8AnP	6	11	137.68	FLVICVMVIELVFANLI	50	M	AC069561.10	51687 ... 50743
1046	OR1P1P	1	17	2.99	LLGDIALLTRLLLVGVI	82	M	AF102538.1	139 ... 675
1047	OR7E12P	7	11	1.92	MAGGEFFSLHIMPAFGL	55	M	AF073989.1	547 ... 1515
1048	OR4A1P	4	11		LHGGVVGHFQVVNGICV	57	M	AB030896.1	1 ... 906
1049	OR10G3	0	14	1.7	LHGSCGAHLQLTDIVVS	91	M	AF259072.1	19582 ... 18644
1050	OR10G1P	3	14	1.7	LHGSCGAHIQLTDIVAS	93	M	AF259072.1	55611 ... 54658
1051	OR10G2	0	14	1.7	LHGSCGAHIQLTDVVAS	91	M	AF259072.1	55611 ... 54658
1052	OR5Tn	0	11	51.94	MVGTCAAHIHALFVIEV	52	M	AF121977.1	262 ... 1197
1053	OR7EnP	8	3	136.02	MVACGVLDLHIIGSFGL	53	R	AF091580.1	7 ... 663
1054	OR7EnP	5	3	136.02	MAGGKFLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
1055	OR4AnP	2	11	50.93	LHAGVVGHVQFMNGICV	61	M	AB030895.1	1 ... 924
1056	OR4C1	1	11	50.93	LHGGIIGHVQFVNSMCL	66	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1057	OR1EnP	7	17	2.9	.....MMMYTLIMGILI	80	M	AF073961.1	32 ... 649
1058	OR7KnP	11	14	5.99	MIGCNFIELYMMIGIFG	49	R	AF091580.1	7 ... 663
1059	OR4CnP	3	11	50.93	LHDGIEGHIQFVNSMCA	61	M	AF102522.1	40 ... 660
1060	OR1RnP	11	17	2.9	MVGISAVHLHLIEGVVA	44	R	M64377.1	1 ... 939
1061	OR5AUn	0	14	1.22	MAATCGANIHCLFANLS	51	M	AC069559.8	85584 ... 84655
1062	OR4Cn	0	11	50.96	LHAGVVGHIQFVNSICI	69	M	AF102522.1	40 ... 660
1063	OR4Cn	0	11	50.96	VHGCIVGHVQLLSICV	57	M	AB030895.1	1 ... 924
1064	OR13Dn P	2	9	86.89	MLGSCWITLRLFTVIVL	58	M	AJ251154.1	2703 ... 1747
1065	OR5n				ASASLTSYVHNEEEVFV	44	M	AL359352.1	111313 ... 112242
1066	OR2Hn				LLGTCVMQVQSLSSLV	83	M	AL078630.1	48786 ... 47851
1067	ORn				.....	25	M	AC074177.4	88434 ... 88916
1068	ORn				.....EINLLLARGKAL	29	M	AF283814.1	1 ... 930
1069	ORn				NNNNNFXXSLHLCCILI	29	M	AC074177.4	128803 ... 129726
1070	ORn				TLLLLTFQHHL.....	27	M	L14569.1	62 ... 667
1071	OR6Fn				..CCCWPIPTSAIAVIS	46	R	M64386.1	130 ... 975
1072	ORn				.....ILLLLL	33	R	U50947.1	418 ... 1350
1073	ORn				..CCCLIPFFFTSGYSW	24	R	M64392.1	1 ... 942
1074	OR10An				PLGECDPPEEQMYVGLVM	51	M	AF247657.1	1 ... 945
1075	ORn				IPNASRRRRR....PP	25	R	M64388.1	1 ... 942
1076	OR2Ln				FLAGAGINAHYVSTFLF	51	M	AF102527.1	22 ... 669
1077	OR10Jn				LTGICGIMVQSNVSVLL	57	M	X92969.1	8035 ... 8961
1078	OR1Kn				LLLLLMVNLYLIKGVVT	50	R	M64377.1	1 ... 939
1079	OR10Dn				LHGSCGLHILLSNVISG	69	M	AC074177.4	12106 ... 13038
1080	ORn				.....CCCI	41	R	M64376.1	1 ... 999

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1081	OR2Ln				SLACGGLNAHFVRTLSF	52	M	AF102537.1	16 ... 669
1082	ORn				HHHHHRLESSSLLLLLL	38	M	AC073945.4	152209 ... 153150
1083	ORn				.....LLLLLS	27	M	AL365336.1	41087 ... 41711
1084	OR2n				.....GGGGGG	57	M	AF102521.1	22 ... 669

5           Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that various changes and modifications can be practiced without departing from the spirit of the invention. Therefore the foregoing descriptions and examples should not be construed as limiting the scope of the invention.

10

          All patents, patent applications, and publications cited herein are hereby incorporated by reference in their entirety. In particular, the following documents are hereby incorporated by reference in their entirety: United States Provisional Patent Applications Serial Nos. 60/145,412, filed July 23, 1999; 60/155,126, filed September 22, 1999; 60/158,495, filed October 8, 1999; 60/158,615, filed October 8, 1999; 60/181,113, filed February 8, 2000; 60/181,115, filed February 8, 2000; 60/184,809, filed February 24, 2000; 60/188,332, filed March 9, 2000; and United States Patent Applications Serial Nos. 09/620,753, filed July 21, 2000; and 09/621,122, filed July 21, 2000.



**CLAIMS**

What is claimed is:

- 5           1.     An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence that is at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through  
10   SEQ ID NO:152 and encoding a polypeptide having olfactory receptor function.
2.     An expression vector comprising a polynucleotide sequence of claim 1.
3.     A host cell comprising the expression vector of claim 2.
- 15           4.     An isolated and purified olfactory receptor polypeptide comprising the translated sequence of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of the translated sequence of SEQ ID  
20   NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152 and having olfactory receptor function.
5.     A host cell expressing a polypeptide of claim 4 or a functional fragment thereof.
- 25           6.     A phage expressing a polypeptide of claim 4 or a functional fragment thereof.
7.     A preparation containing a polypeptide of claim 4, further comprising  
30   biological or synthetic molecules which maintain the functional structure of the polypeptide.

8. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 or a nucleotide sequence having a sequence at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 and encoding a polypeptide having olfactory receptor function.
9. An expression vector comprising a polynucleotide sequence of claim 8:
10. A host cell comprising the expression vector of claim 9.
11. An isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function.
12. A host cell expressing a polypeptide of claim 11 or a functional fragment thereof.
13. A phage expressing a polypeptide of claim 11 or a functional fragment thereof.
14. A preparation containing a polypeptide of claim 11, further comprising biological or synthetic molecules which maintain the functional structure of the polypeptide.
15. A library of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

16. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 50 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through  
5 SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

17. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 100 polynucleotides of SEQ ID NO:1 through  
10 SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

18. A library of olfactory receptors according to claim 15, wherein the library  
15 comprises the expression products of at least 200 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

20 19. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 500 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through  
25 SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

20. A library of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, wherein said polypeptides are functional  
30 olfactory receptors; or functional fragments of said polypeptides.

21. A library of olfactory receptors according to claim 20, wherein the library comprises at least 50 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,

wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

22. A library of olfactory receptors according to claim 20, wherein the library  
5 comprises at least 100 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,  
wherein said polypeptides are functional olfactory receptors; or functional fragments of  
said polypeptides.

23. A library of olfactory receptors according to claim 20, wherein the library  
10 comprises at least 200 polypeptides of SEQ ID NOS of SEQ ID NO: 1085 through SEQ  
ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional  
fragments of said polypeptides.

24. A library of olfactory receptors according to claim 20, wherein the library  
15 comprises at least 500 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,  
wherein said polypeptides are functional olfactory receptors; or functional fragments of  
said polypeptides.

25. A method for determining the binding pattern of a composition with  
20 olfactory receptors, comprising the steps of:  
    exposing the composition to a library according to claim 21; and  
    determining whether the composition binds to each olfactory receptor, thereby  
determining the overall binding pattern of the composition.

25       26. The method of claim 25, wherein the composition consists essentially of one  
compound or chemical.

27. The method of claim 25, wherein the composition comprises at least two  
compounds or chemicals.

30

28. The method of claim 25, wherein the step of determining whether the  
composition binds to each olfactory receptor further comprises a determination of the

approximate binding constant with which the composition binds to each receptor or functional fragment thereof.

29. The method of claim 25, further comprising the step of determining whether  
5 a receptor or functional fragment thereof to which the composition binds is activated.

30. The method of claim 29, further comprising the step of determining the absolute or relative amount by which the receptor or functional fragment thereof is activated.

10

31. A DNA array or a DNA chip comprising DNA segments derived from SEQ ID NO: 153 through SEQ ID NO: 1084.

32. A method of determining differences among individuals with respect to their  
15 olfactory faculties, comprising the steps of comparing the olfactory DNA of the individual against the array or chip of claim 31.

33. A method to determine single nucleotide polymorphisms in olfactory receptors, comprising the steps of uniquely amplifying olfactory receptor sequences from DNA  
20 obtained from one or more individuals, based on primers designed according to the first 25 bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084, and determining the similarities and differences between said amplified DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

FIGURE 1

## SEQ. ID NO:1

```

1  GGNTTATNCC  NCGTTGNACT  GCAGGGGNNC  AACNCACAGN  ACGCCCGNTG  CTGAGGCTAT  AAATGANCGG
71  NNTAAGGAGA  GGAGTGAAGA  CAGTAAAAAA  ACACAGAGAT  AAATTTATCA  ATTGGGAAGC  TTTCAAAGGG
141  CCAAAATATAG  ATGAATATTA  ATGGGCCAAA  GAAGAGAAGC  ACAACAGTAA  TGTGGGCAGA  CAGAGTGGAA
211  AGGGCCTTGG  ACATCCCATC  AGAGGCTTGG  CGATGCACAG  TAGCAAGGAT  GATAGTGTCA  GAAATGAGCA
281  AAAGGAGGAA  ACACATAAGT  GAGAGCAGAC  CACTGTTAGT  GAGCACCAGT  ATCTCAAAAC  CATAGGTGTC
351  TAAGCAGGCA  AGCTTGATCA  CTAGGAGGAG  GTCACAGAAA  AAATTGTCTA  CCCTGTTGGG  TCCACAGAAA
421  GGCAGATTGA  CTTTGAATGC  CAGGTGGGTG  GCTGAGTGTG  AGATGCCAAT  GGCCAGGAA  ACCCCACCA
491  GAACAGTTCA  CACCCTCCGG  TTCATGATGG  TTATGTAGTG  CAGAGGTTTG  CATATAGCAA  TGTATCTATC
561  ATAGGCCATG  GCAACAAGAA  GCACCATCTC  ACTACCCCA  AAAACATGCA  AGN

```

## SEQ. ID NO:2

```

1  GGNNNTNAC  ACGGACTCCA  AGCAGTGGTA  ACAACGCAGA  GTACGCCCGT  TCCTGAGTGA  GTAGATGAAG
71  GGGTTCAGCA  TGGGATTGAT  GACAGTGTTG  AAAATTCCAA  CAGCTTTATC  CTTGTCTGAA  AGCTTGGTTG
141  AACCAGTCG  CATATAGTTA  AAGATACCTG  AACCATAGAA  TATGGCAACC  ACAGTGAGGT  GGGAGCCACA
211  TGTGGAGAAG  GCTTCTTCC  TGCCCTCTAC  AGAGCGAATT  CGCAGGACTG  CAGCTGCCAC  GTGGATATAG
281  GAGATGACAA  TGAGAGCCAT  GGGGGTACCT  GCCATTATAA  AACCACAGC  AAAAAGCAGC  AGCTCATTGA
351  GTTGGGTGCT  GGAGCAGGAG  AGCTGGAAGA  GCTGTGGGAG  GTCACAGTAG  AAGTGATTGA  TCACATTGGG
421  GCCACAGAAG  TTGAGCGTGG  ACATGGCCAC  AGTGTGGGTC  AGTGCCTTGG  TGAAGCACA  AGCCAGGAC
491  GCAGCCATCA  ACATCCTCTG  GACTGTCTGA  CTCATGCGGG  TGCTTGTAGG  TGAGGGGCC  GGCAGATGGG
561  CAGGAATCGG  TCATAGGG

```

## SEQ. ID NO:3

```

1  TGGNNTTTTA  TCNCCNTTGG  AGCTCCNAAG  CAGTGGTAAC  AACGCAGAGT  ACGCCCGTTG  CGAAGCGTGT
71  AGATTAGGGG  GTTCAGTAGG  GGAGTGATGA  CAGTGTAGGT  CACCGAGATC  AGCTGGTCAT  GTTCTCTGGT
141  GTTCTCTGAC  TTGGGCTTGA  GGTAGGCAAT  GGAGGCACAG  CTGTAGTGGA  CAATGACCAC  AGTGAGGTGG
211  GATGCACAGG  TGGCAAAAGC  CTTCTTCCGG  CCCTCAACTG  AAGTAATCTT  GAGGATTGTA  GAGATAATGA
281  GAACATAAGA  AATGAAAACC  AGACCCATAG  GTACAACAAG  CACCAGCACA  CTGATAATCA  AAGTCAGGAT
351  TTCATTGACA  GTGGTGTCAA  TGCAGGAGAG  CTTTCATCACA  GGGCGGATGT  CACAGAAGAA  GTGGGGCACC
421  TTTTCTAGCA  CAGAAGGGTA  ACCTGAATAC  AGATGTCACT  TGCGTTATTG  CTACAATCAG  CCAATGCTG
491  CAAGGCCCCC  AGGACAAGTT  GGATACGCAG  CCTCTTGTTT  ATAATAACCA  TGTATCTCAA  GGGGGTTGCA
561  AGATGGCCAC  ATAGCNGNTC  ATATTCCN

```

## SEQ. ID NO:4

```

1  GTNGTTNTTA  ACNCCATTGG  AGCTCCAAAG  CAGTGGTAAC  AACGCAGAGT  ACGCCCCCAA  TGTATTTTTT
71  TTTGAGAAAC  TTGTCTTTCT  TAGATTTTTG  TTACATCTCT  GTCACAAATC  CAAAATCTAT  TGTTAGTTCC
141  TTGACTCATG  ATACTTCCAT  TTCTTTCTTT  GGGTGTGCTC  TGCAAGCCTT  CTTTTTCATG  GACTTGGCAA
211  CTACGGAGGT  AGCCATCCTT  ACAGTGATGT  CCTGTGACCG  CTATATGGCC  ATCTGCCGGC  CTTTACATTA
281  TGAGGTCATC  ATAAACCAAG  GTGTCTGTCT  GAGGATGATG  GCCATGTCGT  GGCTCAGTGG  GGTGATCTGT
351  GGATTCATGC  ATGTGATAGC  AACATTCTCA  TTACCATTCT  GTGGCGCAA  TAGAATACGT  CAATTTTTCT
421  GTAATATTCC  ACAACTNCTA  AGCCTCTTAG  ACCCCAAAGT  AATTACCATT  GAGATTGGAG  TCATNGGNTT
491  TTGGTACAAG  TCTTNGGATA  ATCCTCTTTG  NTGNAATTAC  TCTCTCTAC  ATGTNCATTT  TTTTTTGNCA
561  TCATGAGGGA  TTCCTTCTAA  AGG

```

## SEQ. ID NO:5

```

1  GNNGNTTNN  NCCNCCNTTG  GACTCCAAAG  CAGTGGTAAC  AACGCAGAGT  ACGCCCGTGT  GTAAATGAAT
71  GGGTTCAACA  TGGGAGTCAT  AACAGTGTAG  GACAATGATA  GCAGCTTCGT  GCCCTCAGGT  GAATTATTTG
141  ATTTAGGCCG  GAAGTAGGTG  AGGCTTAATG  ATATATAGAA  AAGAGAGACA  ACAAGGAGGT  GTGAGGAACA
211  TGTAGAAAAG  GCTTTATTCT  TCCCTTTAGC  TGATGGGATC  TTGAGGATGG  CAGCAGCAAT  GCGAGTATAG
281  GAACACAAGA  TCAGCAAGCA  GGGGATCATG  ACCACCAGAA  TGGTTCCGAC  GATGGCGTAG  ATCTCAAACA
351  GTGCTGTGTC  TGCACAGACC  AGCCTCAGCA  CAGGTGGGCT  GTCACAGAAG  AAGTGGTTCA  CCTTGTGGT
421  GCCACAGAAT  GGAAACTGA  AGAGCCATGT  GGTCTGCACA  GTAGCTACAG  GAAAGCCTGG  GAACCAGGAG
491  GCAGCAGCCA  GTTTGGCAG  AGTCCTTTGG  TTCATGATGA  CTGGGTAGTG  CAAGGGACTN  GCAGATNNNC

```

561 NCATTCGGTC ATATGNCATG GNAG

SEQ. ID NO:6

1 CNTTGGAGCT CCAAAGCAGT GGTAACAACG CAGAGTACGC CCGCTCCGCA GAGAATAGAT GAAAGGGTTC  
 71 AGGGTCGGGG GCACGACTGT GTAGAACGCA GACAGGAAAA CATCCAGAAC GGGGGGAGAA TTTGAAATTG  
 141 GCTTCACATA GGCAATGCTG CCAGATATCA TAAAGAGTGT TACAACCACA AGATGTGGAA TGCAGGTAGA  
 211 AAATGTTTTT GATCTACCCCT CCTTAGAAGG AATCCTCATG ATGACAGAAA AAATGTACAT GTAGGAGAGA  
 281 GTAATTACAA CAAAGGAGAT TATCACAAGA CTTGTACCAA AAACCATGAC TCCAATCTCA ATGGTAATTA  
 351 CTTTGGGGTC TAAGAGGCTT AGGAGTTTGT GGAATATTAC AGAAAAATTG ACGTATTCTA TTGCGCCAC  
 421 AGAATGGTAA TGAGAATGTT GCTATCACAT GCATGAATCC ACAGATCACC CCACTGAGCC ACGACATGGC  
 491 CATCATCCTC AGACAGACAC CTTGGTTTAT GATGACCTCA TAATGTAAAG GCCGGCAGGA TGGCCATATA  
 561 GCGGTCATAG GA

SEQ. ID NO:7

1 GCAGTGGTAA CAACGCAGAG TACCGCCCCC TATGTACTTT TTCTTGGGAA ACTTGTCTGT GTTTGACATG  
 71 GGTTTCTCCT CAGTGACTTG TCCCAAAATG CTGCTCTACC TTATGGGGCT GGGCCGACTC ATCTCCTACA  
 141 AAGACTGTGT CTGCCAGCTT TTCTTCTTCC ATTTCTCTCG GAGCATTGAG TGCTTCTTGT TTACGGTGAT  
 211 GGCCTATGAC CGCTTCACTG CCATCTGTTA TCCTCTGCGA TACACAGTCA TCATGAACCC AAGGATCTGT  
 281 GTGGCCCTGG CTGTGGGCAC ATGGCTGTTA GGGTGCATTG ATTCCAGTAT CTTGACCTCC CTCACCTTCA  
 351 CTTGCCACA CTGTGGTCCC AATGAAGTGG ATCACTTCTT CTGTGACATT CCAGCACTGT TGCCCTTGGC  
 421 CTGTGCTGAC ACATCCTTAG CCCAGAGGGT GAGCTTCACC AACGTTGGCC TCATATCTCT GGCTGCTTTC  
 491 TGCTAAATCT TTTATCCTAC ACTAGAATCA CAAATATCTA TCTTAAGCAT TCGTACAAC

SEQ. ID NO:8

1 GGAACAACGC AGAGTCGCCC CCGATGTACT TGTTCTTCTC CAACCTGTCC TTTGCTGACA TTTGTGTTAC  
 71 TTCCACCACC ATTCCAAAAA TGCTGATGAA CATCCAGACA CAGAACAAAG TCATCACCTA CATAGCCTGC  
 141 CTCATGCAGA TGTATTTTTT CATACTCTTT GCTGGATTTG AAAACTTCCT CCTGTCCGTG ATGGCCTATG  
 211 ACCGGTTTGT GGCCATCTGT CACCCCTGTC ACTACATGGT CATTATGAAC CCTCACCTCT GTGGACTGCT  
 281 GGTCTTGAGC TCCTGGACCA TGAGTGCTCT GTATTCTTG CTACAAATCT TAATGGTAGT ACGACTGTCC  
 351 TTTGTCACAG CCTTAGAAAT CCCCCACTTT TTCTGTGAAC TTAATCAGGT CATCCAACCT GCTTGTTCTG  
 421 ATAGCTTTCT TAATCACATG GTGATATATT TTACAGTTTG CGCTGCTGGG TGGAGGTCCC TGACTGGGAT  
 491 CCTTTACTTC TTACTCTAAG ATAATTTCTT CATACATGCA ATCTCANCAA GNTCAGGG

SEQ. ID NO:9

1 GGGTTTTNAC CCNNTNGGAG CTCCNAGCAG TGGTAACAAC GCAGAGTACG CCCGTTTCGT AGGCTATAAA  
 71 TGAAGGGGTT GAGTGAGGGA GTCACCACTC CATAGAAGAG GGCCATGAAC TTGGGTGAT CCCTTGAGAT  
 141 GGAGGAGGGG GGCTGAAGGT ACATGCTGAT GGCTGGGCCA TAAATAAGA AAACATAAAT AAGATGGGAG  
 211 GAGCATGTCC CAAAGGCCTT TNTCCTTCCC TTGGAAGATT TGATCTTAAA TACAGCACTT NCAATACTAG  
 281 CATAGGAAGC AAGAATTAAG CATANTGGGA CAGCTAACAT AAAAATGCAT ACCACAGAGA GTGTGAGCTC  
 351 GTTAGAACCC TTTTCACCAC AGGCAATCTT TATCAGAACA GGAATCTCAC ACACCAAGTG GTCCAGCTTA  
 421 TTGAGACCAC ACAGTGGNAA TTTGTATTGT GGCAGTGGCC CTCTGAGAAC GGCATAGATT ATACCAANTT  
 491 AACCACNACN GCGGNAACTA ANGATTGAGA CGCNCCTGGAT TCATGATGAG GGTNTAGTGA AGAGGTNTNC  
 561 AGAATGGCCA CATACCGNTC AAA

SEQ. ID NO:10

1 GCTGCTNCCA GCAGTGGTAA CAACGCANAG TACGCCCCCA ATGTATTTGT TCTTCGGCCA TCTGTCTCTC  
 71 CTGGATGTCT GCTTCATCAC CACTACCATC CCACAGATGT TGATCCACCT CGTGGTCAGG GACCACATTG  
 141 TCTCCTTTGT ATGTTGCATG ACCCAGATGT ACTNTGTCTT CTGTGTTGGT GTGGCCGAGA GCATCCTCTT  
 211 GGCTTTTCATG GCCTATGACC GNTATGNTGC TATCTGCTAC CCACTTAACT ATGTCCCGAT CATAAGCCAT  
 281 AAGGTCTGTG TCAGGCTTGT GGGAACTGCC TGGNTCTTTG GGCTGATCAA TGGCATCTTT NTCGGGTATA  
 351 TTTCATTCTT AGAGCCCTTC CGCAGAGACA ACCACATAGA AAGCTTCTTC TGGCAGGCCC CCATAGTGAT  
 421 TTGGCCTCTT TTGTGGGGGA CCCTNANANT AGTCTGTGGG CAAATCTTTN GCCGATGCCA TCGTGGTAAT  
 491 TCTNAGNCCC ATNGGTGCTN ACTGNTACTT ACCTATNTGC ACATTCTGT CCACCATCCT AGNNAAAGTC  
 561 CTCCTTCTN

SEQ. ID NO:11

```

1 GGNNTTTTAC CNCNATTGGA GCTCCAAAGC AGTGGTAACA ACGCAGAGTA CGCCCCCTAT GTACTTGTTC
71 TTGAGAAACT TGTCTTTCTT AGATTTTGT TACATCTCTG TCACAATTCC AAAATCTATT GTTAGTTCCCT
141 TGACTCATGA TACTTCCATT TCTTCTTTG GGTGTGCTCT GCAAGCCTTC TTTTTCATGG ACTTGGCAAC
211 TACGGAGGTA GCCATCCTTA CAGTGATGTC CTATGACCGC TATATGGCCA TCTGCCGGCC TTTACATTAT
281 GAGGTCATCA TAAGCCAAGG TGTCTGTCTG AGGATGATGG CCATGTCTGT GCTCAGTGGG GTGATCTGTG
351 GATTCATGCA TGTGATAGCA ACATTCTCAT TACCATTCTG TGGGCGCAAT AGAATACGTC AATTTTTCTG
421 TAATATTCCA CAGCTCCTAA GCCTCTTAGA CCCCAAAGTA ATTACCATTG AGATTGGAGT CATGGTTTTT
491 GGTACAAGGC TTGNGATAAT CTNCTTTGGT GNAATTACTC TCTCCTACAT GTACATTTTT TCTGCATCAT
561 GAGGATTCCCT TCTAAGGAGG GG

```

## SEQ. ID NO:12

```

1 GGNTTTGACC ACGGAGCTCC AAGCAGTGGT AACAAACGAG AGTACGCCCT CTTGTCCTCG TGCCGATACA
71 TGATGGGGTT CAACATGGGA GTCATAACAG TGTAGACAA TTCTTGCCCT TCTTGCCCT GAGGTGAATT
141 ATTTGATTTA GGCCGGAAGT AGGTGAGGCT TAATGATATA TAGAAAAGAG AGACAACAAG CAGGTGTGAG
211 GAACATGTAG AAAAGGCTTT ATTCTTCCCT TTAGCTGATG GGATCTTGAG GATGGCAGCA GCAATGTGAG
281 TATAGGAACA CAAGATCAGC AAGCAGGGGA TCATGACCAC CAGAATGGTT CCGACGATGG CGTAGATCTC
351 AAAGAGTGCT GTGTCTGCAC AGACCAGCCT CAGNACAGGT GGGCTGTAC AGAAGAAGTG GTTCACCTTG
421 TTGGTGCCAC AGAATGGAAA ACTGAAGAGC CATGTGGTCT GCACAGTAGC TACAGGAAAG CCTGGGAACC
491 AGGAGGTAGC AGCCAGTTTG CACGAGTCCC TTTGGTNNAT GAATGACTGG GGTAGTGCAA GGGACTGCAG
561 ATGGCCACAT ANCGGTCNT

```

## SEQ. ID NO:13

```

1 GNNNTTNNNN CCACTGGAGC TCCAAAGCAG TGGTAACAAC GCAGAGTACG CCCCCAATGT ATTTATTCTT
71 GCTCACCTCT CCTTAGTTGA TATCTGTTTT ACCACCAGTA TTGTCCCCCA GCTGCTGTGG AACCTAAAAG
141 GACCTGACAA AACAATCACA TTCCTGGGTT GTGTCATCCA GCTCTACATC TCCCTGGCAT TGGGCTCCAC
211 TGAGTGTGTC CTCCTGGCTG TAATGGCTTT TGATCGCTAT GCTGCAGTTT GCAAACCTCT CCACTATACC
281 GCCGTAATGA ACCCTCAGCT GTGCCAGGCT CTGGCAGGGG TTGCGTGGCT GAGTGGAGTG GGAACACTC
351 TTATCCAGG CACTGTCACC CTCTGGCTTC CTCGCTGTGG ACACCGATTG CACTAACATT TCTTCGTGAG
421 GTACCCTCCA TGATTAAGCT TGCATGTGTG GACATCCATG ATAATGAGGT TCAGTCTTTT GTTGCTTCAC
491 TGGTCTTGCT CCTCTTGCCC TTAGTGCTAA TACTGCTGCC TATGGACATA TAGCCAAGGT GGCATAAGGA
561 TCAAGTCAGT CCAGCCT

```

## SEQ. ID NO:14

```

1 GGNNTNTNAC TCCATGGACT CCAAGCAGTG GTAACAACGC AGAGTACGCC CATACTGAT GGGGTTCAGT
71 AGGGGAGTGA TGACAGTGTA GGTCAACGAG ATCAGCTGGT CATGTTCTCT GGTGTTCTCT GACTTGGGCT
141 TGAGCTAGG AATGGAGGCA CAGCTGTAGT GGACAATGAC CACAGTGAGG TGGGATGCAC AGGTGGCAA
211 AGCCTTCTTC CGGCCCTCAA CTGAAGCAAT CTTGAGGATT GNAGAGATAA TGAGAACATA AGAATGAAA
281 ACCAGACCCA TAGGTACAAC AAGCACCAGC ACACTGATAA TCAAAGTCAG GATTTTCATTG ACAGTGGTGT
351 CAATGCAGGA GAGCTTCATC ACAGNGCGGA TGTACAGAA GAAGTGGGGC ACCTTTCTAG CACAGAAGGG
421 TAACCTGAAT ACAGATGTCA CTTGCGTTAT TGTACAATC AGCCCAATGC TGCNGGCCCC CAGGACAAGT
491 TGGATACGCA GCCTTNTCGT TCTANTAACC ATGTATCTCA ANGGGCTTGC NGATNNCCAC ATACTNGCAT
561 ANACCATTCG TGNGAGC

```

## SEQ. ID NO:15

```

1 GNCNTNTTA ACNCCATTGG AGCTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCATTA CGAAAAGTGT
71 AGATGAAGGG GTTCAAGAGG GGTGTGATGA TGCAGCTCAG GACGGAGGCA CCTTTGTTGA GCAGTTTGGA
141 CTGAGCCTCT GACATACGAA TGTAGAGAAA GATGGAAGT CCATAGATGA TGACCACCAC TGTAAGATGC
211 GAGGCGCAAG TGGAAAACGC TTTCTTTCGC TCAGCAGCTG TAGGGGCCCT GAGAACAGTG GCAAGAATGC
281 AGGCATAGGA AACTGAGGTC AGAGCCAGTG AGCCAGTAA CACCAACGTA GAGAGCATGA AAGCCACCAG
351 TTTACAGCAG TGGGTGTCCC CACAAGAAAG CCTGAGCAAG GGCCAACTGT CACGAAAGAA GTGGTCAATA
421 CCATTGNGGC CACAGAAAGG CATGGCTGGC CATGAGGACA GTGGGGCAAA GGACCCAGAG GAATNCANCT
491 AGCCAGGAGG CCACACTAGT TTGTGAACAG ACATGGCCAT TNATTAGGGT CTCATAGCGG AGTTGTCGNC
561 AGATTTGCNT GGTNACGATT CAN

```

## SEQ. ID NO:16



```

1 GGNNTTTTAC CNCNATTGGA CTCCAAAGCA GTGGTAACAA CGCAGAGTAC GCCCCCTATG TATTATTCT
71 TGCTCACCTC TCCTTAGTTG ATATCTGTTT TACCACCACT ATTGTCCCC AGCTGCTGTG GAACCTAAAA
141 GGACCTGACA AAACAATCAC ATTCCTGGGT TGTGTCATCC AGCTCTACAT CTCCCTGGCA TTGGGCTCCA
211 CTGAGTGTGT CCTCCTGGCT GTAATGGCTT TTGATCGCTG TGCTGCAGTT TGCAAACCTC TCCACTATAC
281 CGCCGTAATG AACCCCTCAGC TGTGCCAGGC TCTGGCAGGG GTTGCGTGGC TGAGTGGAGT GGGAAACACT
351 CTTATCCAGG GCACTGTCAC CCTCTGGCTT CCCCCTGTG GACACCGATT GCTCCAACAT TTCTTCGTGA
421 GGTACCCTCC ATGATTAAGC TTGCATGTGT GGACATCCAT GATAATGAGG TTCAGCTCTT TGTGTCTTCA
491 CTGGTCTTGC TCCTCTTGCC CTTAGTGCTA ATACTGCTGC CTATGGACAT ATAGCCAANG TGGCATAAAG
561 GATCAAGTCA GTCCAGG

```

## SEQ. ID NO:17

```

1 GNNNNTTNTT CANTCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA
71 GAATTCGCCC TTATTCCGGA GGGTATACAT GAAGGGATTG GTAAGTAGAC GTAAACTCGA AGCCAAGAAC
141 AGAATTTCTC TTAGAAAAGA GAATTGAAAC TAAAGAGAAA GAACTAGCAA AGAAGGAAAT ATTGAATATA
211 CAAGAGAGAG GAGACAGATG ATGGAACAAG ACTCTGAAAG AGGTGGAAGG GATTGAATAC AATCAAAAGT
281 ATGGTGAAGT CTAGTTCCAA GATGGTGGCG TAGGGGCAAG CTGGCTTTGC TTACCCCCCT GGCAGAAAAC
351 CAAAAACAAA TAGCACCAG ATTATCACTA GCAATATCCC AGAACTCACA TATAAGGATG AGACAGTTCC
421 CAGGGCCCAG AGAAGATCAG AAGCACAAGT GGGAGAAGTC AGCTTTGGAT GCTACTTTGT TCTAAGGGAG
491 ACAAGTTGGG AGGATGATTG CAGATGTATA TTCAATGTTA TAAAACAGCC CATAAAACAA AGATTGGAAA
561 ATGTTGAATT TTGCAACCAG GAGCAAATAC TGGGAAAGGC GAATTCAGC CACTTGCGNC C

```

## SEQ. ID NO:18

```

1 GNNNNTTNAN TCANTGCCCT NGGGCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG
71 CAGAATTCGC CTTGTGTGCG CAAGGTGTAA ATGAAAGGGT TTGCGCAGGA GTAAATGAAG GGATTACGCA
141 GGAGTAAATG AAGGGATTAC GCAGGAGTAA ATGAAGGGAT TACGCAGGAG TAAATGAAGG GATTACGCAG
211 GAGTAAATGA AGGGATTACG CAGGAGTAAA TGAAGGGATT ACGCAGGAGT AAATGAAGGG ATTACGCAGG
281 AGTAAATGAA GGGATTACGC AGGAGTAAAT GAAGGGATTA CGCAGGAGTA AATGAAGGGA TTACGCAGGA
351 GTAAATGAAG GGATTACGCA GGAGCAAATA CATAGGAAGG GCGAATTCCA GCACACTGGC GCGCGTTACT
421 AGTGGATCCG AGCTCGGTAC CAAGCTTGAT GCATAGCTTG AGTATTCTAA CGCGTCACTT AAATAGCTTG
491 GCGTAATCAT GGTCATAGCT GTTCTCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG
561 CCCGGAAGCA TAAAGTGTA AGNCTGGGGT GCCTAATGAG TGACTTACTC CATTG

```

## SEQ. ID NO:19

```

1 GNNANTNATT CCATCCATTG TCCCTTCAGA TGCATGCTCG AGCGGCCGCC AGTGTGATGG ATATCTGCAG
71 AATTCGCCCT TCTTGGTTTT TGTGCTGATA GATCATGGGA TTCAGCATGG GGGTGACCAC AGTGTACATC
141 ACTGAGGCTG TTGCACTTGA GTGTGAGTTG CGGGTGGCAG CAGAACTAAG GTACACCCCT AGGATTGCAC
211 CATAAAATAA GGAGACAAC TGAAGGTGAG ATGCACAGGT GGAAGATGCC TTGTACTTCC CCTGAGCTGA
281 TGAGATNGCA TGTATGGAAN GAAATTATNT TANAAGTAAG AGTAAAGNAT NCCAGTCAGG GGNANCNTTC
351 ACCCATCAGN TGCAANTTGT AAAAATTATA TTCAANCNAT NTGNATTTAA NGAAAANCCT TATCANGTAN
421 AACTGCAAGN GNTNTGNATT NANCCCTNGN ANTTAANNNT TCNACAAGAA AATAANGTGC GTTNNAATCT
491 TTNTAAGTCC CTNTCNCCAT TAANGTCNAN TCCNTCCNTA TCCCTTTTCN NATTTTGNAN TCNNGANTAC
561 NNTCTNNNGC NNTCNATTTT TNTNNTNNCT GACCTACTAA CCNATTNAGT TACNACAAGN CCNTTCNANT
631 CTCTATAATT NCTCGCANGT TNTCCCTCTT NNCANNNTCC CNTTNTNTC CCTNTTCCCC ATCTNC

```

## SEQ. ID NO:20

```

1 CCATTGGCCC TCTAGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT CGCCCTTCCT
71 ATGTATTTTC TCTTACTGGG CTTTCTGGT TCTCAAATC TTCAGCTCTC TCTCTTTATG CTTTCTCTGG
141 TGATGTACAT CCTCACAGTT AGTGGTAATG TGGCTATCTT GATGTTGGTG AGCACCTCCC ATCAGTTGCA
211 TACCCCATG TACTTCTTTC TGAGCAACCT CTCCTTCTG GAGATTGGT ATACCACAGC AGCAGTGCCC
281 AAAGCACTGG CCATCCTACT GGAGAGAAGT CAGACCATAT CATTTACAAG CTGTCTTTTG CAGATGTACT
351 TTGTTTTCTC ATTAGGCTGC ACAGAGTACT TCCTCCTGGC AGCCATGGCT TATGACCGCT GTCTTGCCAT
421 CTGCTATCCT TTACACTACG GAGCCATCAT GAGTAGCCTG CTCTCAGCGC AACTGGCCTT GGGCTTCTGG
491 GTGGNTGGGT TCGGGGGCAA TGCAGTGCCC ACAGGCCTTC AATCAAGTGG GCTGNTCCTT CTGGTGGCCC
561 CCGGTGCCAA TCAACCACTT TTTTTTGGG ACAATTGCAN CCCTGGAATT GGGCC

```

## SEQ. ID NO:21

```

1 GNNCTTANTT CAATCCCACC NANCCNTGCC GANGCATGCT CGNGCGGCCG CCAGTGTGAT GGATATCTGC
71 AGAATTCGCC CTTCTATGT ATTTACTCTT ACTGGGCTTT CCTGGNTCTC AAACCTCTCA GCTCTCTCTC
141 TTTATGCTTT TTCTGGTGAT GTACATCCTC ACAGTTAGTG GTAATGTGGC TATCTTGATG NTGGTGAGCA
211 CNTCCCATCA GNTGCATACC CCCATGTTNT TCTTTCTGAG CNACCTCTCC TTCTGGAGA TTTGGTATNC
281 CNCAAGCNGC ANNGCCCCAA GCTTTGCNCA TCTTATTGCN CAGANGCINN CCNNTACANN NACNCTCCTG
351 TTTNTGGCTN CCTTNCCTCT TNCTTCNCTC ANNTACTNCN TCTNCTNTAG TNTCTTTCTT CTCTNCTNCT
421 CNTNNCNCCT NTAATNTTCC NCCTNTTCTN NTTCTNTTT TCCCTNCTCT GTTTCACCCC TACCTCTTAT
491 CCNTNCTNCT NACTTCANNC TCNGNCNNTN NNNCNCNNT AAATNTANGN NNANNTNNTN ATNNTNCTCTT
561 CTCNTTTTAT ATCGCCTCTT CTCNTNCTTC CNNTTCTCTC TCCTCANNCA TATCNANTNT NTTCTACTCT
631 CGTNCNNTAT CTANNCTCCT NTTTCNGTCC TNCTTCTCCT NTCATTTCTA TATTNCTTCT CANACANTNT
701 TCGCATCGTN GCANCATCTC CTCCCATCTC CTGTNCNCTN TTCCN

```

## SEQ. ID NO:22

```

1 GNNNTTAANT CATTCCCCNC TCNATGCATG CTCGAGCGGC CGCCAGNGTG ATGGATATCT GCAGAATTCCG
71 CCCTTGTTTC GGAGGCAGTA GATGAATGGG TTGATGGAAT CTGAGACAGT GCTCTAGAAT CTGTGTTTCA
141 TACAGGATGA GATATAAATG AAACAAATGC TAAATAATGA CACAAGGTAC CTGCGCGAGA GAGGAATCAT
211 CCACCTGGAA GGGTAGGCTG TTTGTGAATA ATGTAGGGTG GGAGAGAAGG CTTTACTAAG GAGATGGGCT
281 TAAAGAATGT GAACGATGTG CTCACAGAGG CCACAGAAGA GAAATTATAG CCAGGAGAAC AACCTGAAAG
351 ACAAAGGACA CGGTGGCATG AGCGCATGTA ACACAATGTA CTCAGGAAAT GGTGGGCATC CTGAGATATG
421 GAGTGGAAAT CAGTACAGGG CTTTGTAAAC TCAGCTTGGA GTCAGATCAC AGAAAGCCTT GACAAGGAAC
491 TGAAAATGGG TTCTGAAGGC CAGAAGCCCA TTCAAGATTC CCAAAGGGAA AAACACAAAT CAGCTTGTTT
561 TCAGGACGTA ATTCTTGCCA GTTGCTAGAA TTACATCAGA AAGGAGGTTT ACNT

```

## SEQ. ID NO:23

```

1 GNNNTNANTC ANNCANTGGG CCCTCTAGAT GCATGCTCGA GCGGCCGCCA GTGTGATGGA TATCTGCAGA
71 ATTCGCCCTT CCTATGTATT TCCTCTTACT GGGCTTTCCT GGTCTCTCAA CTCTTCAGCT CTCTCTCTTT
141 ATGCTTTTTT TGGTGATGTA CATCCCCACA GTTAGTGGTA ATGTGGCTAT CTGTATGTTG GTGAGCACCT
211 CCCATCAGTT GCATACCCCC ATGTACTTCT TTCTGAGCAA CCTCTCCTTC CTGGAGATTT GGTATACCAC
281 AGCAGCAGTG CCCAAAGCAC TGGCCATCCT ACTGGGGAGA AGTCAGACCA TATCATTTAC AAGCTGTCTT
351 TTGCAGATGT ACTTTGTTAT CTCATTAGGC TGCACAGAT ACTTCCTCCT GGCAGCCATG GCTTATGACC
421 GCTGTCTTGC CATCTGCTAT CCTTTACACT ACGGAGCCAT CATGAGTAGC CTGCTCTCAG CGCAGCTGGC
491 CCTGGGCTCC TGGGTGNGGG GGTTCGTGGC CATTGCAAGT GCCCACAAGC CTAATCAGT GGCCCTGTCC
561 NTCTGGGGGC CCGGGGCCA TTNACCACTT TNTTCTGGGA CAATTGCACC CCTGGAATTG G

```

## SEQ. ID NO:24

```

1 TNNTTAANTC ATTCCNTTGN CCCTCNAGAT GCATGCTCGA GCGGCCGCCA GTGTGATGGA TATCTGCAGA
71 ATTCGCCCTT TCCTTGTTAC TGAGGGAGTA GATTAGGGGA TTGATGGAAT CTGAGACAGT GCTCTAGAAT
141 CTGTGTTTCA TACAGGATGA GATATAAATG AAACAAATGC TAAATAATGA CACAAGGTAC CTGCGCGAGA
211 GAGGAATCAT CCACCTGGAA GGGTAGGCTG TTTGTGAATA ATGTAGGGTG GGAGAGAAGG CTTTACTAAG
281 GAGATGGGCT TAAAGAATGT GAACGATGTG CTCACAGAGG CCACAGAAGA GAAATTATAG CCAGGAGAAC
351 AACCTGAAAG ACAAAGGACA CGGTGGCATA AGCGCATGTA ACACAATGTA CTCAGGAAAT GGCTGGCATC
421 CTGAGATATG GAGTGAATA CAGTACAGGG CTTTGTAAAC TCAGCTTGGA GTCAGATCAC AGAAAGCCTT
491 GACAAGGAAC TGAAAATGGG TTCTGAAGGC CAGAAGCCAT TCAAGATTCC CAAAGGGAAA AACACANATC
561 ACTTGTTTTT AGGACGTATT CTTGGGCAGT TGCTAGAATT ACATCAGAAA GG

```

## SEQ. ID NO:25

```

1 GNNNTTANT CCATGCCCCT CTAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
71 GCCCTTGTTT CGCAGCCTAT AAATGAAGGG GTTGATGGAA TCTGAGACAG TGCTCTAGAA TCTGTGTTTC
141 ATACAGGATG AGATATAAAT GAAACAAATG CTAATAATG ACACAAGGTA CCTTGCCGAG AGAGGAATCA
211 TCCACCTGGA AGGGTAGGCT GTTTGTGAAT AATGTAGGGT GGGAGAGAGG GCTTTACTAA GGAGATGGGC
281 TTAAAGAATG TGAACGATGT GCTCACAGAG GCCACAGAAG AGAATTATA GCCAGGAGAA CAACCTGAAA
351 GACAAAGGAC ACCGGTGGCA TAAGCACATG TAACACAATG TACTCAGGAA ATGGCTGGCA TCCTGAGGTA
421 TGGAGTGGAA TACAGTACCG GGGCTTTGTA AACTCAGCTT GGAGTCAGAT CCAGAAAGCC CTTGACAAGG
491 AACTGAAAT TGGGTTCTTG AAGGCCAGAA GCCATTCAAG GATTCCCCAA AGGGGAAAAA CACAAATCAA

```

561 GCTTGTTTTT AGGGACCGTT AATTCTGGGG CCAGGTTGCT TGAATTACCT TCANGAAAGG GAGGTTTACA  
631 CT

## SEQ. ID NO:26

1 GNNCTTATTC ATCCCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG CAGAATTCGC  
71 CCTTTCTTTG TTCCTCAGAG TGTAGATTAG GGGGTTGATG GGGTTGATGG AATCTGAGAC AGTGCTCTAG  
141 AATCTGTGTT TCATACAGGA TGAGATATAA ATGAAACAAA TGCTAAATAA TGACACAAGG TACCTTGCCG  
211 AGAGAGGAAT CATCCACCTG GAAGGGTAGG CTGTTTGTGA ATAATGTAGG GTGGGAGAGA AGGCTTTACT  
281 AAGGAGATGG GCTTAAAGAA TGTGAACGAT GTGCTCACAG AGGCCACAGA AGAGAAATTA TAGCCAGGAG  
351 AACAACTGA AAGACAAAGG ACACGGTGGC ATAAGCGCAT GTAACACAAT GTACTCAGGA AATGGCTGNC  
421 ATNCTNAGAT ATGGAGNGNG AATACCAGTA CANGGCTTTN TANACTCANC TTGGAGTNCA GAATCACANA  
491 ANGCTTGCA AGGAACTGAA AATGGGTTCT GAAAGGCCAG AAGCCNTTNA AGATCCCCAA AGGGAAAAAA  
561 CACAAATCAA GCTTTTTTNA AGNACNGTAA TTCNTGGNGC CAGTTGCTTA GAATTNCCAT CANAAANG

## SEQ. ID NO:27

1 GGNNTAAGCC TTCCCCCTNC GATGCTGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA GAATTCGCCC  
71 TTCCCATGTA TTTCTCTTA CTGGGCTTTC CTGGTTCTCA AACTCTTCAG CTCTCTCTCT TTATGCTTTT  
141 TCTGGTGATG TACATCCTCA CAGTTAGNGG TAATGGGGCT ATCTTGATGN TGGTGAGCAC CNCCCATCAG  
211 TTGCATACCC CCATGTACTT CTTTCTGAGC AACCNNTCCN TCCTGGAGAN TTTGGNATAC CACACGCAAN  
281 NAGNGNCCNA AGGCACTTGG NCNTNCTACA GGNGGAGAAG GCTTGACCAT ANNATTTTAC CATGCCTNGC  
351 CTTANGNCAN ACCCNNTTN TNCCTNTNT TCCNCTNNNN GGTNNNTCAN CCGCANNCTT NNATCNNNTG  
421 NANCTTCATN GAATATGGNN TNNGTNTNTC TTGAGAGCCT CNNGATCNNA TTTTTTCCAN CNNCTAAAGN  
491 GGNGCTTNTC TCTCTNNNAT CTAGCTTNNT GGNCTCTTTT TNTNTNCTNA CCCGTGNTNT CCTATNTGNT  
561 GTCTCTTCCT ACNNNCTGCN NTTATTNTAN ATCANNTCTN NCNTTGCTCT CNTNTACNAC ATNATCATNC  
631 TCNCTCCCN CTNCTNCTCT CTATNNCNTA CCATCNCTCT CTTCTCATTC ANCTCTTNT CATTGNTTGT  
701 TCANTTANNC ACTCTCCNTC NCATCTTCTA TNCACANTT TTNTNTTTT NCTCTCTANT TCTNNTTCCA  
771 NTGTNCACTC CNNTCTTNNC NNTTNCCCTA NCG

## SEQ. ID NO:28

1 GTNNTTNANN NCATTGCCCC TCTNGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT  
71 CGCCCTTCCT ATGTACTTCC TCTTACCGGG CTTTCTGGT TCTCAAACTC TTCAGTCTC TCTCTTTATG  
141 CTTTTTCTGG TGATGTACAT CCTCACGGTT AGTGGTAATG TGGCTATCTT GATGTTGGTG AGCACCTCCC  
211 ATCAGTTGCA TACCCCATG TACTTCTTTC TGAGCAACCT CTCCTTCTG GAGATTGGT ATACCACAGC  
281 AGCAGTGCCC AAAGCACTGG CCATCCTACT GGGGAGAAGT CAGACCATAT CATTTACAAG CTGTCTTTTG  
351 CAGATGTACT TTGTTTTCTC ATTAGGCTGC ACAGAGTACT TCCTCCTGGC AGCCATGGCT TATGACCGCT  
421 GTCTTGCCAT CTGCTATCCT TTACACTACG GAGCCATCAT GAGTAGCCTG CTCTCAGCGC AGCTGGCCCT  
491 GGGCTTCTGG GTGGGTGGGT TTCGGGGCCA TTGCAAGTGC CCACAGCCCT TATCAAGTGG CCTGTCCCTC  
561 TGNGGCCCCC GGGCCCATCA ACCACTTTTT TCTGGGGACA ATTGCACCCT GGAATGCCCC

## SEQ. ID NO:29

1 GTNNTTNANN CCATNCCATT GGGCCCTCTA GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC  
71 AGAATTCGCC CTTTCATGGT TCCGGAACA GTAAATTATG GGGTTCAGTC ATGGTAACAG GAGGAGGCTG  
141 AGTGATGGG CATGGATGGG GGCTGTGAAT GTGGCGGGAG CTCATGGATG TGCTCTTCTG AGTGCTTCAC  
211 GTTCTGTAGT GAAATAAGAA GCAAGGTCAT CACCGAGAGG GAGGAGACAG GCTCGGGTGA GTTTAGTGGA  
281 TATGAATCCA AGAGAGACCA TTCAACTTAG TTGCTATTTT TTTTCTCTC CAGTTATAGT CACTTGATG  
351 AATGTAGATG TGGAGTACTT GATCATAAGA TCCATTTTAT GGCAGAAGAC ATTATTTTTC TGAGCCTTCT  
421 GCTGTCAGTT TCTAAATAAG CAGGCCAGCC GGGCTGTGCA CCTAAATGTC TGTCTGGGAG GAGCAGGCTG  
491 AGAAGTCTTG CAGTCTGCAG GACACCCGAG GAATCGTATT GTGGGAACCG TCCCCAGAA CCACACGAGC  
561 CGTGCTNCTC AGTNCTGACT GGAANAATGA AATTGNAAGC CAAGTNGTTC NNGGANCNNT

## SEQ. ID NO:30

1 GNNNTTNANN CCATTGCGCC CTCTAGATGC ATGCTCGAGC GGCCGCCAGT GTGATGGATA TCTGCAGAAT  
71 TCGCCCTTCC TATGTATTTT TCTTCTAAC GATTGGAATG CCTGGGATTA GGCAGATGAT TTTCTTTTTT  
141 CCCCATACCC CTCTATTATT TAGGTGATTG AGTTTAAATC CCTTTATCTA CACCCCTTCG AACAAGGGCG  
211 AATTCCAGCA CACTGGCGGC CGTTACTAGT GGATCCGAGC TCGGTACCAA GCTTGATGCA TAGCTTGAGT

281 ATTCTAACGC GTCACCTAAA TAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC  
 351 CGCTCACAAT TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG  
 421 CTAATCACA TTAATTGCGT TGCCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT  
 491 TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTCGCGTA TTGGGCGCTC TTCCGCTTTC TCGCTCACTG  
 561 ACTCGCTGGG CTTCGGTCGN TCGCTGCGG CGAGCGGGAT CAGCTCACTC AAAAG

## SEQ. ID NO:31

1 GNNNNNNNNT CANGCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA  
 71 GAATTCGCCCT TTCTATGTA TTTCTCTTCA CTTTCTCCGA CATCACTCAC AGCCACCCCA CCCTCAGCCT  
 141 CTCCCTCCTC CCATGTATTT TCTCTTCAAT CTCTCCTTCT TTGATATCCT GAACTTTCTG TAGCTCTTTA  
 211 TTTTCTCTTC CAATCCCTTC ATATACACGT TTCGTAACAA GGGCGAATTC CAGCACACTG GCGGCCGTTA  
 281 CTAGTGGATC CGAGCTCGGT ACCAAGCTTG ATGCATAGCT TGAGTATTCT AACCGCTCAC CTAAATAGCT  
 351 TGGCGTAATC ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG  
 421 AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCATAATGA GTGAGCTAAC TCACATTAAT TCGGTGCGCT  
 491 CACTGGCCGC TTTCCANGTC GGGAAACCTG TCGGCCAGCT GCATTAAATG AATCGGCCAA CGCNCGGGA  
 561 GAGGCGGTTT GCGTATTGGG CGCTNTTTCG TTCTTCGNTN ACTGATCGNT GG

## SEQ. ID NO:32

1 GNNNNNNNNT TCATNCCATT GGGCCCTCTA GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC  
 71 AGAATTCGCC CTTGTTGCTT AGAGTGTAAG TAAAGGGTT AACATTGGCT TAGAGGTGAA GAGTAAATAC  
 141 ATAGGAAGGG CGAATTCCAG CACACTGGCG GCCGTACTA GTGGATCCGA GCTCGGTACC AAGCTTGATG  
 211 CATAGCTTGA GTATTCTAAC GCGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG TTTCTGTGT  
 281 GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAG CCTGGGGTGC  
 351 CTAATGAGTG AGCTAACTCA CATTAAATTG GTTGCGCTCA CTGCCCGCTT TCCAGTCGGG AAACCTGTCTG  
 421 TGCCAGCTGC ATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT  
 491 CCTCGCTCAC TGACTCGCTG CGCTCGGTG NTCGGCTGCG GCGAGCGGTA TCAAGCTCAC TCAAAGGCGG  
 561 TAATACGGTT ATCCACAGAA TCAGGGGGAT ACGCANGAAA GAACATGTGA GCAAAAT

## SEQ. ID NO:33

1 GNTNTNANTC ATGCCCCCNC CGATGCNTGC NCGAGCGGCC GCCAGTGTGA TGGATATCTG CAGAATTCGC  
 71 CCTTGTGCGG GAGCGAATAT ATGAAGGGGT TAAGGGAAGA GAAAATACAT AGGAAGGGCG AATTCCAGCA  
 141 CACTGGCGGC CGTTACTAGT GGATCCGAGC TCGGTACCAA GCTTGATGCA TAGCTTGAGT ATTCTAACGC  
 211 GTCACCTAAA TAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT  
 281 TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAATCACA  
 351 TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT TAATGAATCG  
 421 GCCAACGCGC CGGGGAGAGG CGGTTTGCGT ATTGGGCGCT CTNCGCTTC CTCGCTCACT GACTCGCTTG  
 491 CGCTCGGTCC GTTCGGCTGC GGCGAGCGGT ATCAANTCAC TCAAAAGGCG GGAATACGGG TTNACACAGA  
 561 AATCAGGGGG ATAACGCNGG AAAGAACATG TGAGCCANAN GGCAGCAAAA GGCNAGGAA T

## SEQ. ID NO:34

1 GNNNNNNNNT CANNCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA  
 71 GAATTCGCCCT TTGTTCCGAA GGCTATAGAT GAAGGGGTTT TAGGTTTTTA GGAACACAGG CTAAGGGGGA  
 141 AGAGAAAATA CATGGGAAGG GCGAATTCCA GCACACTGGC GGCCGTTACT AGTGGATCCG AGCTCGGTAC  
 211 CAAGCTTGAT GCATAGCTTG AGTATTCTAA CGCGTCACCT AAATAGCTTG GCGTAATCAT GGTATAGCT  
 281 GTTCTCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT AAAGTGTAAG  
 351 GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG  
 421 GAAACCTGTC GTGCCAGCTG CATTAAATGAA TCGGCCAACG CGCGGGGAGA GCGGTTTGC GTATTGGGCG  
 491 CTCCTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTG GTCGGCTGCG GCGAGCGGTA TCAGCTCACT  
 561 CAAAGGCGGT AATACGGGTA TCCACAGAAT CANGGGATAA CGCAGGAAAA GACA

## SEQ. ID NO:35

1 GGNNNTNANT CATTGCCCGC CTNGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAAATC  
 71 GCCCTTCCGA TGTATTTTCT TCTACGTTAA GGTATTTTAA ATTGTTACTA ATGCATAAGG GCAACACATT  
 141 CTGTAATGCT GACAAGATGA AAGAGCCAAA AGTAATTAAT GATGCTGTGA CCTCACAAAT ATGTATGTGT  
 211 GGATGTATAT ATATCTATTC AATATATGTA ACTATACATA TGTCTGTTTC TAATTGAAAA CACCAGGTAA

281 TTATCATCTG TAGAAACCCCT AGTGTCTCAG ATAAGTTGGC TAGTTTTTGG TTTCACATAA AGGAACAAAC  
 351 ATTTATAGAT TTATATGTAT ATTAATAATG GTAAAAATTG GCTGGGTGCA GTGGTTCATG CCTATAATAC  
 421 CAGCACTTTG GGAAGCCGAG GTGGGCGGAT TACTTGAGGT AAGGAGCCCA GCCTGACCAA CAAGGTGAAA  
 491 CCCCATCCCT ACTAAAAATA CAAGAATTAG CCCGGGGATG GTGGTGGCCA CCTGTAATCC CAGCTACTTG  
 561 GGAGACTGAA GCCAGGAAAA TCACTTGACC CAGGAAGCNG AGGTTGCAGG NGAG

## SEQ. ID NO:36

1 NGNNNTTGAN TCAATTCNNN GNCGANGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC  
 71 GCCCTTCCTA TGTATTTCCCT TCTAGCCAAC CTCCCACTCA TTGATCTGTC TCTGTCTTCA GTCATAGCCC  
 141 CCAAGATGAT TACTGACTTT TTCAGCCAGC GCAAAGTCAT CTCTTTCAAG GGCTGCCTTG TTCAGATATT  
 211 TCTCCTTCAC TTCTTTGGTG GGAGTGAGAT GGTGATCCTC ATAGCCATGG GCTTTGACAG ATATATAGCA  
 281 ATATGCAAAC CCCTACACTA CACTACAATT ATGTGTGGCA ACGCATGTGT CGGCATTATG GCTGTGCGAT  
 351 GGGGAATTGG CTTTCTCCAT TCGGTGAGCC AGTTGGCCTT TGCCGTGCAC TTACCTTTCT GTGGTCCCAA  
 421 TGAGGTCGAT AGTTTTTATT GTGACCTTCC TAGGGTAACC AAACCTGCCT GTACAGATAC CTACAGGCTA  
 491 GATATTATGG TCATTGCTAA CAGTGGTGTG CTCACTGTGT GGTCTTTTGT CTTCTAATCA TCTCATACAC  
 561 TATCATCTA ATGACCATCC AGCATTGCCC TTTAGATAAG TCGTNCAAAG G

## SEQ. ID NO:37

1 GNNNTNANTC CNNNCCNCCN CTAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC  
 71 GCCCTTCCCA TGTATTTGCT TCTCAGCAAC TTGTCCTTCT CTGACCTCTG CTTCTCTTCC GTGACCATTC  
 141 CCAAGTTGTT ACAGAAACATG CAGAACCAGG ACCCATCCAT CCCCTATGCG GACTGCCTGA CCCAAATGTA  
 211 CTTCTTCTCG TTATTTGGAG ACCTGGAGAA CTTCTCTCCT GTGGCCATGG CCTATGACCG CTATGTGGCC  
 281 ATCTGCTTCC CCCTGCACTA CACCGCCATC ATGAGCCCCA TGCTCTGTCT CGCCCTGGTG GCGCTGTCTT  
 351 GGGTGCTGAC CACCTTCCAT GCCATGTTAC ACACTTTACT CATGGCCAGG TTGTGTTTTT GTGCGAGCAA  
 421 TGTGATCCCC CACTTTTCT GNGATATGTC TGCTCTGCTG AAGCAGGCCT TCTCTGACAC TCGAGTTAAT  
 491 GAATGGGTGA TATTTATCAT GGGAGGGCTC ATTCTTGTC TCCCATTCCT ACTCATTCTT GGGTCCTATG  
 561 CAAGAATTGT CTCCTCATCC TCAAGTCCC TTTNTAANG GTATCTGCAA GGCCCT

## SEQ. ID NO:38

1 NGNNNNNTNA NTCNANGCCN NGNGCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG  
 71 CAGAATTGCG CTTTCCAATG TATTTACTTC TCAGCCAGCT CTCCCTTATG GACCTGATGT ACATCTCCAC  
 141 CACCGTCCCC AAGATGGCGT ACAACTTCCT GTCCGGCCAG AAAGGCATCT CTTTCTGGG ATGTGGTGTG  
 211 CAAAGCTTCT TCTTCTGAC CATGGCGTGT TCTGAAGGCT TACTCCTGAC CTCCATGGCC TACGACCGTT  
 281 ATTTGGCCAT CTGCCACTCT CTCTATTATC CTATCCGCAT GAGTAAAATG ATGTGTGTGA AGATGATTGG  
 351 AGGCTCTTGG AACTTGGGGT CCATCAATC CTTGGCACAC ACAGTCTTTG CCCTTCATAT TCCCTACTGC  
 421 AGGTCTAGGG CTATTGACCA TTTCTTCTGC GATGTCCAG CATGTTGCT TCTTGCTGTA CAGATACTTG  
 491 GGTCTATGAA TATATGGTTT TTGTAAGGAC AAAGCCTCTT TCTTCTTTN CCTTTCATTG GCATCACTTC  
 561 TTCTGNNGGC CGAGTCCTAA TTGCTGGCTA TATAATGCAC TCAAAGGAGG GGAGG

## SEQ. ID NO:39

1 TAGNNNNNTT ANNTCANNGC CNNTGNNNGC TCAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC  
 71 TGCAGAATTC GCCCTTCCAA TGTATTTTCT TCTCAGCAGG AGAGATATTT ATCCTCACTG CCATGTCCTA  
 141 TGACCGCTAT GTAGCCATCT GCTGTCCCCT GAACTACGAG GCTGCACAGA GTACTTCTC CTGGCAGCCA  
 211 TGGCTTATGA CCGCTGTCTT GCCATCTGCT ATCCTTTACA CTACGGAGCC ATCATGAGTA GCCTGCTCTC  
 281 AGCGCAGCTG GCCCTGGGCT CCTGGGTCTG TGGTTTCGTG GCCATTGCAG TGGCCACAGC CCTCATCAGT  
 351 GGCCTGTCTT TCTGTGGCCC CCGTGCCATC AACCATTCTT TCTGTGACAT TGCACCCTGG ATTGCCCTGG  
 421 CCTGCACCAA CACACAGGCA GTAGAGCTTG TGGCCTTTGT GATTGCTGNT GTGGTTATCC TGAGTTCATG  
 491 CCTCATCACC CTTGTCTCCT ATGTGTACAT CATCAGCACC ATCCTTAGGA TCCCTCTGCT AGTGGCCGGA  
 561 GCAAAGCCTT CTCCCGTGCT CCTCGCATCT NAACNGGTG CTCATTGGT ATGGG

## SEQ. ID NO:40

1 CATGCTCGAG CGGNCGCCAG NGNGATGGAT ATCTGCAGAA TTCGCCCTTC CTATGTATTT GCTTCTCAGC  
 71 AGGAGAGATA TTTATCCTCA CTGCCATGTC CTATGACCGC TATGTAGCCA TCTGCTGTCC CCTGAACTAC

141 GAGGTGATTC ATGTGCCCAT TAGAGCTTGA GAAGCACTGC TTGGAAGCCC CTTCTGCCAT CAATGAGGCT  
 211 GCACAGAGTA CTTCTCCTG GCAGCCATGG CTATGACCG CTGCCTTGCC ATCTGCTATC CTTTACACTA  
 281 CGGAGCCATC ATGAGTAGCC TGCTCTCAGC GCAGCTGGCC CTGGGCTCCT GGGTCTGTGG TTTCTGGCC  
 351 ATTGCAGTGC CCACAGCCCT CATCAGTGGC CTGTCTTCT GTGGCCCCCG TGCCATCAAC CACTTCTTCT  
 421 GTGACATTGC ACCCTGGATT GCCCTGGCCT GCACCAACAC ACAGGCAGTA GAAGCTTGNG GCCTTTGTGA  
 491 ATTGCTGNTG TGGGTATCCC GAGTTCATGC CTCATCACCC TGNCTTCTA TGTGTACATC ATCAGGCACC  
 561 ATTCTCAGGA TCCCTTCTGC AAGNGG

## SEQ. ID NO: 41

1 ATGGNNNNNN NNTTTNNNA ANTTTTNCCC ANTTTGGGCG GNCCCCCCT TCTTTAAGGN AATGGGCCCCA  
 71 TTGGGGCCCTT CCCGGAAGGC CCGGGGGCNC CCGGCCCCAA AGGTTTGGGT TGGGAAATGG GGGGAATTTA  
 141 AATTCCCTTTG GGCCAAGGNA AAAATTTTCC NGCCCCCCTT TTTTCCCTT TTTGGTTTTT ANCCGGGGGA  
 211 ANGGGGGGGT TGATTAATTA ATCGGGAAGN TNGGGGGGAA NTTTTTTAA AAAAACCTTG GGGGAAGGTT  
 281 CCAACCCAAC AAGGTTGGTT TTCCANGGGA CCGTTGGGAC CAGGCTTTTN GAATCAAGAA TCCCAAAGGG  
 351 CATTCTTTTG GATTAAGGAA NGGTGCCGGG ACCGGTGAAA GGGAAAAAAC TGGTGGACCC CATACCAAAA  
 421 TGAGAACCAC GGTGAGATGC CGAGGAGCAC GTGGAGAAAG GCTTTGCTTC CGGCCACTGG CAGAGGGGAT  
 491 CCTGAGGATG GTGCTTGATG ATGTACACAT AGGAGACAA GGGTGATGAG GCATGAATC AGGATAACCA  
 561 CAACAGCNAT CACAAAGGCC ACAAGCTCT ACTGCCTGTG TGTGGGTGC AGGCCAGGGC AATCCAGGGG  
 631 TGCAATGTCA CAAGAAAGAA AGTGGTTGAT GGCACGGNG GGCCACAGAA GGACAGGCCA CTTGATGAAG  
 701 GGCTTGTTGG CACTGCAATG GCCACGAAAC CACCAGACCC AGGAACCCAN GGCCAAGCTT GCGCCTGAAG  
 771 AGCAAGGCTA CTCATGAATG GCTTCCGTAG TNGTAAAGGA TAGCAAGATG GCAAAGGCAA GCCGGTCATN  
 841 AAGCCATGGC TTGCCNG

## SEQ. ID NO: 42

1 GNNNTTANNN CATTGCGCCC TCTAGATGCA TGCTCGAGCG GCNCGCCAGT GTGATGGATA TCTGCAGAAT  
 71 TCGCCCTTGT TGCGCAAGGA GTAGATGAAC GGATTCAGGG CAAGGGAGTG CTGAGGAGAT AGACGGGTAT  
 141 AACTGGGCA CAAGTCCATG AGTAATCAAG GCCTGTTATT TAAAAAAA AAAAAAAG CTTGAACAAT  
 211 ATAGAATCCC ATTACCCAGA GATAGACTGG ATGGTGAATT AAATTTCTG GTGAATTTCT TTCCAGATAT  
 281 CTCTCTATG ATATGTATAC ACAAGCAATT TTGGAAGAA AAGATACTTT ATAAGGATAA GCCTGAAAC  
 351 TGCAACGAAT GCAATGTGGA GAATGAAGGC AAGATGTGGC GAAGAAGGGC ACCACAATCT GGTGGCTGAG  
 421 AGAGTGCAAC TGCTACTACA GCTAAAAGGA GAGCTGGAGA AGCTGGTGAG GACAGTAAGA GATGAATCTG  
 491 GTTTAAGACA CGCTGAGTCT CAAATGCCAT GGCTCCCCTA GGTGCTCTCT TCAGATGTAA ATCTTAAGCT  
 561 CAAAGCAGGT GGATGAGAAA TCACATTTCA TAGTCCCTGC ACAGACGGCT NTNTTGAGCT

## SEQ. ID NO: 43

1 GNNNTTANNN TCATTGCCCC GNNNGANGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT  
 71 CGCCCTTCCC ATGTATTTGC TTCTCAGCAA CTGTCTCTTC TCTGACCTCT GCTTCTCTTC CGTGACCATT  
 141 CCAAGTTGT TACAGAACAT GCAGAACCAG GACCCATCCA TCCCCTATGC GGACTGCCTG ACCCAAATGT  
 211 ACTTCTTCTT GTTATTTGGA GACCTGGAGA GCTTCTCTCT TGTGGCCATG GCCTATGACC GCTATGTGGC  
 281 CATCTGCTTC CCCCTGCACT ACACCGCCAT CATGAGCCCC ATGCTCTGTC TCGCCTGGT GGCCTGTCC  
 351 TGGGTGCTGA CCACCTTCCA TGCCATGTTA CACACTTTAC TCATGGCCAG GTTGCTTTTT TGTGCAGACA  
 421 ATGTGATCCC CCACTTTTTC TGTGATATGT CTGCTCTGCT GAAGCTGGCC TTCTCTGACA CTCGAGTTAA  
 491 TGAATGGGTG ATATTTATCA TGGGAGGGCT CATCTTGCA TCCATTCCTA CTCATCCTTG GGTCTATGC  
 561 AAGAAATGCT CCTCATCCTC AAGGCCCTTC TNTAAGGGTA TCTGCAAG

## SEQ. ID NO: 44

1 GNNNTTNANT CNTGCCCTGN CCCNCGCNC NNGCGCCGCG GCGGATGGAT ATCTGCAGAA TTCGCCCTTG  
 71 TTACTAAGAG TATAGATGAA CGGATTCAGG GCAAGGGAGT GCTGAGGAGA TAGACGGGTA TACACTGGGC  
 141 ACAAGTCCAT GAGTAATCAA GGCTGTAT TTAACAAAAA AAAAAAGCT TGAACATAT AGAATCCCAT  
 211 TACCCAGAGA TAGACTGGAT GGTGAATTAA ACTTCTGGT GAATTTCTTT CCAGATATCT CTCTATGCAT  
 281 GTGTATACAC AAGCAATTTT TGGAGAAAA GATACTTTAT AAGGATAAGC CTGAAAACTG CAACGAATGC  
 351 AATGTGGAGA ATGAAGGCAA GATGTGGCGA AGAAGGGCAC CACAACTCTG TGGCTGAGAG AGTGCAACTG  
 421 TCACTACAGC TAAAGGAGA GCTGGAGAAG CTGGTGAGGA CAGTAAGAGA TGAATCTGGN TTAAGACACG  
 491 CTGAGTCTCA GATGCCATGG CTTCCCTAGG TTGCTCTTN CAGATGTAA TCTTAAGCTC AAAGCANGTG  
 561 GATGAGAAAT ACACATTTNA TAGTCACCTG CACAGACGGT TTTTGTAT

## SEQ. ID NO: 45

```

1 CATGCCCGT CCCNCNAGNT NCNNGCNCCG CGGCCGCNAN GGATATCTGN ANAATTCGCC CTTCTATGT
71 ATTTACTTCT CCAACTTCTC CTTCCCATCT CTATCATTAG AACCATTCA TATACACCCT ACGAAACAAG
141 GGCGAATTCC AGCACACTGG CGGCCGTTAC TAGTGGATCC GAGCTCGGTA CCAAGCTTGA TGCATAGCTT
211 GAGTATTCTA ACGCGTCACC TAAATAGCTT GGCGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT
281 TATCCGCTCA CAATTCCACA CAACATACGA GCCGGAAGCA TAAAGTGTAA AGCCTGGGGT GCCTAATGAG
351 TGAGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT
421 GCATTAATGA ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCTCGCTCA
491 CTGACTCGCT GCGCTCGGTC GTTCGGCTGN GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG NAATACGGTT
561 ATCCACAAGA ATCAGGGGGA TAACGCAAGA AAAGACATGT GA

```

## SEQ. ID NO: 46

```

1 GNNNTNATTN ATTGCATTGG GCCCTCTAGA TGCATGCTCG AGCGGCCGCC AGTGTGATGG ATATCTGCAG
71 AATTCGCCCT TAGTGAGTAG ATGAAAGGGT TCAGCATGGG GGTCAACACA GTGTACATCA TAGCCATGAC
141 AGTGTCCTTT AGAGTAGAAC TATTAGCTGA TGAGCATAAG TAGAGACCAA TAACGGTTCC ATAGAACAGT
211 GACACCACAG ATAGGTGGGA GCCACAAGTA GAGAAGGCCCT TGCAGACACC CTTAGAAGAA GGGACCTTGA
281 GGATGGAGGA GACAATTCTT GCATAGGACC CAAGGATGAG TAGGAATGGG ATGACAAGAA TGAGCCCTCC
351 CATGATAAAC ATCACCATT CATTAACTCG AGTGTCAGAG AAGGCCAGCT TCAGCAGAGC AGACATATCA
421 CAGAAAAGGT GGGGGATCAC ATTGTCTGCA CAAAAACACA ACCTGGCCAT GAGTAAAGTG TGTAACATGG
491 CATGGAAGGT GGTCAGCACC CAGGACAGCG CCACCAGGGC GAGACAGAGC ATGGGGCTCA TGAGGGCGGT
561 GTAGTGCAGG GGAAGCAGA TGGCCACATA GCGGTCATAG GCCATGGCCA CAAGGAGGAA

```

## SEQ. ID NO: 47

```

1 CNATGGGCC TCTAGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT CGCCCTTCCA
71 ATGTATTTGC TTCTCAGCAA CTTGTCTTTC TCTGACCTCT GCTTCTCTTC CGTGACCATT CCCAAGTTGT
141 TACAGAACAT GCAGAACCAG GACCCATCCA TCCCCTATGC GGAATGCCTG ACCCAAATGT ACTTCTTCTT
211 GTTATTTGGA GACCTGGAGA GCTTCCTCCT TGTGGCCATG GCCTATGACC GCTATGTGGC CATCTGCTTC
281 CCCCTGCACT ACACCGCCAT CATGAGCCCC ATGCTCTGTC TCGCCCTGGT GGCGCTGTCC TGGGTGCTGA
351 CCACCTTCCA TGCCATGTTA CACACTTTAC TCATGGCCAG GTTGTGTTTT TGTGCAGACA ATGTGATCCC
421 CCACTTTTTC TGTGATTTGT CTGCTCTGCT GAAGCTGGCC TTCCCTGACA CTCGAGTTAA TGAATGGGTG
491 ATATTTATCA TGGGAGGGCT CATTCTTGTC ATCCCATTCC TACTCAATCC TTGGGTCTAT GCAAGAAATT
561 GTCTTCTTCA TNCTCAANGG CCCTTTCTTC TAANGGTATC TTGCAAG

```

## SEQ. ID NO: 48

```

1 ANNNCCNTNG GAGCTCCAAA GCAGTGGTAA CAACGCAGAG TACGCCCCCT ATGTACTTAC TTTTGTTAAG
71 TCCAACCTCC ATCCTCCTTG GCCTTTTGAT TCAATTGATC ACTCCTTCTT CCTCAAAACA CCTTGTTTAC
141 TCATCCTTTC TCAGTCTCCT TTGTGGATTG TTCCTCATTT ATTTGACCTC TTGCTGGTGA ACCCTTTCAT
211 ATACACTCTC CGTAACAAAG AGGGCGTACT TCTGTCTGCT TGAGCGNACT GATGGNACCC AGCTTTTGTG
281 CCCTTTAGTG AGGGNTAATT GCGCGCTTGG CGNAATCATG GNCATAGCTG NTTNCTGNNGN GAAANTGNTA
351 TTTCGNTNAC AATTNCACAC AACATACNAG CCGGGAGCAT AAAGGGNNAA GNCCTGGGGN GCCTAATGAG
421 GGAGCTTACT CACAATAATT GGGGTGNGCC CACTGGCCCC TTTTCAGGCG GGAAAACCTN GCGGGGCCAG
491 CTGGAATAAA TGAATCGGGC CACGCGCCGG GGAGGAGGGC GGGTTNNGGA ATTGGGCGCT TTTCCNTTT
561 CTNGGTAAAT GGAATNGGTN GGCNNNGTCC GTTCGGTTGG GGGGANCGGN NNT

```

## SEQ. ID NO: 49

```

1 AACGCAGAGT ACCGCCCACT ACGTAATCTG TACATGAAAG GGTTTAAAG AGACTGGGAA GAGAGGAATT
71 GGCAAGATCA AGCAGAGGCA ACTCCTTCTA GTCCTTCTAG TACCGCAAGG GGCAGATAAA TGGAAATGGT
141 AACACCTAGA GGAAAGTATA CTTGCCAAAA GCAAAATNCAT AGGGGGGAGT ACATTATCGG GTTGAAAAA
211 GTATTCCATG CAGATAAAAA CAAAAGCAA ATACATCGGG GCGTACTTTC TGTCGTCTTT GAGCGTACTG
281 ATGGTACCCA GCTTTTGNTC CTTTAGTGAG GGTAAATTGC GCGCTTGGCG TAATCATGGT CATAGCTGGT
351 TTCTGTGTGA AATTGTTATC CCGCTCACA TTCACACAAC ATACGAGCCC GGGAGCATAA AGTGTAAGC
421 CTGGGGTGCC TAATGAGTGG AGCTTACTTA CATTAAATTG CGTTGCGCTC ACTGGCCGCT TTTCCAAGTC
491 GGGAAACCTG TCGTGNCAGC TTCANTAATG AATCGGCCAA CGCCGCGGGG AGAGGCGGGT TCGTATTGG
561 GCGCTCTTCC GCTTCTTNGT TNACTGACTT CGG

```



## SEQ. ID NO:50

1 GNNNTTTAAC NCCGGNGCTN CNAGCAGTGG AACAAACGCAG AGTACGCCCC CGATGTACTT TCTTTTTTCAG  
 71 TCTCAAGTCT TCCTCTTCTC CAAAGATTTT GTCTTTTCTA CTACCTGAGC TACCAAATCC CTTGTCTATCA  
 141 ATTTCAATAA CTGTATTCTC TTCATCATT TCACTTCAA CGTGTCATCT CAGAACAAGC TTCATGTTAC  
 211 TTCCAATTTT ATCCTTCTTG TTTGCTGATT CCAAGAATTC CAGTCCCATC TAGGCCCCGA ATGCATTGTT  
 281 CCTGCCACCC TTTTCATATC CTCAATTCCC TTGTATCATC ACTTTCCTTT TATATAGCAC AGATTCCATG  
 351 ATTCATAACA ATAATTATGT TTTTTTTTGC ATGTGCTCTT AATTCCTTT CTTGCTCCTA TTATCTTCTA  
 421 TCATACTTTT CTGGAAACAC TAATTCTGGT GAAATATACT CTTTGTGGAC TTTGCACTTA TGCTCAGTCA  
 491 GCTGAAGATG ATGGCTAGAC AAATACTCAC AATCATGCTG ACTGGCCCAA TTTATAGTCA TGACCACCGA  
 561 TTACAAACCC CTTCAATTTAT TCTCCGCAAC AGGGGCGTCT TCTGCGCTTG AGCGTCCGGT GGGG

## SEQ. ID NO:51

1 GCAGTGGTAA CAACGCAGAG TACGCCCCGT ACAGGAGGCTG TAAATAAAGG GGTTGAGGAA GTAAAGTACT  
 71 TCACAGTACT GGAGCACACA GCATGTGAAT TTCAGCCAAA GGACAAATGC CTCCAAAAAA AGTTAATTCA  
 141 CAGTGCAGCA GGGCGAGGCA CTTGTCTTAT TCCTGCTTTC TCACATTGAC CCTGAAAGGA CTTTTTTTTG  
 211 TTAATCCCAT TTTCACAGAT GGGAAAGGGA CTCTGTATGG TTGTCACTTT TATCCAAAGT CTCATAGCCA  
 281 GTAAGAAGCT GCCCTCAAAG TCCCTACCTT GTCTTCCATT CGACTATTCT GAGGTTTCTA CCCAGAAACC  
 351 CCATACCTCT GCCTTATATT TTAATGAAAA GTATGTCTCC AGGTTTATGT GGAGAATAAC CAAGACCTCA  
 421 GAAACATTTA GTGAAATCA GAGCTAGAAG GAATCTGTTT TTTTGGGAGT TCAGAGAAAC TGACTTGGAT  
 491 AAGACATCAA AGTTGTCTTG TGCAGCAAT TCTCCTCCGG CACATAGTAG GCACTCTGAT AAATTCAAAA  
 561 AGGCTTCTAA GAAGAGGCAG AAGN

## SEQ. ID NO:52

1 GTGAANCCAN NNTAANNCCN ATTGGAGCTC CAAGCAGTGG TAACAACGCA GAGTACGCCC CCGATGTAGT  
 71 TTCTTCTTTC CTTCTTCCC TCCTTCTTTC CTCTTCTCT CTCCCTCTCC CTCTCCCTCT  
 141 CCCTCTCTCT CTCCTTTTTT TTCTCCTTCC TCCTCTCCC CCAATCCGT TCATGACTTC TTCTTCTTCC  
 211 TCTTCTTCTT CTTTCTTTCT TTCTTCTTTT TCTCTAAGCA GGATCCTGGG CTGTTCAAAC CAGAGAGCTG  
 281 TAAGTCTTTT CTTTCCCAT TACTGTTAGA TCCGTTGAAT CGGCTCCAGA AACCAACAA GTTAACCCCTT  
 351 GCATTTACAC GTTTCGTAAC GGGCGTACTT CTGTCGTCTT GAGCGTACTG ATGGTACCCA GCTTTTGTTC  
 421 CCTTTAGTGA GGGTTAATTG CGCGCTTGGC GTAATCATGG TCATAGCTGT TTCCTGTGGG AAATTGTTAT  
 491 CCGCTCACAA TTCCACACAA CATACGAGCC GGGAGCATAA AAGTGTAAG CCTGGGGTGC CTNATGAGTG  
 561 AGCTAACTCA CATTAAATTGC GTTGCGCTTA CTGNCCGTTT TCAGTCNGGA AAN

## SEQ. ID NO:53

1 TNANNCNNNT TAANNCCCAT TGGAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCC CGATGTACTT  
 71 GCTTCTTCTT CTTTGGAGTG GCTGAATGCT TCCTCCTGGC TACCATGGCA TATGACCGCT ATGTGGCCAT  
 141 CTGCAGTCCC TTGCACTACC CAGTCATCAT GAACCAAAGG ACTCGTGCCA AACTGGCTGC TGCCCTCTGG  
 211 TTCCCAGGCT TTCCTGTAGC TACTGTGCAG ACCACATGGC TCTTCAGTTT TCCATTCTGT GGCACCAACA  
 281 AGGTGAACCA CTTCTTCTGT GACAGCCAC CTGTGCTGAG GCTGGTCTGT GCAGACACAG CACTGTTTGA  
 351 GATCTACGCC ATCGTCGGAA CCATTCTGGT GGTCATGATC CCCTGCTTGC TGATCTTGTG TTCCTATACT  
 421 CGCATTGCTG CTGCCATCCT CAAGATCCCA TCAGCTAAAG GGAAGAATAA AGCCTTTTCT ACATGTTTCT  
 491 CACACCTCCT TGGTGGCTCT CTTTTCTATA TATCATTAAG CCTCACCTAC TTCCGGCCTA AATCAAATAA  
 561 TTCACCTGAG GGCACGAAGC TGCTATCATT GCCTACACTG NTATGACTCC A

## SEQ. ID NO:54

1 GTTNTTCCAT GGAATCCCAA GCAGTGGTAA CAACGCAGAG TACGCCCCCT ATGTACTTAC TTCTTGCTGG  
 71 CTTATCATTT ATAGATATCA TTTATTCTTC ATCCATTTC CACAGATCGA TTTGAGACTT GTTCTTTGGG  
 141 AATAATTCCA TATCCTTCCC ATCTTGCTTG GCCAGCTCT TTACAGAGCG CTTTTTGGT GGGTCAGAGG  
 211 TCTTTCTTCT GTTGGTGATG GCCTATGACC TTGCATTACT TGGTTATCAT GAGACAATGG GTGTGTGTTT  
 281 TGCTGCTGGT AGTGTCTCTG GTTGGAGGAT TTCTGCACTC AGTATTTCAA CTTAGTGTTA TTTATGGGCT  
 351 CCCATTCTGT GACCTCAATG TCATTGATCA TTTTTCTGT GATATGCACC CTTTATTGAA ACTGGTCTGT  
 421 ACCGATACCC ATGTTATTGG CCTCTTAGTG GTGGCAATGG AGGACTAGGT TGCACTATTG GGNTTCTGCT  
 491 CTTACTCATC TCTTATGGNN CATCTGCACT CTCTAAAGAA CCTTAGTCAG AAAGGGAGGT GAAAAGCCCT  
 561 CTCAACCTGC AGTTCCACAT AACTGGGGGG TGGTTTCTTC TTTGTN



## SEQ. ID NO:55

```

1 TTANNCCNNT TNAATNCCNT TGGAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCC CAATGTACTT
71 GCTTCTTCTT TTTTGGGGCT GCTGAGTGCT GCCTCTGGC CACCATGGCA TATGACCGCT ACGTGGCCAT
141 CTGTGACCCC TTGCACTACC CAGTCATCAT GGGCCACATA TCCTGTGCCC AGCTGGCAAG CTGCCTCTTG
211 GTTCTCAGGG TTTTCAGTGG CCACTGTGCA AACCACATGG ATTTTCAGTT TCCCTTTTGG TGGCCCCAAC
281 AGGGTGAACC ACTTNTTNTG TGACAGCCCT CCTGTTATTG NACTGGTCTG TGCTGACACC TCTGTGTTTT
351 GAACTGGAGG CTCTTGACAG CCACTGCCTA ATTCAATTCTC TTTCCTTTCT TGCTGATCCT GGGATCCTAT
421 TTCGCATTCT CTTCATATC TTTAAGGATG CCGTCAGCTG AGGGGAAACA TNAGCATTCT NCACCTGTTC
491 CGCCACCTC TTGGGTGGCT CTCTCTTCTA TAGCACTGGC AATCCTTAAC GTATTTTCCG ACCCCAATTC
561 AAGTGCCTTT TTNTGAGAAG CAAAGAACT GGTGTCACT TTTTTTCAC AAGGGGNGAC TTCCAATGTT

```

## SEQ. ID NO:56

```

1 GNGNTTTNNN CCATGGAGCT CCAAAGCAGT GGTAACAACG CAGAGTACGC CCCCCATGTA CTTTCTTCTT
71 CTTTGGAGTG GCTGAATGCT TCCTCTGGC TACCATGGCA TATGACCGCT ATGTGGCCAT CTGCAGTCCC
141 TTGCACTACC CAGTCATCAT GAACCAAGG ACTCGTGCCA AACTGGCTGC TACCTCTGG TTCCCAGGCT
211 TTCCTGTAGC TACTGTGCAG ACCACATGGC TCTTCAGTTT TCCATTCTGT GGCACCAACA AGGTGAACCA
281 CTCTTCTGT GACAGCCAC CTGTGCTGAG GCTGGTCTGT GCAGACACAG CACTCTTTGA GATCTACGCC
351 ATCGTCGGAA CCATTCTGGT GGTCAATGATC CCCTGCTTGC TGATCTGTG TTCCTATACT CACATTGCTG
421 CTGCCATCCT CAAGGTCCCA TCAGCTAAAG GGAAGAATAA AGCCTTTTCT ACATGTTCTT CACACCTCCT
491 TGNTGTCTCT CTTTCTATA TATCATTAAG CCTCACCTAC TTCCGGCCTA AATCAAATAA TTCACCTGAG
561 GGCAAGAAGC TGCTATCATT GNCCTACACT GTTATGACTC CATGTTGAAC CCCATAATTT ATTCATTGAG
631 C

```

## SEQ. ID NO:57

```

1 TTATNNCCAT TGGAGCTCCA AAGCAGTGGT AACAAACGCA GAGTACGCCC CCCATGTATT TTCTTTTCTT
71 TGGGGNAGCT GNATGCTTCC TNCTGGCTAC CATGGNATAT GACCGCTAT GNGGNCATCT GCAGTCCCTT
141 GNNCTCCCAG TCATTATGAA CCAAAGGACA CGGGCCAAAC TGGCTGGTGN TTCCTGGGTC CCAAGCTTTC
211 CTGNAGCTAC TNGCAAGAC CACAATGGCT CTNAGNTTT CCATTCTGNG GCACCAACAA GGTGAACCAC
281 TTNTTCTGN GACAGCCGGC TGTGCTGAAA GCTGGTCTGN TGCAAGACAC AGCACTGTTT GAGATCTACG
351 CCATCGTCGG AACCATTCTG GTGGTCAATG AACCCTGCT TGCTGATCTT GNGTTCCTAT ACTCGNATTG
421 GTGCTGCTAT CCCTCAAGAA CCCATCAAGC TAAANGGGA GCAATAAAGN CCTTTCTCTA CGTGCTCCTT
491 AACACCTCCC TTGGTGGCCT CTCTTTTCTA ATATAATCNT CTAAGCCTCA ACCTACTTCT TGGGCTGNAA
561 NTCAAATAAA TTCTTCTGGA GAGGCAAGAA GGTGGTATTC ATTTATNCTA CACTGGTNGN GACTCCATGN
631 TGGAAT

```

## SEQ. ID NO:58

```

1 GTNATNCCNT TTAATNCCNT TGGAGCTCCA AGCAGTGGTA ACAACGCAGA GTACGCCCCG TCCTCAGACA
71 GTATATGAAT GGGTTAAAAA TGGGCCAGAG CAGATGCAGG AAGATCAAAT AGGAGGCTAC TGCAGTAGAG
141 TCAAATCTAG GGCTGATGGT TTCTTGGGAT GCATAGTAAT AGGTAGATAG AGAAAGTCTT TAGGAGGTAG
211 AATGGACAGG ACTTCACAAT GCATTAAATG TAGGGAGAAA AAAAATGATT CCTGGGTTTC TAGCTTGAGC
281 TAGTAGGGAT AGTGGTAGAA TTTACTGATA TGGAAAACG GAGGAAAAAG AGTTTGGAAG AGAAAGATGG
351 CAAGTTAAAT ACCTGTGGGA AATATAATCA CAGACACTAA ATAGGCAGCT GTGTGGGTGG CAAAGGAGAG
421 CCATGGGCTA GGAACATACA GTGGGATTCC CTGGCATGTC ATTGGTTACT GAAGTCAGAG TGTATGAGAC
491 AGCCTAAGGA GAGAATNCAC ACAGGAGAAG AAAGAACTAA ACATTCACTG GCTGGCCAGA GGATGAGAAA
561 CCAAGAGAT TGGACTGTTT AGGAGCAACA GTGTTGNGAA AAGGGAGAAA NGGTTGAAAT T

```

## SEQ. ID NO:59

```

1 GGNTTTANNC NCTGGAGCTC CAAAGCAGNG GTAACAACGC AGAGTACGCC CATTGCGTAG CGTGATACATA
71 AAGGGGTTGG AGCTGAAGGA GGAGATAAAG AAGAAGACAG CCAGAACCTT GTCCTCTGTC GGAGATCGCA
141 GGGATCTTGG GCCGTAGATA GGTATAAGCA AAGGGTGCAT AGTAGAAAGT CACTACAGTG AGGTGGGTGC
211 TGCAGGTCGA ATAGGCCTTC TTCCTCCCTT CTGCAGAGTG CATGTGGTAG ACAGCAAGGA GAATCCGGCC
281 ATAGGAACAT GCAATACAAA TGAAGGGAAA CACAAGAAAA ATGGTGGTGC TCAAAAACAC CGTGCACTCA
351 TAGACCCAGG TATCCGTGCA GGCTAGGGTC AACATAGCTG GAACATCACA GAAAAATGA TTGATGGCTC
421 TGGACTTGCA ATATGGGATA CGGAGTGCAT ATACCGTGTG AGCACAAGAG TTGATGGAGC CTATCATCCA

```

491 AGATCCTGTT ATCATCAGTG CACACACTCT TTTTCTCATA CGGATGAGAT AGTGGAGAGG AAAGCAAATA  
 561 GCCACATAAC GATCATAGGC CATTGATGTC AGGAGCAGCG CTTCTGCACC TGCTAAAGTC AGGAAGAAGA  
 631 T

## SEQ. ID NO: 60

1 TGTTANTCCN NTTNCTNCC ATTGGAGCTC CCAAGCAGTG GTAACAACGC AGAGTACGCC CTCCTTGT  
 71 CTGAGAGTGT AGATGAAGGG GTTATAGGAG ATAAAGATCA GGGCAATATG TAGGACAAGG ACACAGACAC  
 141 TGACAACAAA GTTGATTATC TCATTGACAG TGGTGTCTGT GCAGGCCAGC TTCAGCAGG GTCTCACATC  
 211 ACAGAAGAAG TGGGAGATGA CAAAGTCATC ACAAAGGGC AGGCCAAACA TAGATGTTAC TTGGACAATA  
 281 GCCATGCCCA GGCCAATCCT CAGTGACCCA GATCCCAGTC AGACACAAGC CCTCTTACCT ATGAATACCG  
 351 TAAGGGGTTG CAGAAGACCA CATAGCAATC ATATCCCATG GCTATGAGAA GAAAGCAGTT GTTGATGCCA  
 421 AAAGTCACAT AGAAGAGCTG AGTGACACAG CTTGTCATGA CAATAAGCTA GTGAGGATTC AAGAGGCGAG  
 491 AAAGCATATG GGGAGTAATG GCCACCATGT AGCAGGTCTC AGAGATAGAC AGCAATGCTT AGGAAAAAGT  
 561 ACATGGGCCG TACTTCTGTC GTCTTGAGCG TACTGATGGT ACCCAGCTTT TGTTCCCTTT

## SEQ. ID NO: 61

1 GTNANNCCN TGTAGCTCCN AAGCNGAGCT AACACNNAG AGAACAACGC AGAGTACGCC CCCGATGTAC  
 71 TTGTTCTTAC TCTTGCTGG ATTTGAAAAC TTCCTCTGT CCGTGATGGC CTATGACCGG TTTGTGGCCA  
 141 TCTGTCACCC CCTGCACTAC ATGGTCATTA TGAACCTCA CCTCTGTGGA CTGCTGGTTC TAGCATCCTG  
 211 GACCATGAGT GCTCTGTATT CCTTGCTACA AATCTTAATG GTAGTACGGC TGTCCTTCTG CACAGCCTTA  
 281 GAAATCCCCC ACTTTTTCTG TGAACCTAAT CAGGTCATCC AACTTGCTTG TTCTGATAGC TTTCTTAATC  
 351 ACATGGTGAT ATATTTTACA GTTGCCTGTC TGGGTGGAG TCCCTCACT GGGATCCTTT ACTCTTACTC  
 421 TAAGATAATT TCTTCCATAC ATGCAATCTC ATCAGCTCAG GGGAAAGTACA AGGCATTTTC ACCTGTGCAT  
 491 CTCACCTCTC AGTTGTCTCC TTATTTTATG GTGCAATCCT AGGGGTGTAC CTTAGTCTGC TGCCACCCGC  
 561 AACTCACACT CAAGTGCAAC AGCCTCAGTG ATGTACACTG GGGCACCCCC AT

## SEQ. ID NO: 62

1 GNNNNNNNAT TTNATGCCNT TNTTGATTCC CNTNNNNNNN NCAAGCAGNG GTAACAACGC AGAGTACGCC  
 71 CCTATGTAT TTCTTCCTAA GATCCAAATA TTAAATAAAA AGACAGTCAT CCCACCACTA ACTAAAGTAG  
 141 TGTTTCCAC ACTTCTCTAT TAAGAAGCAT GTGAGATACT TGTTACAAAC ATAACATCCT GGTCCCACCC  
 211 CAAAGCCACT CAATCAAATA TCCCAGGGAA GGGATCTAGG AATTCCGTAGG TTTAACGAGT GCCCCAAAT  
 281 GATTATTACC GTTGGAGAA TCTAGGCAAC AATGAATTAA GGAAAGCTCT CTACCATTG GTACTGGTAC  
 351 CAGGTTTGTG GATCACAGGG AAGAGGGTAA GCATATCAGA CTAGCAGAGC TGCCAGAACT CGGGCTTTCA  
 421 AAAGAGAGGT GCCACCTCT CCCATGTCCA TGTAAGTAGC AAACAACCTT CTCATGTACA CTCTGAGGAA  
 491 CAAGGGGGCG TACTTCTGTC GTCTTGAGCG TACTGATGGT ACCCAGCTTT TGTCCTTTTA GTGAGGGTTA  
 561 ATTGCGCGCT TGCGGTAATC ATGGTCATAG CTGTTTCTG TG TGAAATTG TTATCCGCTC ACAATTCT

## SEQ. ID NO: 63

1 TGTAGCTCCA AAGCAGTGGT AACACGCAG AGTACGCCCT CTTGGTTACG TAAGGGAATA GATGATGGGG  
 71 TTCAGCATGG GGGTGACTAC AGTGATCATG ACAGTGGCCA CACGGTCCCA CTCTGCTCGC GTCGGGACGT  
 141 GGCCTGGAAG TAGACTGCAA TGACTGTCCT ATAGAAAGAG GCTCACCACA NCCAGGTGGG AGCCACAGGT  
 211 GGGNCACAAG TCCCGGAGCC TCCAGAGGC TTGAGGGCAG CTGGAGCAGC GGNAAGCTTG NTATGGNCCC  
 281 ACAAGGAGGC GAGGATGAGC AGNAAGGGAG TGACCACCAC TTGCNCGGCC CTNNGTGAAG ATGAGCAGCT  
 351 TGATGTGGT GGNTGTCAGA GCACGAGAGC CTTTAAGAGA GGCTTGGTGG GTCACAGAAG AAGTGGGNGC  
 421 ACTTTGTGGG AAAGCACAGA AAGGACAAGC GAGCCATGAG CAGGATATAC AGGAGGGAGT TGTCCTGGG  
 491 ACACGAGCCA TGCCATTCCA ACCAGGGCTG CGCACATNGC CGGGGACATT CTCGTGGGAT AAGGGAAGGG  
 561 GTGCCGGATN GGCACGTATC AGTCATAGGC CTTGGNCGCC AGAAGACAGC TTTNAATTTA CCCCAGG

## SEQ. ID NO: 64

1 GTTANNCCNT NTANCTNCAA NNGAGGTAAC AACGCAGAGT ACGCCCCCA TGTATTTGCT TCTTGTCCAA  
 71 CCGTGCCTTT GTAGAGATCT GCTACACCAC CGTTGTGGTG CCCTTGATGC TTTCCAACAT TTTTGGGGCC  
 141 CAGAAGCCCA TTCCATTGGC TGGATGTGGG GCCCAAATGT TCCTCTTTCT CACACTTGGT GGTGTGACT  
 211 GTTTCCTCTT GCGGATCGTG GCCTATGACC GCTATGTGGC CATCTGCCAC CCTTTGCAT ACCCTCATC  
 281 ATGACCTGCA GTCTGTGCGT GCAGATGCTG GCGGCGCTG TGGGCTGGC CCTCTTCCTC TCCCTGCAGC  
 351 TCACCGCCTT AATCTTCACC TTGCCCTTCT GCGGCTACCG CCAGGAAATT AACCATTCC TCTGCGATGT

421 ACCTCCGTCC TGC GCCTGGC CTGCGCTGCA TCCGTGTTCA CCAGGCTGCC TCTATGTCGT GAGCATCCTC  
 491 GTGCTGACCG TCCCTTCTT GCTCATCTGC GTCTCCTACG TGTTTCATCAC CTGTGCCATC CTGAGCATCC  
 561 GTTCTGCTGA GGGCCGGCAC CAGGCCTTTT CAACTGCTCT TCCGG

## SEQ. ID NO:65

1 TGTAGCTCCN AAGNNGAGNT ANCAACGCAG AGTACGCCCG CGGAATCTAT AGATGAAAGG GTTTGGNGAG  
 71 TCAGAAGAAG GAAGTACATG GGAGTCATAA CAGTGTAGGA CAATGATGGC AGCTTCTTGC CCTCAGGTGA  
 141 ATTATTTGAT TTAGGCCCGGA AGTAGGTGAG GCTTAATGAT ATATAGAAAA GAGAGACAAC AAGGAGGTGT  
 211 GAGGAACATG TAGAAAAGGC TTTATTCTTC CTTTATAGTG ATGGGATCTT GAGGATGGCA GCAGCAATGT  
 281 GAGTATAGGA ACACAAGATC AGCAAGCGGG GGATCATGAC CACCAGAATG GTTCCGACGA TGGCGTAGAT  
 351 CTCAAAGAGT GCTGTGTCTG CACAGACCAG CCTCAGCACA GGTGGGCTGT CACAGAAGAA GTGGTTCACC  
 421 TTGTTGGTGC CACAGAATGG AAAACTGAAG AGCCATGTGG TCTGCACAGT AGCTACAGGA AAGCCTGGGA  
 491 ACCAGGAGGT AGCAGCCAGT TTGGCACGAG TCCTTTGGTT CATGATGACT GGGTAAGTGC AAGGGACTGC  
 561 AGATGGCCAC ATAGCCGGTC ATATGCCATT GGTAGCCAG GANGAAGCT

## SEQ. ID NO:66

1 GTTATNCCTT GTTGCTCCCN AGCAGAGGTA ACAACGCAGA GTACGCCCTT ATTTCTCAGA TATANGATGA  
 71 AGGGGTTTCA AAAAAGAATG AGCAAAGAAA ATCTGGGCCA GGCGGGCATC AAAAGAAATA GTCTTGTGCT  
 141 CAACCAAGAA GTCTGCAATC ATTTTAGGGG TAGCAGAGA GGCAACACAT ACGTCTATAA ATGACAGGTT  
 211 GGCAAGAAGC AAATACATTG GGGGCGTACT TCTGTCGTCT TGAGCGTACT GATGGTACCC AGCTTTTGT  
 281 CCCTTTAGTG AGGGTTAATT GCGCGCTTGG CGTAATCATG TTTCTGTGT GTCATAGCTG TTTCTGTGT GAAATTGT  
 351 TCCGCTCACA ATTCCACACA ACATACGAGC CGGGAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG  
 421 AGCTAACTCA CATTAAATGTC GTTGCGCTCA CTGCCCCGTT TCAGTCGGGA AACCTGTCGT GCCAGCTGCA  
 491 TTAATGAATC GGCCAACGCG CCGGGGAGAG GCGGTTTGC TATTGGGCGC TCTTCCGCTT CTCGCTCACT  
 561 GACTCGCTTG CGCTCGGTCG TTCGGCTTGC GGCGAGCGGT ATCAAGCTCA CTCAAAT

## SEQ. ID NO:67

1 GGGTTTTACN CTGTGCNCCC CCAGCAGNGG TAACAACGCA GAGTACGCC TGTGTGCGAA GAAATAAATG  
 71 AATGGGTTTA AAATAGACGT GAAGATGGTG TAGAATACAG CAAGGACTTT GTCAACTGAG TAACTGCTGA  
 141 AGGGCCACAC ATAGATGAAA ATACACGATC CAAAGAATAA AGTGACCACA GTGATGTGAG CAGTCAATGT  
 211 GGAGTGGGCC TTCACCATGC TTACAGAGGA GCGATTCCCTA ACTGTAATAA GTATTACAGT GTAGGANACA  
 281 ACCAANAGGA GAAAGGAAC CAGAGAAAGA AAGCCACCAT CTGCAACTAT TAGTAGGCTG ACAACATAAG  
 351 TGTCTATGCA GGCTAACTTN GTNGCTAGAG GAAGGTACACA GAAAAAACT ATCTACCTTA TTAGGACCAC  
 421 ANAATGGCAG ATTAACCGTG AATGCCAAT GGCTGGTGGT ATGGATGAAG CCCACAAACC AGGAAATGAG  
 491 GACGAGCACA ACACATACAC AGNAGCTCAT GATTGANATG TAGTGNGGAG GTTNTCTNTN GCTCATANCC  
 561 GTNTNGCCA TNGNACTNG GANCACCATT TTACTTGAGC TGNNGGAGNG AACATGAAAT N

## SEQ. ID NO:68

1 GTTANNCCNN TTTAATNCNA TGGAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCC CGATGTACTT  
 71 GTTCCCTACTC TTTGCTGGAT TTGAAAATT CCTCTGTCC GTGATGGCCT ATGACCGGTT TGTGGCCATC  
 141 TGTCACCCCC TGCACTACAT GGTCATTATG AACCCTCACC TCTGTGGACT GCTGGTTCTA GCATCCTGGA  
 211 CCATGAGTGC TCTGTATTCC TTGCTACAAA TCTTAATGGT AGTACGGCTG TCTTCTGCAC AGCCTTAGAA  
 281 ATCCCCCACT TTTTCTGNGA ACTTAATCAG GTCATCCAAC TTGCTTGTT TGATAGCTTT CTTAATCACA  
 351 TGGTGATATA TTTTACAGTT GCGCTGCTGG GTGGAGGTCC CCTCACTGGG ATCCTTTACT CTTACTCTAA  
 421 GATAATTTCT TCCATACATG CAATCTCAT AGCTTAGGGG AAGNACAAGG CATTTTCCAC CTGTGCATCT  
 491 CACCTTTCAG TTGCTCCTTA TTTTATGGNG CAATCTAGGG GTGACCTTAG TTTTGTCTGNC ACCCGCAACT  
 561 CACACTTAAG TGCAACAACC TCAGTGATGT AACTGGGGT CACCCCATGC C

## SEQ. ID NO:69

1 GNGNNNCAG NTTANNCCCTT GGACTCCAG TAGAGCTACN ANGANTNCGC CNAGCGCGCA NTTNNCCAG  
 71 GGTNNNTN TN GTATACCAA TGAATAGAAA ACAGACACCA CCTTGTCCT GCCTAGCAAG TAGCTGGAGC  
 141 TGGGTCGCAA GTACACGAAA AGGGCTGTCC CAAACAGCAG AGTCACCACC ATCAGATGCG AGGCACACGT  
 211 GTTGCAGGCT TTCCATCGGC CCTCTGCTGA AGGGATCTTC AGGACCGCAG ACACATATGTA ACCATAGGAG  
 281 ATAAGGAGTT GGAGGAACGA TGTTCTCCG ACGGTGACCA CCACGAGGAA ATTCACCACT TGAAGGAGGA  
 351 AGGTGTCAGA GCAAGACAGA GCCAGGACTG GTGGGAGGTT GCAGAAGAAG TGTTGATGA TGTTGGGTCC

421 GCAAAAGTGA AGCCTAAATA TGGAGCTGGC CTGGATCAGG GAGCTCAGGA AGCCACCAAC ATATGCCCCA  
 491 ACCACCATGC GTGTACAGAG GCCCTGGGTC ATGATAGTGG GGTANAGAAG GGGGCTGGAG ATGGCTTGCA  
 561 TATCGGTCGT ATGCCATAGC AGTCANGAGG AGGCACTCAA GACAGACCCA TGCCGACNAA GAAAT

## SEQ. ID NO:70

1 GNNNNNTTTTA CCCCTGNNGC ACANAGCAGT GGTNACAACG CNCGAGTACG CCCCTATGT ATTTTTTCCCT  
 71 ATTCTGGACA CGCTACTCCT GACCGTGATG GCCTATGACC GGTGTGTGGC TGTCTGCCAC CCTCTGCACT  
 141 ATATGATCAT CATGAACCCC CACCTCTGTG GCCTCCTGGT TTTTGTCAAC TGGCTCATTG GTGTCATGAC  
 211 ATCCCTCCTC CATATTTCTC TGATGATGCA TCTAATCTTC TGTAAAGATT TTGAAATTCC ACATTTTTTTC  
 281 TCGCAACTGA CGTACATCCT CCAGCTGGCC TGCTCTGATA CCTTCCTGAA CAGCACGTTG ATATACTTTA  
 351 TGACGGGTGT GCTGGGCGTT TTTCCCTCC TTGGGATCAT TTTCTCTTAT TCACGAATTG CTTTCATCCAT  
 421 AAGGAAGATG TCCTCATCTG GGGGAAAACA AATAGCACTT TCCACCTGTG GGTCTCACCT CTCCGTCGTT  
 491 TCTTTATTTT ATGGGACAGG CATTGGGGTC CACTTCACTT CTGCGGTGAC TCACCCTTCC CAGAAAATCT  
 561 CCGTGGCCTC GGTGATGTCA CTGNGGTCA CCCCATTGTG ACCCTTTCAT TTACACCCTT AGCAAG

## SEQ. ID NO:71

1 GNNNNNNNNN GTTNATNCCN NTTTAAATGC CANTNGAGNT AACAAACGCAN GAGTACNCCN NNGNGTACGC  
 71 CCAGGGTTCA ACCNNTGAAT AGAAAACAGA CACCACCTTG TCCCTGCCTA GCAAGTAGCT GGAGCTGGGT  
 141 CGCAAGTACA CGAAAAGGGC TGTCCCAAAC AGCAGAGTCA CCACCATCAG ATGCGAGGCA CACGTGTTGC  
 211 AGGCTTTCCA TCGCCCTCTG CTGAAGGGAT CTTCAGGACC GCAGACACTA TGTAAACATA GGAGATAAGG  
 281 AGTTGGAGGA ACGATGTTCC TCCGACGGTG ACCACCACGA GGAATTCAC CACTTGACTG AGGAAGGTGT  
 351 CAGAGCAAGA CAGAGCCAGG ACTGGTGGGG AGGTTGCAAG AAGAAGTGGT TGATGATTGT TGGGTCCCCG  
 421 AAAAGTGAAA GCCTAAATAT NGAGCTGGCC TGGATCAGGG GAGCTCAGGA AGCCACAACA TATGCCCCAA  
 491 CCACCATGCG TGTACAGAGG CCCTGGGTCA TGATAGTGGG GGTNGAGAAG GGGGCTTGA GATGGCTGCA  
 561 TATCGGTCGT TGCCATAGCA AGTCAGGAGG AGGCACTTCA GACAGACCCA TGCCNCNAAG AAAAAAACT  
 631 GNC

## SEQ. ID NO:72

1 GNNNNNNNNN NTTNNNNCN TNACTCCNGC AGTGGTAACA ANNANTACGC NCAGCGCGCA GTTAACCCCT  
 71 ACTAANGGTA ANNTNAGCTG GAACACATCA NTACGNTCAN GNNNGCNCNA TGACCGGTTT GTGGNCATNT  
 141 GTCACCCCTT GCACTACATG GGTCAATTATG AACCTCACC TCTGTGGACT GCTGGTTCTA GCATCCTGGA  
 211 CCATGAGTGC TCTGTATTCC TTGCTACAAA TCTTAATGGT AGTACGGCTG TCCTTCTGCA CAGCCTTAGA  
 281 AATCCCCCAC TTTTCTGTG AACTTAATCA GGCATCCAAC TTGCTTGTTT TGATAGCTTT CTTAATCACA  
 351 TGGTGATATA TTTTACAGGT TGGCTGCTG GGTGGAGGTC CCCTGACTGG GATCCTTTAC TCTTACTCTA  
 421 AAGATAATTT CTTNCATACA TGCAATCTCA TCAGCTCAAG GGGAAAGTCAA GGCATTTTTC ACCTGTGCAT  
 491 CTACCCCTCA GTTGCTNCTT ATTTTATGGN GCAATCCTAG GGGTGACCTT AGTTCTGGTG GCACCCGCAA  
 561 CTACACTCAA TGCACAAGCT CAGTGATGTA CACTGTGGCA CCCATGCTGA ACCN

## SEQ. ID NO:73

1 GTNNNNNCCN TTGATTNCCA TTGGAGCTCC AAAGCAGTGG TAACAACGCA GAGTACGCCC CCTATGTATT  
 71 TTTTCTTATT CTGGACACGC TACTCCTGAC CGGGATGGCC TATGACCGGG TTGNGGCTGG CTGCCACCTT  
 141 CTGNANTATA TGATCATCAT GAACCCCCAC CTNTGTGGCC TCCNGGTTTT TGNCACCTGG CTCATTGGTG  
 211 TNATGACATN CCTCCTCCAT ATTTCTCTGA TGATGCATCT AATCTTCTGT AAAGANTTTG AAANTNCACA  
 281 TTTTTTTNTG CGAACTGACG TACATNCTCC AGCTGGCCTG CTCTGATACC TTCCTGAACA GCACGTTGAT  
 351 ATACTTTATG ACGGGTGTGC TGGGCGTTTT TCCTCCTTG GGATCATTTT CTTCTTATTC ACGAATTGNT  
 421 TTNATCCATA AGGAAGAATG TCCTCATNTG GGGGAAAACA AATAAGCACT TTTNCACCTG TGGGNCCTCA  
 491 CCTCTTCCGN CGTTTCTTTA TTTTATGGGG ACAGGCATTT GGGGTCCAC TTTACTTTTT GNGNGACTC  
 561 ACCCCTTCCA GAAAANTTTC CGTGGGCNTC NGGATGTAC ACTGGNGGCA CCCCATGTT GAACCTTTT

FIGURE 2

## SEQ. ID NO: 111

```

gggccntcg ngatatnctt naccctctga tgctgctcga ggggccggca gggatgatga 60
tatctgcaga attcgccctt ctgttaacga ggaatatata aaggggttac tgaggaataa 120
ataaatgggt tactgaggaa taaataaatg gggtactgag gaacaaatac ataggggtga 180
aagaactgta aaatagaaaa aggacctntt gctgctcctc aggatggcgg nacttagggg 240
ccatgtacat gacgatgnng ctgccnntna agagtccac tntcancng cctcagcccg 300
ncttttntct cactnnccnt nttntctnc cctctnnnc tctttntctc ctattcccc 360
ccctccnct cctccctttt gcntnaccat tgnccctnat ccctttaatt cnntcnntcn 420
tctccctctt attccttcnn tnttgcnctt cantctctnc ctctttctcc ccnctttct 480
ctentctnct ctctctctng tcatcctngt tcntctctt ncctanttcc ctctancctt 540
ntcttatnnc tctctatnc cctctcatct cactctctt cctctcntcn tacttnnctc 600
nnctcttcn ctccgtctnc cncctttctt tcntnacgcc acccctcnnt cntnctctct 660
ntctntctt cactctctcc tctccctnnc cntcactntt ctccnctct acntcctatn 720
ctcncttct nncttnactt tgtaacgtc tctctctct ctctacgcac nttttatctc 780
ttatctcnnc catcnccctc nntctnca nctattnact cttttctcnc atactntatn 840
ctcctntcnn cttanctnc ctcccttctn tnancnntc actgcn 886

```

## SEQ ID NO: 112

```

gctgctcgag cgcgcgagcg tcggcagtg nagggnnatn tgccnnntn gcnnttagat 60
nanaggnntn agtatggggg tgaccacagt ggtacataac tgaggctgtt gcacttgagt 120
gtgagttgag ggtggcagca gaactaaggt acaccctag gattgcacca taaaataagg 180
agacaactga gaggtgagat gcacaggtgg aaaatgcctt gtacttcccc tgagctgatg 240
agattgcatg tatggaagaa attatcttag agtaagagta aaggatccca gtcaggggac 300
ctccaccag cagcgcaact gtaaaatata tcaccatgtg attaagaaag ctatcagaac 360
aagcaagtgt gatgacctga ttaagttcac agaaaaagt ggggatttct aaggctgtgc 420
agaaggacag ccgtactacc attagattt gtagcaagga atacagagca ctnatggtcc 480
aggatgccag aaccagcagt cacagagggt gngggtttca tantgnccct gtagngtcag 540
cnnngacna gatggccnca aaccgntctt nggccctcac gnccttgga ggnngttttc 600
tantccacca cnnntnttct nannc 625

```

## SEQ ID NO: 113

```

catgcnngag caggctcgag cgccggcagn gtgagggata tctgcagaat tcgcccttcc 60
tatgtacttt ttctgagcg tatacacaat cccatcatgt actggggaga agncagacca 120
tatcattnac aagctgnctt tngcagatgn actttgnttt ctcattaggc tgncagagt 180
acttctctct ggcagccatg gcttatgacc gctgtcttgc catctgctat cctttacact 240
acggagccat catgagtagc ctgctctcag cgcagctggc cctgggctcc tgggtgngtg 300
gtttcgcgcn cantgcagcg cccacagccc tcagnagcgg tcttgcctt ctgngncccc 360
cgtgccatta accactnctt tngcngcant gnccttgca ttgtcttgc ctgccacca 420
nacagcagna nancntgngn cnnttngatc gctgntnccg tctcngntct cactccttc 480
cacttttnc ntcgattcc nntntcenn tcgncctct gncnntcnn tctctcttc 540
tnaacgcgtc ctccgannng nctnnatgt cgtctctnn ntgngcnng ncagcnnnnn 600
nnccannnn tngtgccgc gctcc 625

```

## SEQ ID NO: 114

```

gnttaagccc tnnccctctn gangcatgct cgagcggccg ccagtgtgat ggatatctgc 60
agaattcgcc cttgttccgc aaacaataga tgaaaggatt aagtgaagga gtgccaccg 120
catagaagag accaaagaac ttgcccctcc cttgggcata cggatttttg ggctggaggt 180
agacagcnat gactgagctg tagaagaggg tgaccacagt gagatgggag gagcaggtcc 240
caaaggcctt tctccatgct gtggcagagt taatcctcag cactgcctgg gcagtggctc 300
cataagagcg aaggatgagg ctgagaggca caaccacgaa gatgacactg gacacagcca 360
actggatttc attgnaggag gcatctccac aggagagtn gnatcagaga tgggancctc 420
acataaaaaa gtcactatc tgntgggtgg gacagaatgn ccatgtggag gntnnatgtn 480

```

```

cgtntennac ctcttatttt tnttnccctt ttctttcgct cnntcccent tntccennct 540
cgccanttec atnncntct ntcnnttttt ttntntnacc ntntntcat ntctctctt 600
tattctcttt ctcttgntct tccctctctt ctctntttcc canctctccc g 651

```

## SEQ ID NO: 115

```

ggntctcggt acaanacttg gccctctaga tgcattgctg agcgggccgc agtgtgatgg 60
atatctgcag aattcgccct tccaatgtat ttattcctgt tatttgagaga cctggagagc 120
ttcctccttg tggccatggc ctatgaccgc tatgtggcca tctgcttccc cctgcaactac 180
accgccatca tgagcccat gctctgtctc gccctgggtg cgctgacctg ggtgctgacc 240
accttccatg ccatgttaca cactttactc atggccagnt tgtgcttntg tncnnacna 300
ttgttgntnc cccactnnnc tntgtntna gtctnctctn cctnnactg ctctcctct 360
tntccnnga gtcctcnggn nncgtngtcg nttncngcnn tcaattgcan tncnnctc 420
atcctttctt tantntcca tntnttcaat nattntctt tatcncnnt ntncctctc 480
anctcctnct tagcttactn tttctgtctc tccngnctc ancttttctn ccataatntc 540
ttctctcncn tntctctcnc tnnnncccn nnntctctgt ntctctgctc cntcttnacg 600
tctnnnctt tatttantnt ctncnctn tctcngctc cancgngta ccngccctat 660
nnntctctc ganntngtc atggcatctn cacattngc cctactatnn ncgatctatn 720
tctnccat ntattncaca tccactgca ctctactcn ctctctancc nccgtacatc 780
gcnctacng ntgnctntn nccgtctntn cgccnctat nntccactt tntctnggtc 840
ccccctctcg 850

```

## SEQ ID NO: 116

```

gatgcattgt cgagcgcccg cagtgtgatg gatattctgca gaattcgccc ttccaatgta 60
cttttctctg aagaacctct ctgttttgga tctgtgctac atctcagta ctgtgcctaa 120
atccatccgt aactccctga ctgcagaaag ctccatctct tatcttggt gtgtggctca 180
agcctatttt ttctctgctt ttgatctgc tgagctggcc ttcttactg tcatgtctta 240
tgaccgctat gttgccattt gccacccct ccaatacaga gccgtgatga catcaggagg 300
gtgctatcag atggcagta ccacctggct aagctgctt tctacgcag ccgtccacac 360
tggaacatg tttcgggagc acgtttgcag atccaatgtg atccaccagt tcttcctga 420
catccctcag gtgttgccc tggtttctg ngaggtttc tttgtagagc tttgaccng 480
ccctgagcct caatgcttg ntctgggatg ctttattccc atgatgatct ccnattttcc 540
anatctctn aanggggctc nagaatccct ttaggaccag antcnagta aaagccttt 600
ccnctgct tcccccaag 620

```

## SEQ ID NO: 117

```

tggcctcng atgcattgt gagcgccgc cagtgtgatg gatattctgca gaattcgccc 60
ttccaatgta tttgttctg ttatttgag acctggagag ctctcctct gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcacta caccgccatc atgagccca 180
tgctctgtct cgccctgggt gcgtgtcct ggggtgtgac cacttccac gccatgttac 240
acactttact catggccagg ttgtgtttt gtgcagaaa tgtgatccc cacttttct 300
gtgatatgtc tgcctgtctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgcat cccattccta ctatccttg ggtcctatgc 420
aagaattgtc tctccatcc tcaaggctcc ttcttctaag ggtatctgca aggccttctc 480
tacttggtgc tcccaccctg tctgnggtgt cactggttct atggaaccgt tattggtctc 540
tacttatgct cntcagctaa tagttctact cttaaaggaca ctgcatggct atgatgtaca 600
ctgtggtgac ccccatgctg aaccctt 628

```

## SEQ ID NO: 118

```

gatgatgtc gagcgngcgc agtngatgg atatctgcag aattcgccct tcccatgtat 60
ttgttctga gcaacctct ctctctggag atttggtata ccacagcagc agtgcccaa 120
gcaactggca tctactggg gagaagacag accatatcat ttacaagctg cttttgcag 180
atgnacnntg ttttctcant angcctaca gngnncatgt ttncgcnngc cntgacttat 240
gacgcgcntn cnnnctatc nnnntntct ntnacnctac ttctcatna tntgncntn 300

```

```

nnttcnccn tggcnncn nntcncggnc ttncctntgn negtctcnc ccttnggcct 360
gcatctctnc ntnttcctnn ccnncggnct ntctttcctt cntacctnt ttctgtntnn 420
tccctccct ctctgnntgc nntcncnncn catctnnntg ntctgatcnc tntctnnnt 480
ccatcnngtn ctnttctctc gtntctctn cncgcncct gcatcaetgn gcattatn 540
cncngtctca tnnctatctt ccttctctgt ccttctcct ctatgcnca cgtcntntn 600
tactatgctc ntctcnnat tnnngcctgt tcnngcnc ccgncntcc anntactctc 660
cangntctc ctnttcctnt ncnctgtcta attcncntnt accgntctn gntctntct 720
cgctnntccc nnttctctc nctcncgnnn ccttcagct ntcnanttct antnngnncn 780
cnc

```

## SEQ ID NO: 119

```

nntagatgca tgctcgagcg gcccgccagt gtgatggata tctgcagaat tcgcccttcc 60
tatgtatttc ttctggcca acctgtcctt ctgggagacc tggtagatct ctgngactgt 120
gccaagtta ctgtttagtt ttgtgtctgc gaacaacagc atctctttca cactctgtat 180
gatacaactg tacttcttca ttgtcncat gngcacagaa tgcgtgcttc tggccgccat 240
ggcctatgac cgntatgtgg ncatctggcg cccactccac taccacaacca taantgagcc 300
atgggctcct gctcnnccct cgtntnnna tanngaaccn acagntagc gncantccc 360
tgtngagaa tctacttcat cntnctgcct tanntntgt gggcccaatg tgcntaanca 420
ctngntctg nggacatttn ctccagnant tnaantctct tntctcnaca agantactgt 480
cnttancctg annatnttn ggnacattnt tctanggnn ttggnacgag cntntctanc 540
accngcactn cncantaant gctncngtgc tantcngtgc cattctgtg nctnccntt 600
tcatingctn nctcccncg aaagcnaant aagtngngt cttnactttc gccccccacn 660
ncatcncant ggcc

```

## SEQ ID NO: 120

```

ggccctctag atgcatgctc gagcgccgc cagtgtgatg gatatctgca gaattcgccc 60
ttcctatgta ttttttctg ttatttggag acctggagag cctcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgtcttc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtctgac cacttccat gccatgttac 240
acactttact catggccagg ttgtgtttt gtgcagacaa tgtgatcccc cacttttct 300
gtgatatgct tgctctgtg aagctggcct tctctgacac tcgagttaat gaatgggtng 360
atatttatca tngagggct cattctgtc atccattcc tactcatcct tgggtcctat 420
gcgagaattg tctcctcct cctcaaaggc ccttctctt aangggatc tgcaaggcct 480
tctctacttg gtggctcccc cctgntctgt ggtgtcactg ttcctattgg aaaccgntat 540
tgggactcta cttatgctca tcangetaat agttttact ttangggaca ctgncaatgg 600
cctntgaagn taccctggg gtggaccccc atnntngaac ccc

```

## SEQ ID NO: 121

```

ggccctctag atgcatgctc gagcgccgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta ctttttctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgtcttc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtctgac cacttccat gccatgttac 240
acactttact catggccagg ttgtgtttt gtgcagacaa tgtgatcccc cacttttct 300
gtgatatgct tgctctgtg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgcct cccattccta ctcatcctg ggtcctatgc 420
aagaattgnc tcttccatc tcaaggncct ttntctaaa gggtagctgc aaggccttct 480
ctanttggtg ctcaccctt gtcttgggn tggcactgnt tctaattgga accggaatt 540
gnancnctna cnttatgctc natcaactta aatagtttct nactttnaaa gggaccactn 600
ntcattggct tanggatngn ncnttgggtt cntggaaatc ccnatcattc ttacnng 657

```

## SEQ ID NO: 122

atgaccctna	gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	60
cttccaatgt	atttgttctt	gtccaacctg	tccttttttg	atattggctt	tatctctaca	120
ataattccca	atatgctaga	tcatattagc	tcaggaatta	agctgatttc	ttatggggag	180
tgtctgacac	aactctatct	ctctggccta	tttgacagatc	tggaacaaca	ctttctcctg	240
gctgtgttgg	cccttgaccg	ctatgtggcc	atcagccatc	ctctccatta	tgccctaacc	300
atgaactccc	aacgctgtgt	cctgttgggt	gctgtgtcat	gggtgatcac	tattttacat	360
gccctagtgc	ataccctcct	agtgaccagg	ctttccttct	gtggtccaaa	tattatccct	420
cacttcttct	gtgatctggc	cccactcctg	aagctggcct	gctccagtac	ttgtgtcaat	480
gatctgggtg	tcattcctgt	ggcaggaaca	ctgctgaatg	cgccctttgc	tgcatnctta	540
tgncctactt	ttacattgca	ttggccatcc	tgagaattga	ttcccnagg	ggtatgcaaa	600
gggcccttnt	ccagctcnc	nn				622

## SEQ ID NO: 123

gcgncgcagt	gtgatggata	tctgcagaat	tcgcccttcc	aatgtatttg	tttctgttat	60
ttggagacct	ggagagcttc	ctccttgttg	ccatggccta	tgaccgctat	gtggccatct	120
gcttccccct	gcactacacc	gccatcatga	gccccatgct	ctgtctcgcc	ctgggtggcg	180
tgctctgggt	gctgaccacc	ttccatgcca	tgttacacac	tttactcatg	gccaggttgc	240
gtttttgtg	agacaatgtg	atccccact	ttttctgtga	tatgtctgct	ctgctgaagc	300
tgcccttctc	tgacactcga	gttaatgaat	gggtgatatt	tatcatggga	gggtcattc	360
ttgtcatccc	attcctactc	atccttgggt	cctatgcaag	aattgtctcc	tccatcctca	420
aggctccctc	ttctaagggt	atctngcaag	gccttctcta	cttgccgctc	cacctgcctg	480
tggtgtcact	gttctatgga	accgttattg	gtctctactt	atgtcatca	gccataaagt	540
tttactctaa	aaggacactt	gtcatggntt	atgatgtacn	ctgtgngnac	ccccatgctn	600
aaccccttn						610

## SEQ ID NO: 124

ccttgggccc	tctagatgca	tgctcgagcg	gccgccagt	tgatggatat	ctgcagaatt	60
cgcccttctt	tattcctgag	tgaatatatg	agggggttg	cactgctgtt	aagagtggac	120
aggaaaatgg	aaactagacg	aacgtgacaa	atccacgtgg	atccagaaaa	ataggaatca	180
ctgaatgcc	aagggcaggt	cacagaggag	gaagaccagc	actctgagca	ggatgggtcat	240
gtacagcctg	gtcaagggca	tcttccggga	tccacaaagg	atcctgacca	gcagaaccgg	300
gctggaccgg	cagagaacca	cacataaaaa	aatcagccat	gtgactgtga	tgaaatctga	360
tgtttcacac	caaacagaat	caagcaccac	tagacaggaa	gccacagAAC	atccattcca	420
ggatgctctg	cagcagggac	agggcccaga	gcaggacaca	cgactgctna	ccaggtnntt	480
tnngtggct	gcnagctctn	cttaggatng	tcccaaggga	ttgncnggn	ccggtncctt	540
gnttgcttnt	cgnnncccta	ncatgcctt	ngctcctgtn	nangettgac	nattggncc	600
cncccacgng	gcttaannnt	ctcnnngncc	atttanancg	tnatnntact	tcccttgtcg	660

## SEQ ID NO: 125

gnccctctag	atgcatgctc	gagcggccgc	cagtgtgatg	gatatctgca	gaattcgccc	60
ttcctatgta	cttcttcttg	ttatttggag	acctggagag	cttcctcctt	gtggccatgg	120
ccatgaccg	ctatgtggcc	atctgcttcc	ccctgcacta	caccgccatc	atgagcccca	180
tgctctgtct	cgccctgggt	gcgctgtcct	gggtgctgac	caccttccat	gccatgttac	240
acactttact	catggccagg	ttgtgttttt	gtgcagacaa	tgtgatcccc	cactttttct	300
gtgatatgtc	tgctctgctg	aagctggcct	tctctgacac	tcgagttaat	gaatgggtga	360
tatttatcat	gggagggtc	attcttgtca	tccattcct	actcatcctt	gggtcctatg	420
caagaattgt	ctcctccatc	ctcaagggtc	cttcttctaa	gggtatctgc	aaggccttct	480
ctacttgnng	ctccacctg	tcttngngng	cactgttcta	tgggaaccgg	tattgggtctc	540
tacttaatgc	tcataaagct	aatagttcta	ctctaaggga	cactgncatg	gctatgatgt	600
acactgtggt	gaccccnat	gctgacccat	tc			632



## SEQ ID NO: 126

tctagatgca	tgctcgagcg	gccgcagtg	gatggatgc	tgcagaattc	gcccttccaa	60
tgtacttggt	cctggcagcc	atggcttatg	accgctgtct	tgccatctgc	tatcctttac	120
actacggagc	catcatgagt	agcctgctct	cagcgagct	ggccctgggc	tcctgggtgt	180
gtggtttcgt	ggccattgca	gtgcccacag	ccctcatcag	tgccctgtcc	ttctgtggcc	240
cccgtgccat	caaccacttc	ttctgtgaca	ttgcaccctg	gattgccctg	gcctgcacca	300
acacacaggc	agtagagctt	gtggcctttg	ngattgctgg	tgtggttatt	ctgagttcat	360
gcctcatcac	ctttgtctcc	tatgtggaca	tcatcagcac	catccttcag	gatccccctt	420
gncagtcccc	ggagnaaaag	ncctttccac	gtgctcctcg	cntctcnncg	nggtgctcna	480
tttggtatgg	gtccacaagn	tnctctttca	cgncgggatt	ntccattcaa	aagatgncct	540
tgnnttttna	ncaaaagctt	ggncnncgnc	ctgaaanact	gnngtngact	tcangnttta	600
aaactccttt	natntcactn	ttanggggaa	naggggcggn	ac		642

## SEQ ID NO: 127

ntgngccctc	tagatgcatg	ctcgagcggc	cgccagtggt	atggatatct	gcangaattc	60
gcccttccca	tgtatttatt	ccttagcctg	ttggattccc	agctgcacag	ctggattgtg	120
ttacacaact	caccttcttc	aagaatgtgg	aaanctataa	ttttttttct	gtgacccatc	180
tcaacttctc	aaccttgcc	gttctgacag	catcatcaat	aacatattat	gtattttaga	240
tatccctata	tttggttttc	ttcccatnnc	agggatcctt	ttgncttacc	atanaattgt	300
cctccctcat	tccaagaatt	ccattgncag	acgggacgna	tnangccttc	tctacctgt	360
cntctnacc	gnnagtcgnt	tncttatctn	tgnantnccc	tnnggcgncn	ncctgncct	420
cagcttngt	cancnttctc	cncacnnntt	cgctcgtgtt	ncctcgtctc	gtctctctnc	480
tctctnctnc	ttctgctc	ccctccanng	tctncttctc	tcagcncct	tnngcncnt	540
gccagcncn	nangntccnc	ccctctccct	cntgtctnct	cncctctntt	cttctntctc	600
tnnctcatnn	nnncgcncnc	ncgtctccn	ccctntctn	tacgactccn	gncgtctctn	660
cgcctacgac	ctccctgtnc	ncnccgg				688

## SEQ ID NO: 128

gcgtgctgcn	agcggggcgg	cagagtgage	ggatatctgc	agaatncgcc	cttccgatgn	60
atttctttct	aagcaactta	tcttctattg	acatctgcta	ctctctgct	gtggctccca	120
atatgctcac	tgacttcttc	tgaggacaga	agaccatata	atttggtggc	tgtgctgctc	180
agtttttttt	ctttgtcggc	atgggtctgt	ctgagtgcct	cctcctgact	gctatggcat	240
acgacggata	tgcagccatc	tccagccccc	ttctctaccc	cactatcatg	acccagggcc	300
tctgtacacg	catggtggtt	gnngcatatg	ttggtggctt	cctgagctcc	ctgatccagg	360
ccagnnccat	atttaggctt	cacttttgcg	gacccaacat	catcaaccac	ttcttctgct	420
acctccacca	gtcctggctc	tgtcttgctc	tgacaccttc	cttnagtcaa	gncgncgaat	480
tnctccgtgg	tgntcaantg	tcgngaggaa	acatcgnttt	cctccaaccc	cttantctcc	540
cangggntac	catagngtct	gcgngtccct	gaagaatcct	tttngccaan	cgggcgaatn	600
gnaagccctn	ccaccgccc					619

## SEQ ID NO: 129

gcgggcagct	gtgatgntat	ctgacgaatt	cgcccttccg	atgtatttat	ttctaagcaa	60
cttatctttc	attgacatct	gctactcttc	tgctgtggct	cccaatatgc	tcactgactt	120
cttctgggag	cagaagacca	tatcatttgt	ggctgtgct	gctcagtttt	tttcttttgt	180
cggcattggg	ctgtctgagt	gcctcctcct	gactgctatg	gcntacgacc	gatatgcngc	240
catctccagc	ccccctctcn	accccaactat	catgacccag	ggcctctgta	cacgcatgga	300
ggtngcgcn	tatgntngtt	gnctnctnng	agctccctga	nccannnctn	ntcacntatt	360
ntaggetcna	ccnntcgngc	tcccgntcca	ncanchnaacc	ccnttcgctc	ctgnanactt	420
ctccancacg	ttcctggctt	ttctgcnntc	gcctcncgnc	nncttatnnc	tnangntca	480
cncctganct	gcnnttctt	ccangcngc	ncgncance	cgntctntct	gnngaancct	540
tncccatnct	gctcnatnct	ncctcatcn	nttctantn	ctctcennct	cncgctcnnt	600

nncttnenct ctnaacctnt cnnatectca cctnngatat cctcncgntc tttegnentc 660  
nttcnctgtc cgannctctc anacnctcc ctanncg 697

## SEQ ID NO: 130

ctctagatgc atgctcgagc ggccgccagt gtgatggata tctgcagaat tcgcccttcc 60  
tatgtattta ttccttagcc acttgccct cactgacatc tccttttcat ctgtcactgt 120  
ccctaagatg ctgatgaaca tgcagactca gcacctagcc gtcttttaca agggatgcat 180  
ttcacagaca tttttttca tttttttgc tgacttagac agtttcctta tcacttcaat 240  
ggcatataac aggtatgtgg ccatctgaca tcctctacat tatgccacca tcatgactca 300  
gagccagtgt gtcattgtgg tggctgggtc ctgggtcatc gcttgtgcgt gtgctctttt 360  
gcgtaccctc ctcttgccc agctttcctt ctgtgtgac cacatcatcc ctactactt 420  
ctgtgacctt ggtgccctgc tcaagttggc ctgtctgac acctccctca atnagtttagc 480  
aatctttaca ggagcattga cnggcattat gcttccattc ctgngcatcc tgggttctta 540  
tgggcanatn tgggggtcac cattctncag anttccttta ccagggcattn tgcaangcct 600  
tggccacttg tggnnccnc tencg 625

## SEQ ID NO: 131

ttggcctcta gatgcattgt cgagcgccgc cagtgtgatg gatattctgca gaattcgccc 60  
ttgatacatg attgggttgc ggaaggaata aatcatcggt ttgcggaagg aataaataca 120  
tcgggttgcg gaaggaataa atacatcggt ttgcggaagg aataaataca tcgggttgcg 180  
gaaggaataa atcatcggt tgcggaagga ataaatacat cgggttgcg aaggaataa 240  
tacatcggt tgcgtaagga ataaatcatt ggttgcgta aggaataaat cattgggttg 300  
cgtaaggaat aaatcattgg gttgcgtaag gaataaatca ttgngttgcg taaggaataa 360  
atctttgtgc tggtagcat ctatcatggg gttacgaaag ggaagaaata cattggaang 420  
ggcgaattcc agcacactgc cgnccgctac tagtgggatc cganctcggt accaagcttt 480  
gatgcntagc ttgagtattt taacgcgcgc aacctaaaat ngcnttggcc ttacnctntg 540  
gaccnagctt gncttcttg cgtnaanttt cnttattcct cctntntntc ttctccccc 600  
ncanaatnnt nncncngntn ancaacnann ttntatannc ctngngctcc cctantc 657

## SEQ ID NO: 132

tggccncta gatgcattgt cgagcgncgc cagngtgang gatattctgca gaattcgccc 60  
ttcctatgta tttattcctt aatgtcctct cgcttcttga ttttgttac tcttctgtgg 120  
tcacacctaa gctcttggc aacttcttg tctctgacaa gtccatctct tttgagggtc 180  
gtgtgtcca gctcgcttc tttgtagtgc atgtgacagc tgagagcttc ctgtggcct 240  
ccatggccta tgaccgcttc ctatccatct gtcaaccctt ccattatggt tctatcatga 300  
ccagggggac ctgtctccag ctggtagctg tgctctatgc atttgggtgga gccaaactccg 360  
ctatccagac tggaaatgtc tttgccctgc ctttctgtgg gcccaaccag ctaacacact 420  
actactgtga cataccaccc cttctccacc tggcttgtgc caacacagcc acagcaagag 480  
ngnccetena tgncttttct gntctggcac ccttctggcn gctgcaggca ttctcacctc 540  
taccggcttg ggcttggggg ccaatnggga ggatgcgcct caagaacagg gagggagaaa 600  
ggaactccca cttntgcctc ccnn 624

## SEQ ID NO: 133

ggagttgata tgaacgggtt aagtgaagga gtgcccactg catagaagag accaaagaac 60  
ttgcccctcc cttgggcata cggatttttg ggctggaggt agacagcaat gactgagctg 120  
cagaagaggg tgaccacagt gagatgggag gagcagggtc naaaggcctt tctccatgct 180  
gtggnagagn taattctcag cactgcctgg gcagtcggt ncataagagg caaggatgag 240  
gctgagaggc acaaccacga agatgacact ggacacangc caactgtatc cattgtagga 300  
ggnatctoca caggagagtn gaatcagaga tgggacnttc acattaanaa gttatttatn 360  
tgctggcggt nacagatgcc caagcggnan ggngntatgg tntcggncna ttnttcgtc 420  
canaccatt atctcangcc acatgtatnt cagcttttna ntncnntnt nagtntagtc 480  
tngntgntnt ncnntattn cennctcttn tccntcann tatcattntc attccttncn 540  
ncncanant atggnncnc cgnacnct cngtnactcc cctnnngncg 590

## SEQ ID NO: 134

```

gnntnnnnnn ntgttancct cgtccctcta gatgcatgct cgagcggccg ccagtgtgat 60
ggatatctgc agaattcgcc cttccgatgt atttatttct acacagacac agtgacaatc 120
tgatctctct tgcttttccc cacacactgc aacctctgcc tccacattca agtgattctc 180
ctgcctcagc ctcttgagta gctggaatta cagatgtgag ccaccatgcc tggcctgtcc 240
agatgttttt gaaacaaccc ccaccagcac tggagggagt caagggaaga caagccaggc 300
atctgagctc ctctgtctct gcctttcctt ctactgtcc ccagggtaac ccgtcaccac 360
ccccatcacg aaccccttca tctacacatt acgtaacaag ggcgaattcc agcacactgg 420
cgcccggttac tagtgatcc gagctcggtta ccaagcttga tgcatagctt gagtattcta 480
acgntcacc taatatagctt ggcgtnatca tngncccnag cttgntttct gtgtgaaatt 540
tgntatccgc tcacaaattc cacacaacat acgagccnga agcaataagn nntaaagcct 600
gnggtgccna angagngagc taactcacia ttaattncgt tggctnactt gcccc 655

```

## SEQ ID NO: 135

```

ttngnccctc tagatgcatg ctcgagcggc cgccagtgtg atggatatct gcagaattcg 60
cccttccctat gtacttgttt ctaagcaacc tctccttctt ggagatttgg tataccacag 120
cagcagtgcc caaagcaccc gccatcctac tggggagaag tcagaccata tcatttacia 180
gctgtctttt gcagatgtac tttgttttct cattaggctg cacagagtac ttctccttgg 240
cagccatggc ttatgaccgc tgtcttgcca tctgctatcc ttactactac ggagccatca 300
tgatgacctt gctctcagcg cagctggccc tgggctcctg ggtggtgtgg ttctgtggcc 360
attgacgtgc ccacagccct catcagtggc ctgtccttct gtggttcccg tgccatcaaa 420
cacttcttct gtgacattgc accctggant gccctggcct gcaccaacac cacaggcagn 480
aagagcttgt ggcctttgng aatcgctgn tggggctanc cttnngtcat gccctnatca 540
ccntttntcn nctatgnngt acantcatta agnccaatc nctcatggga tccccctttg 600
cnagtggccc ggcngncaaa ngnectnctc cccgtncn 639

```

## SEQ ID NO: 136

```

tgnccctcta gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc 60
cttccgatgt atttgtttct agccaacctg tcatnaactg atgcttgntt cacttctgcc 120
tccatcccca aaatgctggc caacattcat acccagagtc agatcatctc gtattctggg 180
tgtctngcac agctatattt cctccttatg tttgngggcc ntgacaactg cctgctggct 240
gtgatgccat angaccgta tgtggccatt tgccaaccac ccattacag cacatctatg 300
agtcccccagc tctgtgcact antgctgcnc gtgtgctgng tgcnanccan ttgtctgcct 360
gctgcacatn ctgttncnc cccnccngg nctctttnnn ccgnaccnc cctacaantc 420
cntatcannt tengetnccc tttcttctcc cccnnttct tncnccttc ctcnnccta 480
ctttcttctc tcnctnct canatnatca gtccnacctc nccttcttt ctctactnan 540
tctctcnct cccnctcacc ngntngtcta gtctgcccgc gcccctcgc tatcnctncc 600
ccccctccg cntccctga tctctctngt ctaccctcnc catctnatcc ctcc 654

```

## SEQ ID NO: 137

```

ctctagatgc atgctcgagc ggccgccagt gtgatggata tctgcagaat tcgcccttcc 60
aatgtatttt tttctaagca acctctcctt cctggagatt tggatatacca cagcagcagt 120
gccc aaagca ctggccatcc cactggggag aagtcagacc atatcattta caagctgtct 180
tttgcatagc tactttgttt tctcattagg ctgcacagag tacttctcc tggcagccat 240
ggcttatgac cgctgtcttg ccattctgcta tcccttacac tacggagcca tcatgagtag 300
cctgctctca gcgcagctgg ccctgggctc ctggncgtgn ggcttngtgn cnttgngcn 360
ctctagcnc tcatgnnnnc cttgccttnt gggncctgn nnatcaccct nttntctgt 420
nacacttgta cctcncgnt tgcctnnnc tgccttctaan tccctnngtt gtantnctn 480
gccttntctc cccttcgctn gttnatcttn anntnctgc ntctntgnc ctctccttcg 540
ttngaccct ntannncnc tcttctctcn anntccctc tatcncccg nttnccctcn 600
ntgtcnccg antangntac ntntcacnnt ntntcnctn ctctcctaac tcttnccg 658

```

## SEQ ID NO: 138

```

ggccccctag atgcatgctc gagcggggcgc cagcgtgatg gatatctgca gaattcgccc 60
ttcccatgta tttgttttcta agcaacctct ccttcctgga gatttggtat accacagcag 120
cagtgcctcaa agcactggcc atcctactgg ggagaagtca gaccatatca tttacaagct 180
gtcttttgca gatgtacttt gttttctcat taggctgcac agagtacttc ctccctggcag 240
ccatggctta tgaccgctgt cttgccatct gctatccctt acactacgga gccatcatga 300
gtagecctgct ctacagcgag ctggccctgg gctcctgggt gngtggnntc gtggccantg 360
tagtgcctcac agccentatc agnggcctgt ccttttgggg ncncccgtn ccatcaacccc 420
ttctttctgt gacatttgcc cccctgcntt nccntggcc ctncaccaan cacngcangg 480
nngnttncnn gnetcggcnc cccctttgac ntantncntt gntgngcgct tatncntgcg 540
tttaatgncc ttaatnaaac tctcncctct catgttnttc nttntntng gnaccaantc 600
ttcnaannna cccctttttc catnnncncg tctacntcnc tctcnccttc ntcgngtttn 660
nnngtcnncc

```

## SEQ ID NO: 139

```

gatgcatgct cgagcgggcc ccagtgtgat ggatatctgc agaattcgcc ctcccgatgt 60
atTTTTTct aagcaacctc tccttcctgg agatttggtat taccacagca gcagtgcctc 120
aagcactggc catcctactg gggagaagtca agaccatatc atttacaagc tgccttttgc 180
agatgtactt tgttttctca ttaggctgca cagagtactt cctcttgcca gccatggctt 240
atgaccgctg cttgccatct gctatccctt acactacgga gccatcatga gtagecctgct 300
ctnagcgag ctgncctggg ctccctgggtg ngtggttcng ngccattcag cgcacacagn 360
cttcatcagt ggncttgtn cttctgngccc ccgncatcn aaccantttc ttctgngana 420
atngtaccct tgnanttgcc ctggccttgt anccancaca tangctcgta tgncttctn 480
ntggccnccn tgnctcgct ngtnnccgng ntancngnc tnnacgtcct ttcnnacact 540
ttnnctctat gttntcaach tcnngncta ttcgctcang atanccactc ttcnannct 600
cggannnta nnttttcnn accntctttc cntnc

```

## SEQ ID NO: 140

```

atgacctctc agatgcatgc tcgagcggcc gccagtgtga tggatatctg cagaattcgc 60
ccttcctatg tatttatttc taagcaacct ctccctcctg gagatttggt tataccacag 120
cagcagtgcc caaagcactg ggccatccta ctggggagaa gtcagacct atcatttaca 180
agctgtcttt tgcagatgta ctttgttttc tcattaggct gcacagagta ctccctcctg 240
gcagccatgg cttatgaccg ctgtcttgcc atctgctatc ctttacacta cggagccatc 300
atgagttagc tgcctcagc gcaagctggc ctgggctcct ggggtgtgtg tttcggnggc 360
cattgcagng cccacagcnc tnatcagtgg gctgtccttt ctgtgggccc ccnggccat 420
tcaacccaen tttcttttg nggatattgg caacccntg gnatttgnc cctnggccct 480
ngcacncaa ccancaccag ggtcngnna caanccttgn cgggcccctt tntgaaatt 540
ggcctnggtg ngggnntaat tcnctttggn tttnaatgcc cttccaatna accttttgn 600
cnttctatg gngnncct tnnattcnag caccacanc ttangggaa cnccttttt 660
gtcaagtng nccgtnann naaaagccnt ntccnnntg cccccccg 709

```

## SEQ ID NO: 141

```

ntgggccctg agatgcangc tcgagcggcc gccagtgtga tggatatctg cagaattcgc 60
ccttccatg tatttttttc taagcaacct ctccctcctg gagatttggt ataccacagc 120
agcagtgcct aaagcactgg ccactctact ggggagaagt cagaccatat catttacaag 180
ctgtcttttg cagatgtact ttgttttctc attaggctgc acagagtact tcctcctggc 240
agccatggct tatgatcgt gtcttgccat ctgctatcct ttacactacg gagccatcat 300
gagtgcctg ctctcagcgc agctggccct gggctcctgg gtctgtggtt tcgtggccat 360
tgaagtgncc acanngcctc atcagntggc cntgtccttc tgcnncccc cgtnncattn 420
nncacttctt tcgtgacatt gccannctnn tnttgccctn gtccttnnc natcatccat 480

```

```

ggcngttngn gctgttgcc ctttcgctca cncngtctgc gccattctc nctgtnncaa 540
nngcctcct cttactctctg cnttctant antnnncct ctttntctc tnnantctnt 600
cctcgatctc ctttcangnc tccgctncac tgctenctna acgtccnttt ctccctntnt 660
nntcnntnnc g 671

```

## SEQ ID NO: 142

```

gggcncttt gggatgcct tgncccttag atgcatgctc gagcgccgc cagtgtgatg 60
gatattctgca gaattcgccc ttccaatgta cttatttcta gccaacctgt cattaactga 120
tgcctgtttc acttctgcct ccattcccaa aatgctggcc aacattcata ccagagtgca 180
gatcatctcg tattctgggt gtcttgaca gctatatttc ctcttatgt tngnggcct 240
tgacaactgc ctgctggctg tgatggcata tgaccgctat gtggccatct gccaaccact 300
ccattacagc acatctatga gtccccagct ctgtgcacta atgctgtgng tngctgngt 360
gctaaccaac tggntgccc tgatgcacac actgttctn atccnccgc tttcttggtc 420
ccntangcc nctcnntcn ttccttntn tntctctacc tctccntcg ngctctnccc 480
cttcccnnt cttcctnttg tactcnctan nctgtttnn cccntcntt ctcttcttc 540
ttctctntcn ctttcgncn tnttntctn tcttgctcct acctgtccn ntcatacctt 600
ttcnaatcg ctntatcnc cgcctatagt ncaattcnnc tncctnctnn attncctacn 660
ncntcctcn ccatcanc taacctnctn cntnntctct ntctctgtcc tcanctctc 720
gncnatctc ntctcccn 739

```

## SEQ ID NO: 143

```

gatgcatgct cgagcgccgc ccagtgtgat ggatattctgc agaattcgcc cttagatagat 60
aattgggttc agcatggggg tcaccacagt gtacatcata gccatgacag tgccttttag 120
agtagaacta ttagctgatg agcataagta gagaccaata acggttccat agaacagtga 180
caccacagac aggtgggagc cacaagtaga gaaggccttg cagataccct tagaagaagg 240
gaccttgagg atggaggaga caattcttgc ataggacca aggatgagta ggaatgggat 300
gacaagaatg agccctcca tgataaatat caccattca ttaactcgag tgtcagagaa 360
ggccagcttc agcagagcag acatatcaca gaaaaagtgg gggatcacat tgtctgcaca 420
aaaaacacac ctggccatga gtaaagtgtg taacatggca tggaagggtg tcagcaccca 480
ggacagcgcc accagncga gacagagcat ggggctcat atggcgngt agtgcnggg 540
gangcagatg nccacantag tgnatnagn ccatggtcac angggagga gctttcagg 600
ctttnaataa c 611

```

## SEQ ID NO: 144

```

gcgtgctcga gcggccgcca gtgtgatgga tatctgcaga attcgccctt gttgcgcaa 60
gagtacatga aggggttaag tgaaggagtg cccactgcat agaagagacc aaagaacttg 120
cccctccctt gggcatacgg atttttggc tggaggtaga cagcaatgac tgagctgtag 180
aagagggtga ccacagtga atgggaggag caggteccaa aggcctttct ccatgctgtg 240
gnagagttaa tcctcagcac tgnctgggca gtggctccat aagaggcang gatgaggctg 300
agaggcaca ccacngaaga tgacactgta cacagccaac tgtattttat tgnaggngn 360
atctccacag gngagncaa tcagntgatg gntccnccc atttcanaag tcactntatn 420
tntnttgnc ngncacgang gtccntnnng agcngttctt gtccnttct nactatcgt 480
tacntccct cntccctnt ntnttctt cncctnctc ttcntttnc cntntccnt 540
gtncntnt atctcccta ntntcttt tntnctnt tngnnccct cctctntct 600
tncntccctc tcnantat cncctgncc cncnntnc c 641

```

## SEQ ID NO: 145

```

ggttgccnnc gnttaggcat tgggcccctc agatgcatgc tcgagcgcc gccagtgtga 60
tgatattctg cagaattcgc ctttccgat tatttgtt taagcaacct ctcttctctg 120
gagatttggt ataccacagc agcagtgcc aaagcactgg ccactctact ggggagaagt 180
cagaccatat catttacaag ctgtcttttg cagatgtact ttgtttctc attaggctgc 240
acagagtact tcctcctggc agccatggct tatgaccgct gtcttgccat cctgctatcc 300
tttactacac ggagccatca tgagtggcn tgctctcagc tgcagctgg cctgggctcc 360
tggtgngct ggtttctcgc cctattntn ncnncnncn centantng ncnctnctc 420

```

```

ctttcttntt tccctttnc tcaactcatnc ctctctctct tttntgtcc tcttnataac 480
nttgtnnttc gnttctcccn ntctntnctt ctctnttget tcnctctect cntttcgnat 540
ccctttgntc tctacnctct tncgnantca cttnnatntc tnttcacng cntectcnnn 600
gatnttcncc tnttactgc tactctctnc tatactnnnc ttntntncat anttctgtctg 660
ctnactnanc tntactcnt tcccanncn tcnctgtcnt ctgactctcn cctctntnt 720
nntnctcac cnnntacatg gttccttntn ntccatctcg tcnntctctc cnnataacgn 780
ttncatactc nctaacttct ctccatcatc ntcaactntc tttctttntc cctngnc 837

```

## SEQ ID NO: 146

```

gatgatgctc gagcgncgca gtgtgatgga tatctgcaga attcgccctt ccaatgtatt 60
tatttctagg caccactgac ttcttcctct tggccgtcat gtctctggat cgttacctgg 120
caatctgccg accactccgc tatgagaccc tgatgaatgg ccatgtctgt tcccaactag 180
tgctggcctc ctggctagct ggattcctct gggctccttg cccactgtc ctcatggcca 240
gcctgccttt ctgtggccc aatggatttg accacttctt tcgtgacagt tggcccttgc 300
tcaggctttc ttgtggggac accacactgc tgaaactggn ggctttcatg ctctctacgt 360
tgggtggtact gggcccaacng gctctgacct cagntttcta ngcccgcat ctgtccactg 420
ttctnagngc ccnncanngc ttgccngagc gaagcanaag atnnttttca cattgcgcac 480
tcggaantta aaggggtgg cgcnnncan nctgggnngc ttcatctnt ctttttactt 540
tnccanngnn tnntngctca ntccctntnc tentcncaat cntnnngcn ctctgntnn 600
gtanactgcc nttaattnga ccnctttccc naenncac 639

```

## SEQ ID NO: 147

```

catagatgca tgctcgagcg gccgcagtgt gatggatata tgcagaattc gcccttccga 60
tgtaagtctt ttctaggcac cactgaactt ttcctcttgg ccgtcatgtc tctggatcgt 120
tacctggcaa tctgccgacc actccgctat gagaccctga tgaatggcca tgtctgttcc 180
caactagtgc tggcctcctg gctagctgga ttcctctggg tcccttgccc cactgtctc 240
atggccagcc tgcccttctg tggccccaat ggtattgacc acttctttcg tgacagttgg 300
cccttgctca ggctttcttg tggggacacc cacctgctga aactggnggc tttcatgctc 360
tctacgttgg tgttactggg ctcaactggc ctgacctcag ntctntange ctgcattctt 420
gtcactgtct caggnccct nnagntgctg ngcgaaggaa agecgtttc acttgcgcct 480
cncatcttaca ggggtggcat catctnangg ggngnntgca tccttnncta nntnncagg 540
tcccagctat antccaaagt nctnaaaaca ngancctcgg nangannct nntattctac 600
ccttctctgt aacctncc 618

```

## SEQ ID NO: 148

```

cntagatgca ngctcgagcg ggcgccagcg tgnngnanat ctgcagaatt cgcccttcca 60
atgtattttt tctcactaac ttgtctttcc tagatctctg cttcaccacc agttctatcc 120
cccagctgct tttcaatcta ggcagcccag gcaagactat cagccacacg ggctgtgcca 180
tccagctctt catgttctg ggcctgggtg gcaagagtgt attctcttgg cagccgtggc 240
ctatgaccgc ttcatgcaa tctgcaagcc ccttcaactat tctgtcatta tgcacctca 300
gctgtgctgg aagttggtgt ctgtggccc ggggtgttg actcncagt tntctaggta 360
tgccctcctgn gactatgaag cttgtcacga tgcggaagat gtaagnttg ancntnccn 420
ttntngnat gccngcntcn tataaaaanc annctggcg ggacacagt cttngnata 480
gcattnngtc nccttnatnn catennattt gcctngngt cctcgttcc cantntncan 540
tcntctntng gcttanctt ctnaccngn nctntntan ctactcctn ttnttctc 600
cttctanctc tncatcttct ttncntcca tcc 633

```

## SEQ ID NO: 149

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttgttcccta 60
agactataca tgaatgggtt tagcatcggg ttgaaagaac tgtaaaatag aaaaaggacc 120
ttctgctgct cctcaggatg gcgggactta gggccatgt acatgacgat ggcgctgcca 180
aagaagagtc ccactacgca gaggtgggag gagcaggtgg agaaggcctt tctgcggccc 240
tcccagact ggtacctcag gatggccgcc aggatgtgtg agtaggagac cagcaccagg 300

```

```

cagagtgggc ccaccaggat gaacatgcag gctgcaaaga tgaccacctg gttgagccag 360
gtatcagcac aggccagcct gaggacagac aggatttcac aagaagaagt ggttgatttc 420
acgaggccca canaaagggc agtcttagga tgaggntcac atggaccata gccaggaggg 480
agccacattg tcccaggaag ngntgnccag agtgatgcag acttttcagg tcntgatgat 540
ngnnttattc ggagagnntg nnagacnggt cancgttccc gntcgttaga caattanac 600
ccancngng ccttcantna tgtc 624

```

## SEQ ID NO: 150

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttccaatgt 60
atttatttct ctctgacctc tccttcttgg acctctgctt taccacaagt tgggtccccc 120
agatgctggg caacctctgg ggcccaaaga agaccatcag ctctctggga tgctctgtcc 180
agctcttcat ctctctgtcc ctggggacca ctgagtgcac cctcctgaca gtgatggcct 240
ttgaccgata cgtggctgtc tgccagcccc tcactatgc caccatcatc ccccccgcc 300
tgtgctggca gctggcatct gtggcctggg ttatgagtct ggttcaatcg atagtccaga 360
catcatccac cctccacttg cccttctgtc cccaccagca gatagatgac tttttatgtg 420
aggtcccatc tctgattcga ctctcctgng gagatacctc ctacaatgaa atccagtgtn 480
ctgtgtccag tgtcatcttt ggtggntgtg cctctcagcc tcatccttgc ctcttatgga 540
gccactgccc aggcnggggc tgaggattaa ctttgcenna gccatggaag aaaggtcttt 600
nggacctngn n 611

```

## SEQ ID NO: 151

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc ctttctttat 60
ttcgaagagt atacactagt ggattgaaga gaaacaaata cataggaagg gcgaattcca 120
gcacactggc ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg 180
agtattctaa cgcgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttctgtg 240
tgaaattggt atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300
gcctgggggt cctaataagt gagctaactc acattaattg cgttgcgctc actgtccgct 360
ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcggnaga 420
ggccggnntg cgtattgggc gctcttccgc ttctcgctca ctgactcgct gcgctcggga 480
cgctccgctg cggcgagcgg tatcagctta ctcaanggcc gtantacggt tattcncagg 540
aatnnggggt taacgcncng naaagaacat tgtnggccan angncaagcn taatgccag 600
gaaccgntan aacgntccc 619

```

## SEQ ID NO: 152

```

ctcgagcggc gcagtgtgat ggatatctgc agaattcgcc cttcctatgt attatttctc 60
cataatttat ctattgccga tatctgcttc tcttccatca cagcgcccaa ggttctggcg 120
gaccttctgt ctgaaagana gacctctcc ttcaatcatt gctccactca gatgtttcta 180
ttccacctta ttggaggggc ggntgtatnt nnnccntggt nccnatgcg cctncttttc 240
cctntctnt tonantcttt ncgcctctc tcatgcnnc ccttcentct tattctgtc 300
gnaatacgt ntctcgnct nctgtctgct catccttgc gttncgtntn canctcatcg 360
ctgtctgtcg taactnttnc ntctgtgtc tgcgngntca tncacnctc caancgtctn 420
ccctcactnc tcttntctg ctctctctn cncggtgtct tancttcttg ccctgntacg 480
nncgcgct catatncng tncgtgtat ccctctnatn ttntctntc cctctntnc 540
cntctcacnn acttctntgt ctctctccan ncttcgacnn ctctctnate tccacnacgc 600
actntctnt ctatatccgc tcttaccgct ctcnncnnan cacncttnc tctgcatatc 660
agntntctc ncacnncat nttcttcta cncctctcnc tgcncacag atctntcnc 720
nctctgtct cgttgnctc cctgncactn cgcaatcnc catatncgtc tctctcncnt 780
cgccacttat ntngcanct tctctgctt nctctncgat ntccctcnc nntctcncnn 840
ctnatnatcg nttattcnaa tcatactccg tactgtttct gtntcttnt cntgncnct 900
agcttctctc tattcantct acnttctnt cgctntctat ccacnctct cactcncct 959

```

## SEQUENCE LISTING

<110> DigiScents; Yeda Research  
 Bellenson, Joel; Smith, Dexter; Lancet, Doron; Glusman, Gustavo;  
 Fuchs, Tania; Yanai, Itai

<120> OLFACTORY RECEPTOR SEQUENCES

<130> 422852000200

<140> 06/158,615

<141> 1999-10-08

<160> 2747

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 613

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 8, 11, 17, 28-29, 34, 40, 48, 67, 71, 613

<223> N can be any nucleotide

<400> 1

ggnttatncc	ncgttgnact	gcaggggnnc	aacncacagn	acgcccngtg	ctgaggctat	60
aaatganccg	nttaaggaga	ggagtgaaga	cagtaaaaaa	acacagagat	aaatttatca	120
attgggaagc	tttcaaaggg	ccaaataag	atgaatatta	atgggccaaa	gaagagaagc	180
acaacagtaa	tgtgggcaga	cagagtggga	agggccttgg	acatcccatc	agaggcttgg	240
cgatgcacag	tagcaaggat	gatagtgtca	gaaatgagca	aaaggaggaa	acacataagt	300
gagagcagac	cactgttagt	gagcaccagt	atctcaaaac	catagggtgc	taagcaggca	360
agcttgatca	ctaggaggag	gtcacagaaa	aaattgtcta	ccctgttggg	tccacagaaa	420
ggcagattga	ctttgaatgc	caggtgggtg	gctgagtgtg	agatgccaat	ggcccaggaa	480
acccccacca	gaacagttca	caccctccgg	ttcatgatgg	ttatgtagtg	cagaggtttg	540
catatagcaa	tgtatctatc	ataggccatg	gcaacaagaa	gcaccatctc	actaccccca	600
aaaacatgca	agn					613

<210> 2

<211> 578

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 4, 6, 8

<223> N can be any nucleotide

<400> 2

ggmntntnac	acggactcca	agcagtggta	acaacgcaga	gtacgcccgt	tcctgagtga	60
gtagatgaag	gggttcagca	tgggattgat	gacagtgttg	aaaattccaa	cagctttatc	120
cttgtctgaa	agcttggttg	aaccagtcg	catatagtta	aagatacctg	aaccatagaa	180
tatggcaacc	acagtgaggt	gggagccaca	tgtggagaag	gctttcttcc	tgccctctac	240
agagcgaatt	cgcaggactg	cagctgccac	gtggatatag	gagatgacaa	tgagagccat	300
gggggtacct	gccattataa	aaccacagc	aaaaagcagc	agctcattga	gttgggtgct	360
ggagcaggag	agctggaaga	gctgtgggag	gtcacagtag	aagtgtattga	tcacattggg	420
gccacagaag	ttgagcgtgg	acatggccac	agtgtgggtc	agtgcggttg	tgaaagcaca	480
agcccaggac	gcagccacca	acatcctctg	gactgtctga	ctcatgcggg	tgcttgtagg	540
tgaggggccc	ggcagatggg	caggaatcgg	tcataggg			578



<210> 3  
 <211> 588  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 4, 5, 13, 16, 27, 576, 578, 588  
 <223> N can be any nucleotide

<400> 3  
 tggnttttta tcnccnttgg agctccnaag cagtggtaac aacgcagagt acgcccgttg 60  
 cgaagcgtgt agattagggg gttcagtagg ggagtgtga cagtgtagggt caccgagatc 120  
 agctgggtcat gttctctggt gttctctgac ttgggcttga ggtaggcaat ggaggcacag 180  
 ctgtagtggg caatgaccac agtgaggtgg gatgcacagg tggcaaaagc cttcttccgg 240  
 ccctcaactg aagtaatctt gaggattgta gagataatga gaacataaga aatgaaaacc 300  
 agacccatag gtacaacaag caccagcaca ctgataatca aagtcaggat ttcattgaca 360  
 gtggtgtcaa tgcaggagag cttcatcaca gggcggatgt cacagaagaa gtggggcacc 420  
 ttttctagca cagaagggta acctgaatac agatgtcact tgcgttattg ctacaatcag 480  
 cccaatgctg caaggccccc aggacaagtt ggatacgcag cctcttggtc ataataacca 540  
 tgtatctcaa gggggttgca agatggccac atagcngntc atattccn 588

<210> 4  
 <211> 583  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3, 7, 13, 437, 485, 488, 506, 521, 524, 545, 558  
 <223> N can be any nucleotide

<400> 4  
 gtngttntta acnccattgg agctccaaag cagtggtaac aacgcagagt acgcccccaa 60  
 tgtatttttt ttgagaaac ttgtctttct tagatttttg ttacatctct gtcacaattc 120  
 caaaatctat tgttagttcc ttgactcatg atacttccat ttctttcttt gggtgtgctc 180  
 tgcaagcctt ctttttcatg gacttggaac ctacggaggt agccatcctt acagtgtatgt 240  
 cctgtgaccg ctatatggcc atctgccggc ctttacatta tgagggtcatc ataaaccaag 300  
 gtgtctgtct gaggatgatg gccatgtcgt ggctcagtggt ggtgatctgt ggattcatgc 360  
 atgtgatagc aacattctca ttaccattct gtgggcgcaa tagaatacgt caatttttct 420  
 gtaattattc acaactncta agcctcttag accccaaagt aattaccatt gagattggag 480  
 tcatnggntt ttgggtacaag tcttgngata atcctctttg ntgnaattac tctctcctac 540  
 atgtncattt ttttttgnca tcatgaggga ttccttctaa agg 583

<210> 5  
 <211> 584  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2, 5, 8-9, 11, 14, 17, 550, 557-559, 561, 576, 582  
 <223> N can be any nucleotide

<400> 5  
 gnggnttnnt nccnccnttg gactccaaag cagtggtaac aacgcagagt acgcccgtgt 60  
 gtaaataaat gggttcaaca tgggagtcac aacagtgtag gacaatgata gcagcttcgt 120  
 gccctcaggt gaattatttg atttaggccg gaagtaggtg aggccttaatg atatatagaa 180  
 aagagagaca acaaggaggt gtgaggaaca thtagaaaag gctttattct tccctttagc 240  
 tgatgggcatc ttgaggatgg cagcagcaat gcgagtatag gaacacaaga tcagcaagca 300

ggggatcatg	accaccagaa	tggttccgac	gatggcgtag	atctcaaaca	gtgctgtgtc	360
tgcacagacc	agcctcagca	caggtgggct	gtcacagaag	aagtgggttca	ccttggttgg	420
gccacagaat	ggaaaactga	agagccatgt	ggtctgcaca	gtagctacag	gaaagcctgg	480
gaaccaggag	gcagcagcca	gtttggcacg	agtcctttgg	ttcatgatga	ctgggtagtg	540
caagggactn	gcagatnnnc	ncattcggtc	atatgncatg	gnag		584

&lt;210&gt; 6

&lt;211&gt; 572

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 6

cnttggagct	ccaaagcagt	ggtaacaacg	cagagtacgc	ccgctccgca	gagaatagat	60
gaaaggggtc	agggctcggg	gcacgactgt	gtagaacgca	gacaggaaaa	catccagaac	120
ggggggagaa	tttgaaattg	gcttcacata	ggcaatgctg	ccagatatca	taaagagtgt	180
tacaaccaca	agatgtggaa	tgcaggtaga	aaatgttttt	gatctaccct	ccttagaagg	240
aatcctcatg	atgacagaaa	aaatgtacat	gtaggagaga	gtaattacaa	caaaggagat	300
tatcacaa	cttgtaccaa	aaaccatgac	tccaatctca	atggtaatta	ctttggggtc	360
taagaggctt	aggagtttgt	ggaatattac	agaaaaattg	acgtattcta	ttgcgcccac	420
agaatggtaa	tgagaatgtt	gctatcacat	gcatgaatcc	acagatcacc	ccactgagcc	480
acgacatggc	catcatcctc	agacagacac	cttggtttat	gatgacctca	taatgtaaag	540
gccggcagga	tggccatata	gcggtcatag	ga			572

&lt;210&gt; 7

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 7

gcagtggtaa	caacgcagag	taccgcccc	tatgtacttt	ttcttgggaa	acttgtctgt	60
gtttgacatg	ggtttctcct	cagtgacttg	tcccaaatg	ctgctctacc	ttatggggct	120
gggcccga	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttcctcgg	180
gagcattgag	tgcttcttgt	ttacggtgat	ggcctatgac	cgcttactg	ccatctgtta	240
tcctctgcga	tacacagtca	tcatgaaccc	aaggatctgt	gtggccctgg	ctgtggggcac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtggtccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggt	gagcttcacc	aacgttggcc	tcatatctct	480
ggctgctttc	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

&lt;210&gt; 8

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 537, 542

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 8

ggaacaacgc	agagtgcgcc	ccgatgtact	tgttcttctc	caacctgtcc	tttgtgaca	60
tttgtgttac	ttccaccacc	attccaaaaa	tgctgatgaa	catccagaca	cagaacaaag	120
tcataccta	catagcctgc	ctcatgcaga	tgtatTTTTT	catactcttt	gctggatttg	180
aaaacttctt	cctgtccgtg	atggcctatg	accggtttgt	ggccatctgt	cacccctgc	240
actacatggt	cattatgaac	cctcacctct	gtggactgct	ggttctggca	tcctggacca	300

tgagtgtctt	gtattccttg	ctacaaatct	taatggtagt	acgactgtcc	ttctgcacag	360
ccttagaaat	ccccacttt	ttctgtgaac	ttaatcaggt	catccaactt	gcttgttctg	420
atagctttct	taatcacatg	gtgatataatt	ttacagtttg	cgctgtctggg	tggagggtccc	480
tgactgggat	cctttacttc	ttactctaag	ataatttctt	catacatgca	atctcancaa	540
gntcaggg						548

<210> 9  
 <211> 583  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 8, 13, 14, 16, 25, 232, 271, 305, 438, 488, 497, 500, 505, 512, 524, 544, 558, 578  
 <223> N can be any nucleotide

<400> 9	
gggttttnac	ccnntnggag
aggctataaa	tgaaggggtt
ttgggttgat	cccttgagat
taaaataaga	aaactacaat
ttggaagatt	tgatcttaaa
catantggga	cagctaacat
ttttcaccac	aggcaatctt
ttgagaccac	acagtggnaa
ataccaantt	aaccacnacn
ggtntagtga	agaggttntc
	agaatggcca
	cataccgntc
	aaa
	60
	120
	180
	240
	300
	360
	420
	480
	540
	583

<210> 10  
 <211> 569  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 7, 28, 174, 232, 237, 314, 341, 445, 447, 449, 470, 494, 497, 503, 510, 515, 527, 553, 554, 569  
 <223> N can be any nucleotide

<400> 10	
gctgctncca	gcagtggtaa
tctgtctctc	ctggatgtct
cgtygtcagg	gaccacattg
ctgtgttggt	gtggccgaga
tatctgtctac	ccacttaact
gggaactgcc	tgntctttg
agagcccttc	cgagagaga
ttggcctctt	ttgtggggga
tcgtggtaat	tctnagnccc
ccaccatcct	agnnaaagtc
	ctccttctn
	60
	120
	180
	240
	300
	360
	420
	480
	540
	569

<210> 11  
 <211> 582  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3-4, 12, 14, 504, 513, 522  
 <223> N can be any nucleotide

<400> 11  
 ggnmttttac cncnattgga gctccaaagc agtggttaaca acgcagagta cgtccccctat 60  
 gtacttggtc ttgagaaact tgtctttctt agatttttgt tacatctctg tcacaattcc 120  
 aaaatctatt gttagttcct tgactcatga tacttccatt tctttctttg ggtgtgctct 180  
 gcaagccttc tttttcatgg acttggaac tacggaggta gccatcctta cagtgtatgtc 240  
 ctatgaccgc tatatggcca tctgccggcc ttacattat gaggtcatca taagccaagg 300  
 tgtctgtctg aggatgatgg ccatgtcgtg gctcagtggt gtgatctgtg gattcatgca 360  
 tgtgatagca acattctcat taccattctg tgggcgcaat agaatacgtc aatttttctg 420  
 taatattcca cagtcctaa gcctcttaga ccccaaagta attaccattg agattggagt 480  
 catggttttt ggtacaaggc ttgngataat ctncctttgt gnaattactc tctcctacat 540  
 gtacattttt tctgcatcat gaggattcct tctaaggagg gg 582

<210> 12  
 <211> 579  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3, 384, 528, 572, 578  
 <223> N can be any nucleotide

<400> 12  
 ggnnttgacc acggagctcc aagcagtggt aacaacgcag agtacgcctt cttgtcctcg 60  
 tgccgataca tgatggggtt caacatggga gtcataacag tgtaggacaa tgatagcagc 120  
 ttcttgccct cagggtgaatt atttgattta ggccggaagt aggtgaggct taatgatata 180  
 tagaaaagag agacaacaag gaggtgtgag gaacatgtag aaaaggcttt attcttccct 240  
 ttagctgatg ggatcttgag gatggcagca gcaatgtgag tataggaaca caagatcagc 300  
 aagcagggga tcatgaccac cagaatggtt ccgacgatgg cgtagatctc aaagagtgtc 360  
 gtgtctgcac agaccagcct cagnacaggt gggctgtcac agaagaagtg gttcaccttg 420  
 ttggtgccac agaattgaaa actgaagagc catgtggtct gcacagtagc tacaggaaag 480  
 cctgggaacc agggaggtagc agccagtttg cagcagtcctc tttggttnat gaatgactgg 540  
 ggtagtgcaa gggactgcag atggccacat ancggctc 579

<210> 13  
 <211> 577  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-4, 7-10  
 <223> N can be any nucleotide

<400> 13  
 gnnnttnnnn ccactggagc tccaaagcag tggttaacaac gcagagtacg cccccaatgt 60  
 atttattctt gctcacctct ccttagttga tatctgtttt accaccagta ttgtcccca 120  
 gctgtgtgg aacctaaaag gacctgacaa aacaatcaca ttcctgggtt gtgtcatcca 180  
 gctctacatc tccctggcat tgggtccac tgagtgtgtc ctctggctg taatggcttt 240  
 tgatcgctat gctgcagttt gcaaacctct ccactatacc gccgtaatga accctcagct 300  
 gtgccaggct ctggcagggg ttgctgtggt gagtggagtg ggaaacactc ttatccaggg 360  
 cactgtcacc ctctggcttc ctctgtgtgg acaccgattg cactaacatt tcttcgtgag 420  
 gtaccctcca tgattaagct tgcattgtgt gacatccatg ataattgaggt tcagctcttt 480  
 gttgtctcac tggctctgct cctcttggcc ttagtgctaa tactgtgctc tatggacata 540  
 tagccaagggt ggcataagga tcaagtcagt ccagcct 577

<210> 14  
 <211> 577  
 <212> DNA  
 <213> Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3-4, 6, 8, 252, 375, 474, 506, 515, 532, 541, 545-546, 556, 562, 573

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 14

ggnntntnac	tccatggact	ccaagcagtg	gtaacaacgc	agagtacgcc	catacatgat	60
ggggttcagt	aggggagtga	tgacagtgtg	ggtcaccgag	atcagctggg	catgttctct	120
ggtgttctct	gacttgggct	tgaggtaggc	aatggaggca	cagctgtagt	ggacaatgac	180
cacagtgagg	tgggatgcac	aggtggcaaa	agccttcttc	cggccctcaa	ctgaagcaat	240
cttgaggatt	gnagagataa	tgagaacata	agaaatgaaa	accagaccca	taggtacaac	300
aagcaccagc	acactgataa	tcaaagtcag	gatttcattg	acagtgggtg	caatgcagga	360
gagcttcatc	acagngcgga	tgacacagaa	gaagtggggc	acctttctag	cacagaaggg	420
taacctgaat	acagatgtca	cttgcgttat	tgctacaatc	agcccaatgc	tgcnngcccc	480
caggacaagt	tggatagcga	gccttntcgt	tctantaacc	atgtatctca	angggcttgc	540
ngatnnccac	atactngcat	anaccattgc	tgngagc			577

&lt;210&gt; 15

&lt;211&gt; 583

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2, 5, 7, 13, 427, 485, 488, 532, 559, 569, 574, 583

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 15

gncgntntta	acnccattgg	agctccaaag	cagtggtaac	aacgcagagt	acgcccatta	60
cgaaaagtgt	agatgaaggg	gttcaagagg	ggtgtgatga	tgcagctcag	gacggaggca	120
cctttgttga	gcagtttgga	ctgagcctct	gacatacgaa	tgtagagaaa	gatggaactg	180
ccatagatga	tgaccaccac	tgtaagatgc	gaggcgcaag	tggaaaacgc	tttccttcgc	240
tcagcagctg	tagggggcct	gagaacagtg	gcaagaatgc	aggcatagga	aactgaggtc	300
agagccagtg	agcccagtaa	caccaacgta	gagagcatga	aagccaccag	tttcagcagg	360
tgggtgtccc	cacaagaaag	cctgagcaag	ggccaactgt	cacgaaagaa	gtgggtcaata	420
ccattgnggc	cacagaaagg	catggctggc	catgaggaca	gtggggcaaa	ggaccagag	480
gaatncanct	agccaggagg	ccacactagt	ttgtgaacag	acatggccat	tnattagggt	540
ctcatagcgg	agttgtcgnc	agatttgcnt	ggtnacgatt	can		583

&lt;210&gt; 16

&lt;211&gt; 577

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3-4, 12, 14, 549

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 16

ggnnttttac	cncnattgga	ctccaaagca	gtggtaacaa	cgcagagtac	gccccctatg	60
tattttattct	tgctcacctc	tccttagttg	atatctgttt	taccaccagt	attgtccccc	120
agctgctgtg	gaacctaaaa	ggacctgaca	aaacaatcac	attcctgggt	tgtgtcatcc	180
agctctacat	ctccctggca	ttgggctcca	ctgagtgtgt	cctcctgggt	gtaatggctt	240
ttgatcgctg	tgctgcagtt	tgcaaacctc	tccactatac	cgccgtaatg	aacctcagc	300
tgtgccaggc	tctggcaggg	gttgctgtgc	tgagtggagt	gggaaacact	cttatccagg	360
gcactgtcac	cctctggctt	ccccgctgtg	gacaccgatt	gctccaacat	ttcttcgtga	420
ggtaccctcc	atgattaagc	ttgcatgtgt	ggacatccat	gataatgagg	ttcagctctt	480

tggtgcttca ctggtcttgc tectcttgc cttagtgtca atactgctgc ctatggacat 540  
 atagccaang tggcataaag gatcaagtca gtccagg 577

<210> 17  
 <211> 621  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-5, 8, 13, 618  
 <223> N can be any nucleotide

<400> 17  
 gnnnntntt cantccattg ggccctctag atgcatgtc gagcggccgc cagtgtgatg 60  
 gatatctgca gaattcgccc ttattccgga gggatacat gaagggattg gtaactagac 120  
 gtaaaactga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa 180  
 gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag 240  
 actctgaaag aggtggaagg gattgaatac aatcaaaagt atggtgactg ctagtccaa 300  
 gatggtggcg taggggcaag ctggcttgc ttacccccct ggcagaaaac caaaaacaaa 360  
 tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc 420  
 caggggccag agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt 480  
 tctaagggag acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc 540  
 cataaaacaa agattggaaa atgttgaatt ttgcaaccag gagcaaatac tgggaaaggg 600  
 gaattccagc cacttgcneg c 621

<210> 18  
 <211> 615  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-5, 8, 10, 14, 21, 583  
 <223> N can be any nucleotide

<400> 18  
 gnnnnttnan tcantgcctt ngggccctct agatgcatgc tegagcgccc gccagtgtga 60  
 tggatatctg cagaattcgc ccttggttgc caaggtgtaa atgaaagggg ttgcgcagga 120  
 gtaaatgaag ggattacgca ggagtaaatt aagggtattc gcaggagtaa atgaagggat 180  
 tacgcaggag taaatgaagg gattacgcag gagtaaattg agggattacg caggagtaaa 240  
 tgaagggatt acgcaggagt aaatgaaggg attacgcagg agtaaattgaa gggattacgc 300  
 aggagtaaat gaagggatta cgcaggagta aatgaaggga ttacgcagga gtaaatgaag 360  
 ggattacgca ggagcaaata cataggaagg gcgaattcca gcacactggc ggccgttact 420  
 agtggatccg agctcgggtac caagcttgat gcatagcttg agtattctaa cgcgtcacct 480  
 aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg tgaaattgtt atccgctcac 540  
 aattccacac aacatacgag cccggaagca taaagtgtaa agnctggggg gcctaattgag 600  
 tgacttactc catta 615

<210> 19  
 <211> 696  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-3, 5, 7, 287, 300, 309, 313, 328, 331, 343, 345, 347, 360, 366,  
 386, 388, 391, 394, 401, 407, 416, 420, 428, 432, 434, 437, 441,  
 443, 448, 450, 452, 457-458, 463, 476, 484-485, 493, 503, 506, 514,  
 518, 520, 524, 528, 540, 541, 548, 550, 553-554, 557, 561-562,

566-568, 571-572, 575, 582, 584-585, 587-588, 603, 607, 614, 620, 623, 627, 629, 641, 648, 652, 661-662, 665-666, 668, 672, 675, 678, 684, 695

<223> N can be any nucleotide

<400> 19

gnnantnatt	ccatccattg	tcccttcaga	tgcattgctg	agcggccgcc	agtgtgatgg	60
atatctgcag	aattcgccct	tcttggtttt	tgtgctgata	gatcatggga	ttcagcatgg	120
gggtgaccac	agtgtacatc	actgaggctg	ttgcacttga	gtgtgagttg	cgggtggcag	180
cagaactaag	gtacaccctt	aggattgcac	cataaaataa	ggagacaact	gagaggtgag	240
atgcacaggt	ggaagatgcc	ttgtacttcc	cctgagctga	tgagatngca	tgtatggaan	300
gaaattatnt	tanaagtaag	agtaaagnat	nccagtcagg	ggnancnttc	acccatcagn	360
tgcaanttgt	aaaaattata	ttcaancnat	ntgnatttaa	ngaaaancct	tatcangtan	420
acactgcnna	gntntgnatt	nanccctnng	anttaanntt	tcnacaagaa	aataangtgc	480
gttnnaatct	ttntaagtcc	ctntcnccat	taangtcnan	tcntccnta	tcccttttctn	540
nattttgnan	tcnngantac	nntctnnngc	nntcnatttc	tntnntnnt	gacctactaa	600
ccnattnagt	tacnacaagn	ccnttcnant	ctctataatt	nctgcgagt	tntccctctt	660
nncanntncc	cntttnttnc	cctnttcccc	atctnc			696

<210> 20

<211> 615

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 495, 545, 582, 600

<223> N can be any nucleotide

<400> 20

ccattggccc	tctagatgca	tgctcgagcg	gccgccagtg	tgatggatat	ctgcagaatt	60
cgcccttcct	atgtattttc	tcttactggg	ctttcctggg	tctcaaactc	ttcagctctc	120
tctctttatg	ctttttctgg	tgatgtacat	cctcacagtt	agtggtaatg	tggtctatctt	180
gatgttggtg	agcacctccc	atcagttgca	tacccccatg	tacttctttc	tgagcaacct	240
ctccttctctg	gagatttggg	ataccacagc	agcagtgccc	aaagcactgg	ccatcctact	300
ggagagaagt	cagaccatat	catttacaag	ctgtcttttg	cagatgtact	ttgttttctc	360
attaggtctg	acagagtact	tcttctctgg	agccatggct	tatgaccgct	gtcttgccat	420
ctgctatcct	ttactactag	gagccatcat	gagtagcctg	ctctcagcgc	aactggcctt	480
gggcttctgg	gtggntgggt	tcgggggcaa	tgacgtgccc	acaggccttc	aatcaagtgg	540
gctgntcctt	ctggtggccc	ccggtgccaa	tcaaccactt	tntttttggg	acaattgcan	600
ccctggaatt	ggccc					615

<210> 21

<211> 745

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-3, 8, 21, 23, 26, 33, 43, 116, 201, 212, 222, 239, 252, 279, 282, 288, 292-293, 308, 320, 325, 328-330, 333-334, 339-341, 344, 354, 360, 365, 372, 377, 382-383, 388, 390, 394, 397, 402, 415, 418, 422, 424-425, 427, 431, 436, 441, 445, 450, 451, 457, 466, 493, 495, 498, 501, 508-509, 513, 515, 517-518, 520-523, 525, 528-529, 535, 538, 540-542, 544-546, 548-550, 553, 555, 565, 584, 586, 592-593, 607-608, 615, 617, 619, 621, 634, 636-637, 644-645, 651, 656, 662, 671, 685, 693, 697, 699, 710, 714, 735, 737, 740, 745

<223> N can be any nucleotide

<400> 21

gnncttantt caateccacc nancentgcc gangcatgct cgngcggccg ccagtgtgat	60
ggatatctgc agaattcgcc ctctctatgt atttactctt actgggcttt cctggntctc	120
aaactcttca gctctctctc tttatgcttt ttctggatgt gtacatcctc acagttagt	180
gtaatgtggc tatcttgatg ntggtagca cntcccatca gntgcatacc cccatgttnt	240
tctttctgag cnacctctcc ttcttgaga ttgggtatnc cncaagcngc anngcccaaa	300
gctttgcnc tcttattgcn cagangcnnn ccnntacann nacnctcctg tttntcgctn	360
ccttncctct tcttctctc anntactnctn tctnctntag tntctttctt ctctntctct	420
cntnnncct ntaatnttcc ncctnttctn nttctnttt tccctnctct gtttcacccc	480
tacctcttat centnctnct nacttcannc tcngncnntn nnnncnctt aaatntangn	540
nnannntnnn atntnctctt ctccntttat atcgccctt ctctncttcc cnnttctctc	600
tcctcannca tatchantnt nttctactct cgtncnntat ctannctcct nttctngtcc	660
tcttctcct ntcatttcta tattncttct canacantnt tcgcatcgtn gcancatctc	720
ctcccatctc ctgtncnctn ttccn	745

&lt;210&gt; 22

&lt;211&gt; 614

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; 2-4, 9, 19, 23, 47, 613

&lt;222&gt; (3)...(3)

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 22

gnnnntaant cattccccnc tcnatgcatg ctcgagcggc cgccagngtg atggatatct	60
gcagaattcg cccttgtttc ggaggcagta gatgaatggg ttgatggaat ctgagacagt	120
gctctagaat ctgtgtttca tacaggatga gatataaatg aaacaaatgc taaataatga	180
cacaaggtag cttgccgaga gaggaatcat ccacctggaa gggtaggctg tttgtgaata	240
atgtagggtg ggagagaagg ctttactaag gagatgggct taaagaatgt gaacgatgtg	300
ctcacagagg ccacagaaga gaaattatag ccaggagaac aacctgaaag acaaaggaca	360
cggtagcatg agcgcatgta acacaatgta ctgaggaat ggctggcatc ctgagatatg	420
gagtggaaata cagtacaggc ctttgtaaac tcagcttggg gtcagatcac agaaagcctt	480
gacaaggaac tgaaaatggg ttctgaaggc cagaagccca ttcaagattc ccaaagggaa	540
aaacacaaat cagcttggtt tcaggacgta attcttgga gttgctagaa ttacatcaga	600
aaggaggttc acnt	614

&lt;210&gt; 23

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2-4, 6, 8, 12-13, 16, 507, 561, 583, 592

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 23

gnnnntnanc anncantggg ccctctagat gcatgctcga gcggccgcca gtgtgatgga	60
tatctgcaga attcgccctt cctatgtatt tcctcttact gggctttcct ggttctcaaa	120
ctcttcagct ctctctctt atgcttttct tggtagtgta catccccaca gttagtggta	180
atgtggctat cttgatgttg gtgagcacct cccatcagtt gcataccccc atgtacttct	240
ttctgagcaa cctctccttc ctggagattt ggtataccac agcagcagtg cccaaagcac	300
tggccatcct actggggaga agtcagacca tatcatttac aagctgtctt ttgcagatgt	360
actttgttat ctcataggc tgcacagagt acttcctcct ggcagccatg gcttatgacc	420
gctgtcttgc catctgctat cctttacact acggagccat catgagtagc ctgctctcag	480
cgcagctggc cctgggctcc tgggtgnggg ggttcgtggc cattgcaagt gccacaagc	540
cctaatacagt ggcctgtcc ntctgggggc ccccgggcca ttnaccactt tnttctggga	600
caattgcacc cctggaattg g	621

&lt;210&gt; 24



<211> 612  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-3, 8, 16, 20, 26, 557  
 <223> N can be any nucleotide

<400> 24  
 tnnttaantc attcctnttgn cccctcnagat gcatgctcga gcggccgcca gtgtgatgga 60  
 tatctgcaga attcgccctt tccttggttac tgagggagta gattagggga ttgatggaat 120  
 ctgagacagt gctctagaat ctgtgtttca tacaggatga gatataaatg aaacaaatgc 180  
 taaataatga cacaaggtac cttgccgaga gaggaatcat ccacctggaa gggtaggctg 240  
 tttgtgaata atgtaggggtg ggagagaagg ctttactaag gagatgggct taaagaatgt 300  
 gaacgatgtg ctcacagagg ccacagaaga gaaattatag ccaggagaac aacctgaaag 360  
 acaaaggaca cgggtggcata agcgcattgta acacaatgta ctcaggaaat ggctggcatc 420  
 ctgagatatg gagtggaata cagtacaggg ctttgtaaac tcagcttgga gtcagatcac 480  
 agaaagcctt gacaaggaac tgaaaatggg ttctgaaggc cagaagccat tcaagattcc 540  
 caaagggaaa aacacanatc acttgttttc aggacgtatt cttgggcagt tgctagaatt 600  
 acatcagaaa gg 612

<210> 25  
 <211> 632  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-5, 9, 614  
 <223> N can be any nucleotide

<400> 25  
 gnnnnttant ccatgccctt ctagatgcat gctcgagcgg ccgccagtgt gatggatattc 60  
 tgcagaattc gcccttggtt cgcagcctat aaatgaaggg gttgatggaa tctgagacag 120  
 tgctctagaa tctgtgtttc atacaggatg agatataaat gaaacaaatg ctaaataatg 180  
 acacaaggta ccttgccgag agaggaatca tccacctgga agggtaggct gtttgtgaat 240  
 aatgtaggggt gggagagagg gctttactaa ggagatgggc ttaaagaatg tgaacgatgt 300  
 gctcacagag gccacagaag agaaattata gccaggagaa caacctgaaa gacaaaggac 360  
 accggtggca taagcacatg taacacaatg tactcaggaa atggctggca tcctgaggta 420  
 tggagtggaa tacagtaccg gggctttgta aactcagctt ggagtcagat ccagaaagcc 480  
 cttgacaagg aactgaaaat tgggttcttg aaggccagaa gccattcaag gattcccaa 540  
 aggggaaaaa cacaaatcaa gcttgttttc agggaccgtt aattctgggg ccaggttgct 600  
 tgaattacct tcangaaagg gaggttcaca ct 632

<210> 26  
 <211> 628  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-3, 419, 423, 426, 437, 439, 453, 460, 463, 469, 478, 489, 492,  
 536, 539, 579, 583, 586, 594, 598, 616, 623, 627  
 <223> N can be any nucleotide

<400> 26  
 gnncttattc atccccctct agatgcatgc tcgagcggcc gccagtgtga tggatatctg 60  
 cagaattcgc cctttctttg ttctcagag tgtagattag ggggttgatg ggggttgatg 120  
 aatctgagac agtgctctag aatctgtgtt tcatacagga tgagatataa atgaaacaaa 180  
 tgctaaataa tgacacaagg taccttgccg agagaggaat catccacctg gaagggtagg 240

ctgtttgtga ataatgtagg gtgggagaga aggctttact aaggagatgg gcttaaagaa	300
tgtgaacgat gtgctcacag aggccacaga agagaaatta tagccaggag aacaacctga	360
aagacaaagg acacgggtggc ataagcgcac gtaacacaat gtactcagga aatggctgnc	420
atnctnagat atggagngng aataccagta canggctttt tanactcanc ttggagtnc	480
gaatcacana angccttgca aggaactgaa aatgggttct gaaaggccag aagccttna	540
agattcccaa agggaaaaaa cacaaatcaa gcttttttna agnacngtaa ttcntggngc	600
cagttgctta gaattnccat canaaang	628

<210> 27  
 <211> 803  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3-4, 19, 168, 190, 202, 245-246, 250, 260, 266, 280, 281, 284, 286, 289, 301, 303, 305, 313, 332-333, 348, 355, 357, 360, 365-366, 370, 372, 376, 379, 384, 387-390, 394-396, 400, 406-407, 411-412, 416-418, 421, 423, 430, 439-440, 442-443, 446, 448, 462-463, 468-469, 480, 482-483, 490, 493, 498, 506-508, 518-519, 523, 532, 534, 536, 539, 547, 549, 556, 559, 573-575, 580-581, 587, 590, 595-596, 600-601, 603, 612, 614, 618, 623, 629, 633, 640, 643, 646, 655-656, 658, 666, 682, 689, 696, 704, 708-709, 718, 721, 732, 738-739, 743, 746, 751, 759, 764-765, 771, 775, 782-783, 788-789, 791-792, 795, 801  
 <223> N can be any nucleotide

<400> 27	
ggnttaagcc ttccccctnc gatgctgctc gagcgggccgc cagtgtgatg gatattctgca	60
gaattcgccc ttcccatgta tttcctctta ctgggctttc ctggttctca aactcttcag	120
ctctctctct ttatgctttt tctgggtgatg tacatctca cagttagnng taatggggct	180
atcttgatgn ttggtgagcac cncctatcag ttgcataccc ccatgtactt ctttctgagc	240
aaccnntccn tcttgagagan tttggnatac cacacgcaan nagnngccna aggcacttgg	300
nctnctaca ggnggagaag gcttgaccat annattttac catgcctngc cttangncan	360
accnntctn tncctntnt tccnctnnn ggtnnntcan ccgcannctt nnatcnntg	420
nanctcatn gaatatgggn tngtntntc ttgagagcct cnngatcna ttttttccan	480
cnntaaagn ggngcttntc tctctnnnat ctagcttntt ggntctcttt tntntctna	540
cccggtntnt cctatntgnt gtctcttct acnnctgcn nttatntan atcanntctn	600
ncttctctc cntntacnac atnatcatnc tcnctcccn ctntcnctct ctatnncnta	660
ccatcnctct cttctcatte anctctttnt cattgnttgt tcanttannc actctcctc	720
ncatcttcta tncactannt ttntntttt nctctctant tctnnttcca ntgtncactc	780
cnntctnnnc nntncccta ncg	803

<210> 28  
 <211> 620  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3, 4, 7, 9, 10, 11, 24, 563  
 <223> N can be any nucleotide

<400> 28	
gtnttnnann ncattgcccc tctngatgca tgctcgagcg gccgccagtg tgatggatat	60
ctgcagaatt cgcccttctt atgtacttcc tcttaccggg ctttctctgt tctcaaactc	120
ttcagctctc tctctttatg ctttttcttg tgatgtacat cctcacgggt agtggtaatg	180
tggtatcttt gatgttggtg agcacctccc atcagttgca taccctcatg tacttctttc	240
tgagcaacct ctcttctctg gagatttggt ataccacagc agcagtgcc aaagcactgg	300
ccatcctact ggggagaagt cagaccatat catttacaag ctgtcttttg cagatgtact	360
ttgttttctc attaggctgc acagagtact tctctctggc agccatggct tatgaccgct	420
gtcttgccat ctgctatctt ttacactacg gagccatcat gagtagcctg ctctcagcgc	480
agctggccct gggcttcttg gtgggtgggt ttgggggcca ttgcaagtgc ccacagccct	540

tatcaagtgg cctgtccttc tgnnggcccc gggcccatca accacttttt tctggggaca 600  
attgcaccct ggaatggccc 620

<210> 29  
<211> 620  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 3-5, 7-9, 15, 567, 574, 585, 596, 606, 611-612, 616, 618-619  
<223> N can be any nucleotide

<400> 29  
gtnnntnnnt ccatnccatt gggccctcta gatgcatgct cgagcggccg ccagtgtgat 60  
ggatatctgc agaattcgcc ctttcattggt tccggaaaca gtaaattatg gggttcagtc 120  
atggtaacag gaggaggctg agtgtatggg catggatggg ggctgtgaat gtggcgggag 180  
ctcatggatg tgctcttctg agtgcttcac gtttctgagt gaaataagaa gcaaggatcat 240  
caccgagagg gaggagacag gctcgggtga gtttagtgga tatgaatcca agagagacca 300  
ttcaacttag ttgtctattt tttttttctc cagttagatg cacttgcagc aatgtagatg 360  
tggagtactt gatcataaga tccattttat ggcagaagac attatttttc tgagccttct 420  
gctgtcagtt tctaaataag caggccagcc gggctgtgca cctaaatgct tgtctgggag 480  
gagcaggctg agaagtcttg cagtctgcag gacaccgag gaatcgatg gtgggaaccg 540  
tccccgagaa ccacacgagc cgtgctnctc agtnctgact ggaanaatga aattgnaagc 600  
caagtngtcc nnggancnnt 620

<210> 30  
<211> 616  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 2-4, 7, 9-10, 580  
<223> N can be any nucleotide

<400> 30  
gnnnntnnnn ccatgagcc ctctagatgc atgctcgagc ggccgcccagt gtgatggata 60  
tctgcagaat tcgcccttcc tatgtatttc tcttcctaac gattggaatg cctgggatta 120  
ggcagatgat tttctttttc ccccatatcc ctctattatt taggtgattg agtttaaate 180  
cctttatcta cacccttcgg aacaagggcg aattccagca cactggcggc cgttactagt 240  
ggatccgagc tcggtaccaa gcttgatgca tagcttgagt attctaacgc gtcacctaaa 300  
tagcttgagg taatcatggt catagctggt tcctgtgtga aattgttatc cgctcacaat 360  
tccacacaac atacgagccg gaagcataaa gtgtaaagcc tgggggtgcct aatgagttag 420  
ctaactcaca ttaattgcgt tgcgctcact gcccgcttcc cagtcgggaa acctgtcgtg 480  
ccagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc 540  
ttccgcttcc tcgctcactg actcgtggg cttcgggtcgn tcggctgcgg cgagcgggat 600  
cagctcactc aaaagg 616

<210> 31  
<211> 612  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 2-9, 13, 507, 554, 585, 598, 600, 609  
<223> N can be any nucleotide

<400> 31  
gnnnnnnnnt cangccattg ggcctcttag atgcatgctc gagcggccgc cagtgtgatg 60  
gatatctgca gaattcgccc ttcctatgta tttctcttca ctttctccga catcactcac 120

agccacccca	ccctcagcct	ctccctcctc	ccatgtatct	tctcttcaat	ctctccttct	180
ttgatatacct	gaactttctg	tagctcttta	ttttctcttc	caatcccttc	atatacacgt	240
ttcgtaacaa	gggcgaattc	cagcacactg	gcggccgtta	ctagtggatc	cgagctcggt	300
accaagcttg	atgcatagct	tgagtattct	aacgcgtcac	ctaaatagct	tggcgtaatc	360
atgggtcatag	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	acaacatacg	420
agccggaagc	ataaagtgtg	aagcctgggg	tgccataatga	gtgagctaac	tcacattaat	480
tgcggtgcgt	cactggccgc	tttccangtc	gggaaacctg	tcggccagct	gcattaaatg	540
aatcgcccaa	cgcncggga	gaggcggttt	gcgtattggg	cgctntttcg	ttcttcgntn	600
actgatcgnt	gg					612

&lt;210&gt; 32

&lt;211&gt; 616

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2-9, 15, 521, 596

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 32

gnnnnnnnnt	tcatnccatt	gggccctcta	gatgcatgct	cgagcgggcg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttgttgctt	agagtgtaaa	taaaaggggt	aacattgggt	120
tagaggtgaa	gagtaaatac	ataggaaggg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttctgtgtg	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgctt	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaacgc	gcggggagag	gcgggtttcg	tattggggcg	480
tcttcgctt	cctcgctcac	tgactcgctg	cgctcggtcg	ntcggtcgcg	gcgagcggtg	540
tcaagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcagggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

&lt;210&gt; 33

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2, 4, 6, 8, 19, 27, 31, 464, 526, 554, 578, 598, 600, 615

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 33

gntntnanc	atgccccnc	cgatgcntgc	ncgagcgggc	gccagtgtga	tggatatctg	60
cagaattcgc	ccttgttgcg	gagcgaatat	atgaaggggt	taagggaaga	gaaaatacat	120
aggaagggcg	aattccagca	cactggcggc	cgttactagt	ggatccgagc	tcggtaccaa	180
gcttgatgca	tagcttgagt	attctaacgc	gtcacctaaa	tagcttggcg	taatcatggt	240
catagctggt	tctgtgtga	aattgttata	cgctcacaat	tccacacaac	atacgagccg	300
gaagcataaa	gtgtaaagcc	tgggtgcct	aatgagttag	ctaactcaca	ttaattgcgt	360
tgcgctcact	gcccgctttc	cagtcgggaa	acctgtcggtg	ccagctgcat	taatgaatcg	420
gccaacgcgc	cggggagagg	cggtttgcgt	attgggcgct	cttncgcttc	ctcgctcact	480
gactcgcttg	cgctcggtcc	gttcggctgc	ggcgagcggt	atcaantcac	tcaaaaggcg	540
ggaatacggg	ttncacaga	aatcaggggg	ataacgcngg	aaagaacatg	tgagccanan	600
ggcagcaaaa	gggcnaggaa	t				621

&lt;210&gt; 34

&lt;211&gt; 614

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

<220>  
 <221> variation  
 <222> 2-9, 13-14, 593  
 <223> N can be any nucleotide

<400> 34  
 gnnnnnnnt cannccattg ggccctctag atgcatgctc gagcgggccgc cagtgtgatg 60  
 gatattctgca gaattcgccc ttgttccgaa ggctatagat gaagggggtt taggttttta 120  
 ggaacacagg ctaaggggga agagaaaata catgggaagg gcgaattcca gcacactggc 180  
 ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg agtattctaa 240  
 cgcgtcacct aaatagcttg gcgtaatcat ggcatagct gtttcctgtg tgaaattgtt 300  
 atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa gcctgggggtg 360  
 cctaattgagt gagctaactc acattaattg cgttgcgctc actgcccgtt ttccagtcgg 420  
 gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcggggaga ggcggtttgc 480  
 gtattgggag ctcttcgctc tcctcgctca ctgactcgct gcgctcggtc gtcgggtgag 540  
 gcgagcggta tcagctcact caaaggcggg aatacgggta tccacagaat cangggataa 600  
 cgcaggaaaa gaca 614

<210> 35  
 <211> 614  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3-4, 7, 9, 23, 599, 611  
 <223> N can be any nucleotide

<400> 35  
 ggnnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatatc 60  
 tgcagaattc gcccttccga tgtattttct tctacgttaa ggtattttta attgttacta 120  
 atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat 180  
 gatgctgtta cctcacaat atgtatgtgt ggatgtatat atatctatc aatatatgta 240  
 actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct 300  
 agtgtctcag ataagttggc tagttttttg tttcacataa aggaacaaac atttatagat 360  
 ttatatgtat attaaaaatg gtaaaaaattg gctgggtgca gtggttcatt cctataatac 420  
 cagcactttg ggaagccgag gtgggcggat tacttgaggt aaggagccca gcctgaccaa 480  
 caagggtgaa ccccatccct actaaaaata caagaattag cccggggatg gtggtggcca 540  
 cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng 600  
 aggttgagg ngag 614

<210> 36  
 <211> 611  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 1, 3-5, 10, 18-20, 22, 26, 605  
 <223> N can be any nucleotide

<400> 36  
 ngnnnttgan tcaattcnnn gncgangcat gctcgagcgg ccgccagtgt gatggatatc 60  
 tgcagaattc gcccttccga tgtattttct tctagccaac ctcccactca ttgatctgtc 120  
 tctgtcttca gtcatagcc ccaagatgat tactgacttt ttcagccagc gcaaagtcat 180  
 ctctttcaag ggctgccttg ttcagatatt tctccttcac ttctttgggtg ggagtggatg 240  
 ggtgatcctc atagccatgg gctttgacag atatatagca atatgcaaac cctacacta 300  
 cactacaatt atgtgtggca acgcatgtgt cgccattatg gctgtcgcag ggggaattgg 360  
 ctttctccat tcggtgagcc agttggcctt tgccgtgcac ttacccttct gtggtcccaa 420  
 tgaggtcgat agtttttatt gtgaccttcc tagggtaacc aaacttgcct gtacagatac 480  
 ctacaggcta gatattatgg tcattgctaa cagtgggtgt ctcactgtgt ggtcttttgt 540

cttctaataca tctcatatac tatcatccta atgaccatcc agcattgccc tttagataag 600  
tcgtncaaag g 611

<210> 37  
<211> 616  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 2-4, 6, 8, 12-14, 17, 19-20, 442, 595, 599  
<223> N can be any nucleotide

<400> 37  
gnnnntnanc cnnncncnn ctagatgcat gctcgagcgg ccgccagtgt gatggatatac 60  
tgcagaattc gcccttccca tgtatttgct tctcagcaac ttgtccttct ctgacctctg 120  
cttctcttcc gtgaccattc ccaagttgtt acagaacatg cagaaccagg acccatccat 180  
ccctatgcg gactgcctga cccaaatgta cttcttctctg ttatttgagg acctggagaa 240  
cttctcctt gtggccatgg cctatgaccg ctatgtggcc atctgcttcc cctgcaacta 300  
caccgccatc atgagcccca tgcctgtctc cgccctgggt gcgctgtcct ggggtgctgac 360  
caccttccat gccatgttac acactttact catggccagg ttgtgttttt gtgcagacaa 420  
tgtgatcccc cactttttct gngatatgtc tgcctgtctg aagcaggcct tctctgacac 480  
tcgagttaat gaatgggtga tatttatcat gggagggtc attcttgtca tcccatcct 540  
actcattctt gggctctatg caagaattgt ctctcatcc tcaaggctcc tttntaang 600  
gtatctgcaa ggcct 616

<210> 38  
<211> 615  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 1, 3-6, 9, 11, 14, 16, 20, 21, 23, 540, 566  
<223> N can be any nucleotide

<400> 38  
ngnnnnntna ntcnangcnn ngngccctct agatgcatgc tcgagcggcc gccagtgtga 60  
tggatatctg cagaattcgc ccttccaatg tatttacttc tcagccagct ctcccttatg 120  
gacctgatgt acatctccac caccgtcccc aagatggcgt acaacttctt gtccggccag 180  
aaaggcatct ctttcttggg atgtggtgtg caaagcttct tcttcttgac catggcgtgt 240  
tctgaaggct tactcctgac ctccatggcc tacgaccgtt atttgccat ctgccactct 300  
ctctattatc ctatccgcat gagtaaaatg atgtgtgtga agatgattgg aggctcttgg 360  
acactggggg ccatcaactc cttggcacac acagtctttg cccttcataat tccctactgc 420  
aggcttaggg ctattgacca tttcttctgc gatgtcccag ccattgttgc tcttgctgta 480  
cagatacttg ggtctatgaa tatatggttt ttgtaaggac aaagcctctt tcttcttttn 540  
cctttcattg gcatcacttc ttctgngggc cgagtccata ttgctggcta tataatgcac 600  
tcaaaggagg ggagg 615

<210> 39  
<211> 615  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 4-8, 12-13, 17-18, 22-23, 26-28, 469, 591, 596  
<223> N can be any nucleotide

<400> 39  
tagnnnnntt anntcanngc cnnngnnngc tcagatgcat gctcgagcgg ccgccagtgt 60

gatggatata	tgcagaattc	gcccttccaa	tgtattttct	tctcagcagg	agagatat	120
atcctcactg	ccatgtccta	tgaccgctat	gtagccatct	gctgtcccct	gaactacgag	180
gctgcacaga	gtacttccct	ctggcagcca	tggcttatga	ccgctgtctt	gccatctgct	240
atcctttaca	ctacggagcc	atcatgagta	gcctgtcttc	agcgcagctg	gccctgggct	300
cctgggtctg	tggtttcgtg	gccattgcag	tggccacagc	cctcatcagt	ggcctgtcct	360
tctgtggccc	ccgtgccatc	aaccacttct	tctgtgacat	tgcaccctgg	attgccctgg	420
cctgcaccaa	cacacaggca	gtagagcttg	tggcctttgt	gattgctgnt	gtggttatcc	480
tgagttcatg	cctcatcacc	cttgtctcct	atgtgtacat	catcagcacc	atccttagga	540
tcccctctgc	agtggccgga	gcaaagcctt	ctcccgtgct	cctcgcatct	naacngngtg	600
ctcatttggt	atggg					615

&lt;210&gt; 40

&lt;211&gt; 586

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 14, 21, 23, 479, 498, 534, 584

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 40

catgctcgag	cggnccgag	ngngatggat	atctgcagaa	ttcgcccttc	ctatgtattt	60
gcttctcagc	aggagagata	tttatcctca	ctgccatgct	ctatgaccgc	tatgtagcca	120
tctgctgtcc	cctgaactac	gaggtgattc	atgtgcccat	tagagcttga	gaagcactgc	180
ttggaagccc	cttctgccat	caatgaggct	gcacagagta	cttcctcctg	gcagccatgg	240
cttatgaccg	ctgccttgcc	atctgctatc	ctttacacta	cggagccatc	atgagtagcc	300
tgtctcagc	gcagctggcc	ctgggctcct	gggtctgtgg	tttcgtggcc	attgcagtgc	360
ccacagccct	catcagtggc	ctgtccttct	gtggcccccg	tgccatcaac	cacttcttct	420
gtgacattgc	accctggatt	gccctggcct	gcaccaacac	acaggcagta	gaagcttgng	480
gcctttgtga	attgctgntg	tgggtatccc	gagttcatgc	ctcatcacc	ttgncttcta	540
tgtgtacatc	atcaggcacc	attctcagga	tcccttctgc	aagngg		586

&lt;210&gt; 41

&lt;211&gt; 857

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 5-12, 16-18, 22, 27, 32, 42, 60, 99, 159, 171, 202, 212, 240, 242, 251, 306, 330, 371, 568, 669, 750, 802, 840, 856

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 41

atggnnnnnn	nnnttnnnna	anttttnccc	antttggggc	gnccccccct	tctttaaggn	60
aatgggccc	ttgggccctt	cccgggaaggc	ccgggggnc	ccggccccaa	aggtttgggt	120
tgggaaatgg	ggggaattta	aattcctttg	ggccaaggna	aaaattttcc	ngccccctt	180
tttttcccct	tttggttttt	anccggggga	angggggggt	tgattaatta	atcgggaagn	240
tnggggggaa	nttttttaaa	aaaaaccttg	ggggaagggt	ccaacccaac	aaggttgggt	300
ttccanggga	ccgttgggac	caggcttttn	gaatcaagaa	tcccaaagg	cattcttttg	360
gattaaggaa	nggtgccggg	accggtgaaa	gggaaaaaac	tggtggaccc	cataccaaaa	420
tgagaaccac	ggtgagatgc	cgaggagcac	gtggagaaag	gctttgcttc	cggccactgg	480
cagaggggat	cctgaggatg	gtgcttgatg	atgtacacat	agggagacaa	gggtgatgag	540
gcatgaactc	aggataacca	caacagcnat	cacaaaggcc	acaaagctct	actgcctgtg	600
tgttgggtgc	aggccagggc	aatccagggg	tgcaatgtca	caagaaagaa	agtggttgat	660
ggcacgggng	ggccacagaa	ggacaggcca	cttgatgaag	ggcttggtgg	cactgcaatg	720
gccacgaaac	caccagaccc	aggaaccan	ggccaagctt	gcgcctgaag	agcaaggcta	780
ctcatgaatg	gcttccgtag	tngtaaagga	tagcaagatg	gcaaaggcaa	gccggtcatn	840
aagccatggc	ttgccng					857

&lt;210&gt; 42

<211> 620  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-4, 8-10, 43, 611, 613  
 <223> N can be any nucleotide

<400> 42  
 gnnnttannn cattgcgccc tctagatgca tgctcgagcg gcncgccagt gtgatggata 60  
 tctgcagaat tcgcccttgt tgcgcaagga gtagatgaac ggattcaggg caagggagtg 120  
 ctgaggagat agacgggtat aactgggca caagtccatg agtaatcaag gcctgttatt 180  
 taaaaaaaaa aaaaaaaaaa cttgaacaat atagaatccc attaccaga gatagactgg 240  
 atggtgaatt aaactttctg gtgaatttct ttccagatat ctctctatgc atatgtatac 300  
 acaagcaatt tttggaagaa aagatacttt ataaggataa gcctgaaaac tgcaacgaat 360  
 gcaatgtgga gaatgaaggc aagatgtggc gaagaagggc accacaatct ggtggctgag 420  
 agagtgaac tgtcactaca gctaaaagga gagctggaga agctgggtgag gacagtaaga 480  
 gatgaatctg gtttaagaca cgctgagtct caaatgccat ggctccccta ggttgccctc 540  
 tcagatgtaa atcttaagct caaagcaggt ggatgagaaa tcacatttca tagtccctgc 600  
 acagacggct ntnttgagct 620

<210> 43  
 <211> 608  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-5, 10, 22-24, 27, 592  
 <223> N can be any nucleotide

<400> 43  
 gnnntttaan tcattgcccc gnnngangca tgctcgagcg gccgccagt tgatggatat 60  
 ctgcagaatt cgccttccc atgtatttgc ttctcagcaa cttgtccttc tctgacctct 120  
 gcttctcttc cgtgaccatt cccaagtgtg tacagaacat gcagaaccag gacctcca 180  
 tcccctatgc ggactgcctg acccaaatgt acttcttctt gttatttgga gacctggaga 240  
 gcttctctct tgtggccatg gcctatgacc gctatgtggc catctgcttc cccctgcact 300  
 acaccgccat catgagcccc atgctctgtc tcgccctggg gcgctgtcc tgggtgctga 360  
 ccacctcca tgccatgta cacttttac tcatggccag gttgtgttt tgtgcagaca 420  
 atgtgatccc ccacttttct tgtgatgtgt ctgctctgct gaagctggcc ttctctgaca 480  
 ctgaggttaa tgaatgggtg atatttatca tgggagggct cattcttgca tccattccta 540  
 ctcatccttg ggtcctatgc aagaaatgct cctcatcctc aaggcccttc tntaagggtg 600  
 tctgcaag 608

<210> 44  
 <211> 608  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-5, 7, 9, 12, 20, 24, 26, 29, 31-32, 480, 530, 557, 579  
 <223> N can be any nucleotide

<400> 44  
 gnnntnant cntgccctgn ccncngcnc nngcgccg cgatggat atctgcagaa 60  
 ttgcgccctg ttactaagag tatagatgaa cggattcagg gcaagggagt gctgaggaga 120  
 tagacgggta tacactgggc acaagtccat gagtaatcaa ggcctgttat ttaaaaaaaa 180  
 aaaaaaagct tgaacaatat agaatcccat taccagaga tagactggat ggtgaattaa 240  
 actttctggt gaatttcttt ccagatatct ctctatgcat gtgtatacac aagcaatttt 300



tggaagaaaa	gatactttat	aaggataagc	ctgaaaactg	caacgaatgc	aatgtggaga	360
atgaaggcaa	gatgtggcga	agaagggcac	cacaatctgg	tggtctgagag	agtgcaactg	420
tcactacagc	taaaaggaga	gctggagaag	ctgggtgagga	cagtaagaga	tgaatctggn	480
ttaagacacg	ctgagtcctca	gatgccatgg	cttccctagg	ttgcctcttn	cagatgtaaa	540
tcttaagctc	aaagcangtg	gatgagaaat	acacatttna	tagtcacctg	cacagacggt	600
tttttgat						608

&lt;210&gt; 45

&lt;211&gt; 602

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 14, 16, 19, 21, 23-24, 27, 38, 40, 50, 52, 520, 551

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 45

catgccccgt	ccncnagnt	ncnngcncgg	cgggccgcnan	ggatatctgn	anaattcgcc	60
cttctctatgt	atttacttct	ccaactttctc	cttcccatct	ctatcattag	aaccattca	120
tatacaccct	acgaaacaag	ggcgaattcc	agcacactgg	cgggccgttac	tagtggatcc	180
gagctcggta	ccaagcttga	tgcatagctt	gagtattcta	acgcgtcacc	taaatagctt	240
ggcgtaatca	tggtcatagc	tgtttctctgt	gtgaaattgt	tatccgctca	caattccaca	300
caacatacga	gccggaagca	taaagtgtaa	agcctggggg	gcctaattgag	tgagctaact	360
cacattaatt	gcgttgcgct	cactgcccgc	tttccagtcg	ggaaacctgt	cgtgccagct	420
gcattaatga	atcgccaac	gcgcggggag	agggcggttg	cgtattgggc	gctcttccgc	480
ttctcgtca	ctgactcgct	gcgctcggtc	gttcggctgn	ggcgagcggt	atcagctcac	540
tcaaaggcgg	naatacggtt	atccacaaga	atcaggggga	taacgcaaga	aaagacatgt	600
ga						602

&lt;210&gt; 46

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2-4, 6, 10

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 46

gnnntnattn	attgcattgg	gccctctaga	tgcatgctcg	agcgcccgcc	agtgtgatgg	60
atatctgcag	aattcgccct	tagtgagtag	atgaaagggt	tcagcatggg	ggtcaccaca	120
gtgtacatca	tagccatgac	agtgtccttt	agagtagaac	tattagctga	tgagcataag	180
tagagaccaa	taacgggttc	atagaacagt	gacaccacag	atagggtggga	gccacaagta	240
gagaaggcct	tgagacacc	cttagaagaa	gggaccttga	ggatggagga	gacaattctt	300
gcataggacc	caaggatgag	taggaatggg	atgacaagaa	tgagccctcc	catgataaac	360
atcaccatt	cattaactcg	agtgtcagag	aaggccagct	tcagcagagc	agacatatca	420
cagaaaagg	gggggatcac	attgtctgca	caaaaacaca	acctggccat	gagtaaagt	480
tgtaacatgg	catggaagg	ggtcagcacc	caggacagcg	ccaccagggc	gagacagagc	540
atggggctca	tgagggcggt	gtagtgcagg	gggaagcaga	tgggccacata	gcggtcatag	600
gccatggcca	caaggaggaa					620

&lt;210&gt; 47

&lt;211&gt; 607

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2, 572, 578, 594

<223> N can be any nucleotide

<400> 47

cnatgggccc	tctagatgca	tgctcgagcg	gccgccagtg	tgatggatat	ctgcagaatt	60
cgcccttcca	atgtatttgc	ttctcagcaa	cttgctcttc	tctgacctct	gcttctcttc	120
cgtgaccatt	cccaagtgt	tacagaacat	gcagaaccag	gacccatcca	tcccctatgc	180
ggactgcctg	acccaaatgt	acttcttcct	gttatttggg	gacctggaga	gcttctctct	240
tgtggccatg	gcctatgacc	gctatgtggc	catctgcttc	cccctgcaact	acaccgccat	300
catgagcccc	atgctctgtc	tcgccctggg	ggcgctgtcc	tgggtgctga	ccaccttcca	360
tgccatgtta	cacactttac	tcatggccag	gttgtgtttt	tgtgcagaca	atgtgatccc	420
ccacttttct	tgtgatttgt	ctgctctgct	gaagctggcc	ttccctgaca	ctcgagttaa	480
tgaatgggtg	atatttatca	tgggagggct	cattcttgtc	atcccatccc	tactcaatcc	540
ttgggtctat	gcaagaaatt	gtcttcttca	tnctcaangg	ccctttcttc	taanggtatc	600
ttgcaag						607

<210> 48

<211> 613

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 7, 9, 257, 266, 295, 313, 322, 331, 334, 338, 340, 345, 348, 356, 358, 365, 378, 397, 398, 402, 410, 447, 480, 536-537, 557, 563, 576, 580, 584-586, 606, 610-612

<223> N can be any nucleotide

<400> 48

annnccntng	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttttgttaa	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	120
cttcaaaa	ccttggtcac	tcacctcttc	tcagctctct	ttgtggatcc	ttcctcattt	180
atttgacctc	ttgctgggtg	accctttcat	atacactctc	cgtaacaaag	agggcgtact	240
tctgtcgtct	tgagcgnact	gatgggnacc	agcttttgtt	cccttttagt	agggntaatt	300
gcgcgcttgg	cgnaatcatg	gncatagctg	ntnctgngn	gaaantgnta	tttcgntnac	360
aattncacac	aacatacnag	ccgggagcat	aaaggggnna	gncctggggg	gcctaataag	420
ggagcttact	cacaataaatt	gggggtgngcc	cactggcccc	ttttcaggcg	ggaaaacctn	480
gcggggccag	ctggaataaaa	tgaatcgggc	cacgcgcggg	ggaggagggc	gggttnngga	540
attgggcgct	ttttccnttt	ctnggttaat	ggactnggtn	ggcnnngtcc	gttcggttgg	600
ggggancggn	nnt					613

<210> 49

<211> 593

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 177, 298, 506, 515, 578, 582

<223> N can be any nucleotide

<400> 49

aacgcagagt	accgcccact	acgtaatctg	tacatgaaag	ggtttaaaag	agactgggaa	60
gagaggaatt	ggcaagatca	agcagaggca	actccttcta	gtccttctag	taccgcaagg	120
ggcagataaa	tggaatgggt	aacacctaga	ggaaagtata	cttgccaaaa	gcaaatncat	180
aggggggagt	acattatcgg	gttgaaaaaa	gtattccatg	cagataaaaa	ccaaaagcaa	240
atacatcggg	ggcgctacttc	tgctgtcttt	gagcgctact	atggtagcca	gcttttgnct	300
ctttagttag	gggttaattgc	gcgcttggcg	taatcatggg	catagctggg	ttctgtgtga	360
aattgttatc	ccgttcacaa	ttcacacaac	atacagagcc	gggagcataa	agtgtaaagc	420
ctgggggtgc	taatagttgg	agcttactta	cattaaattg	cgttgcgctc	actggccgct	480
tttccaagtc	gggaaacctg	tcgtgncagc	ttcantaatg	aatcggccaa	cgccgcgggg	540
agaggcgggt	tgctgtattg	gcgctcttcc	gcttcttngt	tnactgactt	cgg	593

<210> 50  
 <211> 624  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-4, 11, 16, 20, 22  
 <223> N can be any nucleotide

<400> 50  
 gnnntttaac nccggngctn cnagcagtgg aacaacgcag agtacgcccc cgatgtactt 60  
 tctttttcag tctcaagtct tctctttctc caaagatttt gtctttttcta ctacctgagc 120  
 taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcatt caacttcaaa 180  
 cgtgtcatct cagaacaagc ttcatgttac ttccaatttt atccttcttg tttgctgatt 240  
 ccaagaattc cagtcccatc taggcccgcga atgcattgtt cctgccaccc tttcatatc 300  
 ctcaattccc ttgtatcatc actttccttt tatatagcac agattccatg attcataaca 360  
 ataattatgt ttttttttgc atgtgctctt aatttccttt cttgctccta ttatcttcta 420  
 tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcaactta 480  
 tgctcagtca gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540  
 tttatagtcg tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600  
 tctgcgcttg agcgtccggt gggg 624

<210> 51  
 <211> 584  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 584  
 <223> N can be any nucleotide

<400> 51  
 gcagtggtaa caacgcagag tacgcccgtt acggaggctg taaataaagg ggttgaggaa 60  
 gtaaagtact tcacagtact ggagcacaca gcatgtgaat ttcagccaaa ggacaaatgc 120  
 ctccaaaaaa agttaattca cagtgcagca gggcgaggca cttgtcttat tcgctgggtc 180  
 tcacattgac cctgaaagga cttttttttg ttaatcccat tttcacagat gggaaaggga 240  
 ctctgtatgg ttgtcacttt tatccaaagt ctcatagcca gtaagaagct gccctcaaag 300  
 tccctaccct gtcttccatt cgactattct gaggttcaga cccagaaacc ccatacctct 360  
 gccttatatt ttaatgaaaa gtatgtctcc aggtttatgt ggagaataac caagacctca 420  
 gaaacattta gtgaaaatca gagctagaag gaatctgttt ttttgcgagt tcagagaaac 480  
 tgacttggat aagacatcaa agttgtcttg tgcagcaaat tctcctcgg cacatagtag 540  
 gcactctgat aaattcaaaa aggcttctaa gaagaggcag aagn 584

<210> 52  
 <211> 613  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 6, 10-12, 16-17, 20, 553, 594, 607, 613  
 <223> N can be any nucleotide

<400> 52  
 gtgaanccan nntaannccn attggagctc caagcagtgg taacaacgca gagtacgccc 60  
 ccgatgtagt ttcttcttcc ctctcttccc tcttctctc cttcttctct ttctctctct 120  
 ctctctctcc ctctctctct cctctctctc ctcttcttcc ttctctctcc tctctctccc 180  
 cccaatccgt tcatgacttc ttcttcttcc tcttcttctt ctttcttctt ttcttctttt 240

tctctaagca	ggatcctggg	ctgttcaaac	cagagagctg	taagtctttt	ctttcccat	300
tactgttaga	tccgttgaat	cggctccaga	aaccaaaca	gttaaccctt	gcatttacac	360
gtttcgtaac	ggcggtactt	ctgtcgtctt	gagcgtactg	atggtagcca	gcttttggtc	420
ccttttagtga	gggttaattg	cgcgcttgcc	gtaatcatgg	tcatagctgt	ttcctgtggg	480
aaattgttat	ccgctcaca	ttccacacaa	catacgagcc	gggagcataa	aagtgtaaag	540
cctgggggtgc	ctnatgagtg	agctaactca	cattaattgc	gttgcgctta	ctgnccgttt	600
tcagtcngga	aan					613

&lt;210&gt; 53

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2, 4-5, 7-9, 14-15, 601

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 53

tnannnnnt	taanncccat	tggagctcca	aagcagtgg	aacaacgcag	agtagcccc	60
cgatgtactt	gcttcttctt	ctttggagtg	gctgaatgct	tcctcctggc	taccatggca	120
tatgaccgct	atgtggccat	ctgcagtccc	ttgcactacc	cagtcacat	gaaccaaagg	180
actcgtgcca	aactggctgc	tgccctcctg	ttccaggct	ttcctgtagc	tactgtgcag	240
accacatggc	gtttcagttt	tccattctgt	ggcaccaaca	aggtgaacca	cttcttctgt	300
gacagccac	ctgtgctgag	gctggctctg	gcagacacag	cactgtttga	gatctacgcc	360
atcgctggaa	ccattctggg	ggcatgata	ccctgcttgc	tgatcttggt	ttcctatact	420
cgcattgctg	ctgccatcct	caagatccca	tcagctaaag	ggaagaataa	agccttttct	480
acatgttctt	cacacctcct	tgggtggctt	ctttctata	tatcattaag	cctcacctac	540
ttccggccta	aatcaaataa	ttcacctgag	ggcacgaagc	tgctatcatt	gcctacactg	600
ntatgactcc	a					611

&lt;210&gt; 54

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 4, 483, 509-510, 606

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 54

gtntttccat	ggactcccaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttcttgctgg	cttatcattt	atagatatca	tttattcttc	atccatttcc	cacagatcga	120
tttcagactt	gttctttggg	aataattcca	tatccttccc	atcttgcttg	gccagctct	180
ttacagagcg	cctttttggg	gggtcagagg	tctttcttct	gttggtgatg	gcctatgacc	240
ttgcattact	tggttatcat	gagacaatgg	gtgtgtgttt	tgctgctggg	agtgtcctgg	300
gttggaggat	ttctgcactc	agtatttcaa	cttagtggtt	tttatgggct	cccattctgt	360
gacctcaatg	tcattgatca	ttttttctgt	gatatgcacc	ctttattgaa	actgggtctgt	420
accgataccc	atgttattgg	cctcttagtg	gtggcaatgg	aggactaggt	tgactattg	480
ggnttctgct	cttactcatc	tcttatggnn	catctgcact	ctctaaagaa	ccttagtcag	540
aaagggaggt	gaaaagccct	ctcaacctgc	agttccacat	aactgggggg	tggtttcttc	600
tttgtn						606

&lt;210&gt; 55

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

<222> 4-5, 8-9, 12, 16, 19, 295, 298, 321, 472, 481, 573, 617

<223> N can be any nucleotide

<400> 55

ttannccnnt tnaatncnt tggagctcca aagcagtggg aacaacgcag agtacgcccc	60
caatgtactt gctttcttct ttttggggct gctgagtgtc gcctcctggc caccatggca	120
tatgaccgct acgtggccat ctgtgacccc ttgcactacc cagtcacatcat gggccacata	180
tcctgtgccc agctggcaag ctgcctcttg gttctcaggg ttttcagtgg ccactgtgca	240
aaccacatgg attttcagtt tccctttttg tggccccaac aggggtgaacc acttnttntg	300
tgacagccct cctgttattg nactgggtctg tgctgacacc tctgtgtttt gaactggagg	360
ctcttgacag ccactgccta attcattctc tttcctttct tgctgacccct gggatccctat	420
ttcgcattct ctctactatc ttttaaggatg ccgtcagctg aggggaaaca tnagcattct	480
ncacctgttc cgccacctc ttgggtggct ctctcttcta tagcactggc aatccttaac	540
gtattttccg accccaattc aagtgccttt ttntgagaag caaagaaact ggttgctact	600
tttttttcac aagggngac ttccaatggt	630

<210> 56

<211> 631

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4, 8-10, 493, 582

<223> N can be any nucleotide

<400> 56

gngntttnnn ccatggagct ccaaagcagt ggtaacaacg cagagtacgc ccccatgta	60
ctttcttctt ctttggagtg gctgaatgct tcctcctggc taccatggca tatgaccgct	120
atgtggccat ctgcagtcct ttgcactacc cagtcacatcat gaaccaaagg actcgtgcca	180
aactggctgc tacctcctgg ttcccaggct ttctgtagc tactgtgcag accacatggc	240
tcttcagttt tccattctgt ggacaccaaca aggtgaacca cttcttctgt gacagccac	300
ctgtgctgag gctgggtctg gcagacacag cactcttga gatctacgcc atcgtcggaa	360
ccattctggt ggtcatgac ccctgcttgc tgatcttctg ttctatact cacattgctg	420
ctgccatcct caaggtcca tcagctaaag ggaagaataa agccttttct acatgttct	480
cacacctcct tgntgtctct cttttctata tatcattaag cctcacctac ttccggccta	540
aatcaaataa ttcactgag ggcaagaagc tgctatcatt gncctacact gttatgactc	600
catgttgaac ccataattt attcattcag c	631

<210> 57

<211> 637

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 5-6, 76, 82, 92, 106, 122, 125, 142-143, 190, 214, 223, 244, 247, 259, 283, 290, 320, 402, 416, 455, 470, 529, 558, 561, 607, 618, 620, 630

<223> N can be any nucleotide

<400> 57

ttatnnccat tggagctcca aagcagtggg aacaaccgca gagtacgccc cccatgtatt	60
ttctttttct tggggnagct gnatgcttcc tntgggtac catggnatat gaccggctat	120
gnggncatct gcagtcctt gnntcccag tcattatgaa ccaaaggaca cgggccaac	180
tggtggtgn ttctgggtc ccaagcttct ctgnagctac tngcaagac cacaatggct	240
cttnagnttt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc	300
tggtgtgaaa gctgggtctg tgcaagacac agcactgttt gagatctacg ccacgtcgg	360
aaccattctg gtgtcaatg aaccctgct tgctgatctt gngttcctat actcgnattg	420
gtgtgctat ccctcaagaa ccatcaagc taaangggaa gcaataaagn ctttctcta	480
cgtgtcctt aacacctccc ttggtggcct ctcttttcta atataatcnt ctaagcctca	540
acctacttct tgggcctnaa ntcaaataaa ttcttctgga gaggcaagaa ggtggtattc	600

atttatncta cactggtn gn gactccatgn tggaact

637

&lt;210&gt; 58

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3, 6, 9, 16, 19, 507, 597, 611

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 58

gtnatnccnt ttaatnccnt tggagctcca agcagtggtgta acaacgcaga gtacgcccgt	60
tcctcagaca gtatatgaat gggttaaaaa tgggccagag cagatgcagg aagatcaaat	120
aggaggctac tgcaagtagag tcaaatctag ggctgatggt ttcttgggat gcatagtaat	180
aggtagatag agaaagtctt taggaggtag aatggacagg acttcacaat gcattaaatg	240
tagggagaaa aaaaatgatt cctgggttct tagcttgagc tagtagggat agtggtagaa	300
tttactgata tggaaaactg gaggaaaaag agtttggaag agaaagatgg caagttaaat	360
acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag	420
ccatgggcta ggaacataca gtgggattcc ctggcatgtc attggttact gaagtcagag	480
tgatagagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg	540
gctggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttgngaa	600
aaggagagaaa nggttgaaat t	621

&lt;210&gt; 59

&lt;211&gt; 631

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3, 8, 9, 11, 29

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 59

ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag	60
cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt	120
gtcctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aaggggtgcat	180
agtagaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttctccctt	240
ctgcagagtg catgtggttag acagcaagga gaatccggcc ataggaacat gcaatacaaa	300
tgaagggaaa cacaagaaaa atggtggtgc tcaaaaacac cgtgcactca tagaccagag	360
tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc	420
tggacttgca atatgggata cggagtgcac ataccgtgtg agcacaagag ttgatggagc	480
ctatcatcca agatcctgtt atcatcagtg cacacactct ttttctcata cggatgagat	540
agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg	600
cttctgcacc tgctaaagtc aggaagaaga t	631

&lt;210&gt; 60

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 6, 10-11, 15, 18

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 60

tgttantccn ntttctncc attggagctc ccaagcagtg gtaacaacgc agagtacgcc	60
ctccttgttt ctgagagtgt agatgaaggg gttataggag ataaagatca gggcaatatg	120

taggacaagg	acacagacac	tgacaacaaa	gttgattatc	tcattgacag	tggtgtctgt	180
gcaggccagc	ttcagcaggg	gtctcacatc	acagaagaag	tgaggagatga	caaagtcac	240
acaaaagggc	aggccaaaca	tagatgttac	ttggacaata	gccatgccca	ggccaatcct	300
cagtgaacca	gatccagtc	agacacaagc	cctcttacct	atgaataccg	taaggggttg	360
cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcca	420
aaagtcacat	agaagagctg	agtgacacag	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcaggtctc	agagatagac	540
agcaatgctt	aggaaaaagt	acatgggccc	tactttctgtc	gtcttgagcg	tactgatggt	600
accagcttt	tgttccctt					620

&lt;210&gt; 61

&lt;211&gt; 612

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3, 5-6, 9-10, 20, 25, 37-38

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 61

gtnannccnn	tgtagctccn	aagcngagct	aacaacnnag	agaacaacgc	agagtacgcc	60
cccgatgtac	ttgttcctac	tctttgctgg	atttgaaaac	ttcctcctgt	ccgtgatggc	120
ctatgaccgg	tttgtggcca	tctgtcacc	cctgcactac	atggtcatta	tgaaccctca	180
cctctgtgga	ctgctgggtc	tagcatcctg	gaccatgagt	gctctgtatt	ccttgctaca	240
aatcttaatg	gtagtacggc	tgctcttctg	cacagcctta	gaaatcccc	actttttctg	300
tgaacttaat	caggtcatcc	aacttgcttg	ttctgatagc	tttcttaatc	acatgggtgat	360
atattttaca	gttgcgctgc	tggttgagg	ttccctcact	gggatccttt	actcttactc	420
taagataatt	tcttccatac	atgcaatctc	atcagctcag	gggaagtaca	aggcattttc	480
acctgtgcat	ctcacctctc	agttgtctcc	ttattttatg	gtgcaatcct	aggggtgtac	540
cttagtctgc	tgccacccgc	aactcacact	caagtgcac	agcctcagtg	atgtacactg	600
gggcaccccc	at					612

&lt;210&gt; 62

&lt;211&gt; 628

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 2-8, 13, 19, 22, 32, 35-41, 49

&lt;223&gt; N can be any nucleotide

&lt;400&gt; 62

gnnnnnnnat	tnatgcctt	tnttgattcc	cntnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttcccac	acttctctat	taagaagcat	gtgagatact	180
tggtacaaac	ataacatcct	ggccccaccc	caaagccact	caatcaaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tggtggagaa	300
tctaggcaac	aatgaattaa	ggaaagctct	ctaccatttg	gtactggtag	cagggtttgag	360
gatcacaggg	aagagggtaa	gcatatcaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccatgtcca	tgtaagtagc	aaacaaccct	ctcatgtaca	480
ctctgaggaa	caagggggcg	tactttctgtc	gtcttgagcg	tactgatggt	accagcttt	540
tggtcccttta	gtgagggtta	attgcgcgct	tggcgtaatc	atggtcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

&lt;210&gt; 63

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

<220>  
 <221> variation  
 <222> 191, 214, 263, 271, 277, 303, 325, 333, 363, 418, 528, 570, 596, 614  
 <223> N can be any nucleotide

<400> 63  
 tgtagctcca aagcagtggg aacaacgcag agtacgccct cttgggttacg taagggaata 60  
 gatgatgggg ttcagcatgg ggggtgactac agtgtacatg acagtggcca cacggtccca 120  
 ctctgctcgc gtcgggacgt ggcctggaag tagactgcaa tgactgtcct atagaaagag 180  
 gtcaccaca nccaggtggg agccacaggt gggncacaag tcccggagcc tcccagaggc 240  
 ttgagggcag ctggagcacg ggnaagcttg ntatggnccc acaaggaggc gaggatgagc 300  
 agnaagggag tgaccaccac ttgcngcgcc ctnggtgaag atgagcagct tggatgtggg 360  
 ggntgtcaga gcacgagagc ctttaagaga ggcttgggtg gtcacagaag aagtgggngc 420  
 actttgtggg aaagcacaga aaggacaagc gagccatgag caggatatac aggagggagt 480  
 tgtccgtggg acaccagcca tgccattcca accagggctg cgcacatngc cggggacatt 540  
 ctggtgggat aaggggaagg gtgccggatn ggcacgtatc agtcataggc cttggncgcc 600  
 agaagacagc tttnaattta ccccagg 627

<210> 64  
 <211> 605  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 5-6, 9, 11, 14, 17, 21-22  
 <223> N can be any nucleotide

<400> 64  
 gttannccnt ntanctncaa nngaggtaac aacgcagagt acgccccca tgtatttgct 60  
 tcttgtccaa cctgtccttt gtagagatct gctacaccac cgttgtggg cccttgatgc 120  
 tttccaacat ttttggggcc cagaagccca ttccattggc tggatgtggg gcccaaatgt 180  
 tcctctttct cacacttggg ggtgctgact gtttctctt ggcgatcgtg gcctatgacc 240  
 gctatgtggc catctgccac cctttgcact acccctcatc atgacctgca gtctgtgcgt 300  
 gcagatgctg ggcggcgctg tgggcctggc cctcttctc tccctgcagc tcaccgcctt 360  
 aatcttcacc ttgcccttct gcggctaccg ccaggaaatt aaccacttcc tctgcgatgt 420  
 acctccgtcc tgccgctggc ctgcgctgca tccgtgttca ccaggctgcc tctatgtcgt 480  
 gagcatctc gtgctgaccg tccccttctt gctcatctgc gtctcctacg tgttcacac 540  
 ctgtgccatc ctgagcatcc gttctgctga gggccggcac caggcctttt caactgctct 600  
 tccgg 605

<210> 65  
 <211> 609  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 10, 14-15, 19, 22, 67, 603  
 <223> N can be any nucleotide

<400> 65  
 tgtagctccn aagnngagnt ancaacgcag agtacgcccg cggaatctat agatgaaagg 60  
 gtttgngag tcagaagaag gaagtacatg ggagtcataa cagtgtagga caatgatggc 120  
 agcttcttgc cctcaggtga attatttgat ttaggccgga agtaggtgag gcttaatgat 180  
 atatagaaaa gagagacaac aaggaggtgt gaggaacatg tagaaaaggc ttattcttc 240  
 ccttttagctg atgggatctt gaggatggca gcagcaatgt gagtatagga acacaagatc 300  
 agcaagcggg ggatcatgac caccagaatg gttccgacga tggcgtagat ctcaaagagt 360  
 gctgtgtctg cacagaccag cctcagcaca ggtgggctgt cacagaagaa gtgggttcacc 420  
 ttgttgggtg cacagaatgg aaaactgaag agccatgttg tctgcacagt agctacagga 480  
 aagcctggga accaggaggt agcagccagt ttggcacgag tcctttgggt catgatgact 540



gggtaagtgc aagggactgc agatggccac atagccggtc atatgccatt ggtagcccag 600  
gangaagct 609

<210> 66  
<211> 617  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 6, 20  
<223> N can be any nucleotide

<400> 66  
gttatncctt gttgctcccn agcagaggta acaacgcaga gtacgcccct atttctcaga 60  
tatangatga aggggttcag aaaaagaatg agcaaagaaa atctgggcca ggcgggcatc 120  
aaaagaaata gtcttggtgt caaccagaaa gtctgcaatc attttagggg tagcagaaga 180  
ggcaacacat acgtctataa atgacagggt ggcaagaagc aaatacattg ggggcgtact 240  
tctgtcgtct tgagcgtact gatggtaccc agcttttgtt cccttttagtg agggttaatt 300  
gcgcgcttgg cgtaatcatg gtcatactgt ttctctgtgt gaaattgtta tccgctcaca 360  
attccacaca acatacgagc cgggagcata aagtgtaaag cctgggggtgc ctaatgagt 420  
agctaactca cattaattgc gttgcgctca ctgcccgtt tcagtcggga aacctgtcgt 480  
gccagctgca ttaatgaatc ggccaacgcg ccggggagag gcggtttgcg tattgggcgc 540  
tcttcgctt ctcgctcact gactcgcttg cgctcggtcg ttcggcttgc ggcgagcgg 600  
atcaagctca ctcaaat 617

<210> 67  
<211> 621  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 10, 17, 28, 277, 286, 370, 373, 422, 513, 527, 536, 545, 548, 550, 558,  
563, 566, 572, 574, 579, 583, 603-604, 609, 621  
<223> N can be any nucleotide

<400> 67  
gggttttacn ctgtgcnccc ccagcagngg taacaacgca gtagtgcgcc ttgttgcgaa 60  
gaaataaatg aatgggttta aaatagacgt gaagatggtg tagaatacag caaggacttt 120  
gtcaactgag taactgctga agggccacac atagatgaaa atacacgatc caaagaataa 180  
agtgaccaca gtgatgtgag cagtcaatgt ggagtgggcc ttcaccatgc ttacagagga 240  
gcgattccta actgtaataa gtattacagt gtagganaca accaanagga gaaaggaact 300  
cagagaaaga aagccaccat ctgcaactat tagtaggctg acaacataag tgtctatgca 360  
ggctaacttn gtngctagag gaaggtcaca gaaaaaaact atctacctta ttaggaccac 420  
anaatggcag attaacctgt aatgccaaact ggctggtggt atggatgaag cccacaaacc 480  
aggaaatgag gacgagcaca acacatacac agnagctcat gattganatg tagtgnggag 540  
gtttncntn gctcatance gtnttngcca tngnaactng gancaccatt ttacttgag 600  
tgnnggagng aacatgaaat n 621

<210> 68  
<211> 611  
<212> DNA  
<213> Homo Sapien

<220>  
<221> variation  
<222> 5-6, 9-10, 17, 19, 298, 464, 519, 549  
<223> N can be any nucleotide

<400> 68  
 gttannccnn tttaatncna tggagctcca aagcagtggt aacaacgcag agtacgcccc 60  
 cgatgtactt gttcctactc tttgctggat ttgaaaactt cctcctgtcc gtgatggcct 120  
 atgaccgggtt tgtggccatc tgtcaccccc tgcactacat ggtcattatg aacctcacc 180  
 tctgtggact gctggttcta gcacccctga ccatgagtgc tctgtattcc ttgtacaaa 240  
 tcttaatggt agtacggctg tcttctgcac agccttagaa atccccact ttttctgnga 300  
 acttaatcag gtcacccaac ttgcttggtc tgatagcttt cttaatcaca tgggtgatata 360  
 ttttacagtt gcgctgctgg gtggagggtc cctcactggg atcctttact cttactctaa 420  
 gataatttct tccatacatg caatctcatc agcttagggg aagnacaagg cattttccac 480  
 ctgtgcatct cacccttcag ttgctcctta ttttatggng caatctaggg gtgaccttag 540  
 ttttctgnc acccgcaact cacacttaag tgcaacaacc tcagtgatgt acactgggggt 600  
 caccatgc c 611

<210> 69  
 <211> 625  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2, 4-6, 11, 15-16, 40, 42, 45, 47, 52, 61, 64-66, 74-75, 77, 80, 586,  
 618  
 <223> N can be any nucleotide

<400> 69  
 gngnnncgag nttannccctt ggactcccag tagagctacn angantncgc cnagcgcgca 60  
 nttnnnccag ggtntntntn gtatcaccaa tgaatagaaa acagacacca ccttgtccct 120  
 gcctagcaag tagctggagc tgggtcgcaa gtacacgaaa agggctgtcc caaacagcag 180  
 agtcaccacc atcagatgag aggcacacgt gttgcaggct ttccatcggc cctctgctga 240  
 agggatcttc aggaccgcag acactatgta accataggag ataaggagtt ggaggaacga 300  
 tgttctctcg acggtgacca ccacgaggaa attcaccact tgactgagga aggtgtcaga 360  
 gcaagacaga gccaggactg gtgggagggt gcagaagaag tgggtgatga tgttgggtcc 420  
 gcaaaagtga agcctaaata tggagctggc ctggatcagg gagctcagga agccaccaac 480  
 atatgcccc accaccatgc gtgtacagag gccctgggtc atgatagtgg ggtanagaag 540  
 ggggctggag atggcttgca tatcggctcg atgccatagc agtcangagg aggcactcaa 600  
 gacagacca tgccgacnaa gaaat 625

<210> 70  
 <211> 626  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-5, 17-18, 24, 34, 42, 584  
 <223> N can be any nucleotide

<400> 70  
 gnnnnnttta cccctgnngc acanagcagt ggtnacaaag cncgagtacg cccctatgt 60  
 attttttctt attctggaca cgctactcct gaccgtgatg gcctatgacc ggtttgtggc 120  
 tgtctgccac cctctgcact atatgatcat catgaacccc cactctgtg gcctcctggg 180  
 ttttgcacc tggctcattg gtgtcatgac atccctctc catatttctc tgatgatgca 240  
 tctaattctt tgtaaagatt ttgaaattcc acattttttc tgcgaactga cgtacatcct 300  
 ccagctggcc tgctctgata ccttcttgaa cagcacgttg atatacttta tgacgggtgt 360  
 gctggggcgtt tttccctctc ttgggatcat tttctcttat tcacgaattg cttcatccat 420  
 aaggaagatg tcctcatctg ggggaaaaca aatagcactt tccacctgtg ggtctcacct 480  
 ctccgtcggt tctttatatt atgggacagg cattggggtc cacttcactt ctgcggtgac 540  
 tcacccttcc cagaaaatct ccgtggcctc ggtgatgtca ctgnggtcac ccccatggtt 600  
 accctttcat ttacaccctt agcaag 626

<210> 71

<211> 633  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-10, 4, 7, 10-11, 33, 35, 39, 50, 57, 60, 61-62, 65, 84-85, 441, 615, 617, 632  
 <223> N can be any nucleotide

<400> 71  
 gnnnnnnnnn gtnnatnccn nttttaatgc cantngagnt aacaacgcan gagtacnccn 60  
 nngngtacgc ccagggttca accnntgaat agaaaacaga caccaccttg tccctgccta 120  
 gcaagtagct ggagctgggt cgcaagtaca cgaaaagggc tgtcccaaac agcagagtca 180  
 ccaccatcag atgcgaggca cacgtgttgc aggctttcca tcgccctctg ctgaagggat 240  
 cttcaggacc gcagacacta tgtaaccata ggagataagg agttggagga acgatgttcc 300  
 tccgacggtg accaccacga ggaaattcac cacttgactg aggaagggtg cagagcaaga 360  
 cagagccagg actggtgggg aggttgcaag aagaagtggg tgatgattgt tgggtcccgc 420  
 aaaagtgaag gcctaaatat ngagctggcc tggatcaggg gagctcagga agccacaaca 480  
 tatgccccaa ccaccatgcg tgtacagagg ccctgggtca tgatagtggg ggtngagaag 540  
 ggggcctgga gatggctgca tatcggtcgt tgccatagca agtcaggagg aggcacttca 600  
 gacagaccca tgccncnaag aaaaaaact gnc 633

<210> 72  
 <211> 614  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 2-11, 14-17, 19-20, 22, 28, 42-43, 45, 51, 76, 82-83, 85, 101, 106, 110, 112-114, 117, 119, 135, 139, 434, 507, 520, 614  
 <223> N can be any nucleotide

<400> 72  
 gnnnnnnnnn nttnnnnnncn tnactccngc agtggttaaca annantacgc ncagcgcgca 60  
 gttaaccctc actaanggta anntnagctg gaacacatca ntacgntcan gnnngcncna 120  
 tgaccggttt gtggnatnt gtcacccctt gcactacatg ggtcattatg aaccctcacc 180  
 tctgtggact gctggttcta gcacccctga ccatgagtg cctgtattcc ttgctacaaa 240  
 tcttaattgg agtacggctg tccttctgca cagccttaga aatccccccac tttttctgtg 300  
 aacttaatca ggcattcaac ttgcttgttc tgatagcttt cttaatcaca tgggtgatata 360  
 ttttacaggt tgcgctgctg ggtggaggtc ccctgactgg gatcctttac tcttactcta 420  
 aagataattt cttncataca tgcaatctca tcagctcaag gggaagtcaa ggcatttttc 480  
 acctgtgcat ctacccctca gttgctnctt attttatggg gcaatccctag ggggtgacct 540  
 agttctggtg gcacccgcaa ctacactcaa tgcacaagct cagtgatgta cactgtggca 600  
 cccatgctga accn 614

<210> 73  
 <211> 630  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> variation  
 <222> 3-6, 8-10, 17, 124, 144, 146, 173, 184, 193, 212, 220, 266, 274, 276, 288, 306, 419, 423, 448, 474, 485, 500, 552, 555, 576, 588, 591, 606  
 <223> N can be any nucleotide

<400> 73  
 gtnnnnnnnn ttgattneca ttggagctcc aaagcagtg taacaacgca gagtacgccc 60  
 cctatgtatt ttttctatt ctggacacgc tactcctgac cgggatggcc tatgaccggg 120

ttgnggctgg	ctgccaccct	ctgnantata	tgatcatcat	gaacccccac	ctntgtggcc	180
tcnnggtttt	tgncacctgg	ctcattgggtg	tnatgacatn	cctcctccat	atttctctga	240
tgatgcacct	aatcttctgt	aaagantttg	aaantncaca	ttttttntg	cgaactgacg	300
tacatnctcc	agctggcctg	ctctgatacc	ttcctgaaca	gcacgttgat	atactttatg	360
acgggtgtgc	tgggcgtttt	tccctccttg	ggatcatttt	cttcttattc	acgaattgnt	420
ttnatccata	aggaagaatg	tcctcatntg	ggggaaaaca	aataagcact	tttncacctg	480
tgggnctcaa	cctcttccgn	cgtttcttta	ttttatgggg	acaggcattt	gggggtccac	540
tttacttttt	gnngngactc	accccttcca	gaaaanttte	cgtgggcntc	ngggatgtac	600
actgngggca	cccccatgtt	gaaccctttt				630

&lt;210&gt; 74

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Unknown: Synthetic construct

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3,12

&lt;223&gt; N can be any nucleotide

&lt;221&gt; variation

&lt;222&gt; 9

&lt;223&gt; y = t/u or c

&lt;400&gt; 74

ccnatgtayt tntccta

18

&lt;210&gt; 75

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Unknown: Synthetic construct

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3, 12

&lt;223&gt; N can be any nucleotide

&lt;221&gt; variation

&lt;222&gt; 9

&lt;223&gt; y = t/u or c

&lt;400&gt; 75

ccnatgtayt tntcctc

18

&lt;210&gt; 76

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Unknown: Synthetic construct

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 3, 12

&lt;223&gt; N can be any nucleotide

&lt;221&gt; variation

&lt;222&gt; 9

&lt;223&gt; y = t/u or c

&lt;400&gt; 76

ccnatgtayt tntcctg

18

<210> 77  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 77  
ccnatgtayt tntctcctt

18

<210> 78  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 78  
ccnatgtayt tntctctta

18

<210> 79  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 79  
ccnatgtayt tntctcttc

18

<210> 80  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 80

ccnatgtayt tncctcttg

18

<210> 81

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 81

ccnatgtayt tncctcttt

18

<210> 82

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 82

ccnatgtayt tnccttcta

18

<210> 83

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 83

ccnatgtayt tncctcttc

18

<210> 84  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 84  
ccnatgtayt tncttctg

18

<210> 85  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 85  
ccnatgtayt tncttctt

18

<210> 86  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 86  
ccnatgtayt tnctttta

18

<210> 87  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 87  
ccnatgtayt tnccttttc

18

<210> 88  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 88  
ccnatgtayt tnccttttg

18

<210> 89  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 89  
ccnatgtayt tnccttttt

18

<210> 90  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 90  
ccnatgtayt tnttccta

18

<210> 91  
<211> 18  
<212> DNA



<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 91

ccnatgtayt tnttcttc

18

<210> 92

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 92

ccnatgtayt tnttcttg

18

<210> 93

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 93

ccnatgtayt tnttcctt

18

<210> 94

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 94  
ccnatgtayt tnttctta

18

<210> 95  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 95  
ccnatgtayt tnttcttc

18

<210> 96  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 96  
ccnatgtayt tnttcttg

18

<210> 97  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 97  
ccnatgtayt tnttcttt

18

<210> 98  
<211> 18

<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 98  
ccnatgtayt tntttcta

18

<210> 99  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 99  
ccnatgtayt tntttctc

18

<210> 100  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<400> 100  
ccnatgtayt tntttctg

18

<210> 101  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<210> 105  
<211> 18  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 12  
<223> N can be any nucleotide

<221> variation  
<222> 9  
<223> y = t/u or c

<210> 106  
<211> 31  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 4, 7, 10, 13, 20, 23, 26  
<223> N can be any nucleotide

<220>  
<221> variation  
<222> 1, 2, 8, 12, 15  
<223> y = t or c

<220>  
<221> variation  
<222> 11, 29  
<223> r = a or g

<400> 106  
yytngtnytn ryncygatan atnatnggrt t

31

<210> 107  
<211> 28  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 6, 9, 12, 17, 23  
<223> N can be any nucleotide

<220>  
<221> variation  
<222> 1  
<223> y = t or c

<220>  
<221> variation  
<222> 3, 14, 20, 26  
<223> r = a or g

<220>  
<221> variation  
<222> 8  
<223> k = t or g

<220>  
<221> variation  
<222> 13  
<223> w = t or a

<400> 107  
ytrttncckna gnwrtanatr aanggrtt

28

<210> 108  
<211> 32  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 9, 12, 15, 21, 24, 27  
<223> N can be any nucleotide

<220>  
<221> variation  
<222> 3, 23  
<223> y = t or c

<220>  
<221> variation  
<222> 6, 18, 30  
<223> r = a or g

<220>  
<221> variation  
<222> 11  
<223> k = t or g

<220>  
<221> variation  
<222> 17  
<223> w = t or a

<220>  
<221> variation  
<222> 26  
<223> s = g or c

<400> 108  
tcytrtttnc knagngwrta naynasnggr tt

32

<210> 109  
<211> 32  
<212> DNA  
<213> Unknown: Synthetic construct

<220>  
<221> variation  
<222> 3, 9, 12, 15, 21, 24, 27  
<223> N can be any nucleotide

<220>  
<221> variation  
<222> 6, 14, 18, 30  
<223> r = a or g

<220>  
 <221> variation  
 <222> 11  
 <223> k = t or g

<220>  
 <221> variation  
 <222> 5, 16  
 <223> s = g or c

<400> 109  
 tcntsrttnc knarnsarta natnatnggr tt

32

<210> 110  
 <211> 27  
 <212> DNA  
 <213> Unknown: Synthetic construct

<220>  
 <221> variation  
 <222> 4, 7, 10, 16, 22  
 <223> N can be any nucleotide

<220>  
 <221> variation  
 <222> 1, 9, 13, 19, 25  
 <223> r = a or g

<220>  
 <221> variation  
 <222> 6  
 <223> k = t or g

<220>  
 <221> variation  
 <222> 12  
 <223> w = t or a

<220>  
 <221> variation  
 <222> 11  
 <223> s = g or c

<400> 110  
 rttncnknarn swrtanatra anggrrtt

27

<210> 111  
 <211> 886  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 7, 11, 16, 18, 21, 209, 231, 258, 259, 266, 267, 269, 282, 287, 289,  
 301, 308, 314, 315, 316, 319, 321, 325, 329, 337, 338, 339, 346, 368, 383,  
 385, 393, 398, 412, 413, 416, 417, 420, 439, 440, 442, 447, 453, 459, 474,  
 479, 484, 488, 499, 508, 513, 521, 526, 536, 541, 549, 559, 574, 579, 587,  
 590, 596, 597, 601, 602, 610, 618, 622, 633, 635, 648, 649, 650, 652, 654,

661, 666, 688, 690, 692, 698, 705, 713, 720, 724, 726, 731, 732, 736, 771,  
788, 790, 795, 801, 802, 807, 811, 817, 829, 836, 840, 846, 849, 850, 855,  
859, 870, 872, 874, 877, 878, 886

<223> n = any nucleotide

<400> 111

```

gggtccntcg ngatatntt naccctctga tgctgctcga gcgcccgga gggatgatga 60
tatctgcaga attcgccctt ctgttacgca ggaatatata aaggggttac tgaggataa 120
ataaatgggt tactgaggaa taaataaatg gggtactgag gaacaaatac atagggttga 180
aagaactgta aaatagaaaa aggacctntt gctgctctc aggatggcgg nacttagggg 240
ccatgtacat gacgatgnng ctgccnntna agagtccac tntcancng cctcagccc 300
ncttttntct cacnnncnt nttntctnc cctctnnnc tcttntctc ctattcccc 360
ccctccnct cctccctttt gentnaccat tgnccctnat cctttaatt cnntcnntcn 420
tctccctct attcctcnn tntcgnctt cantctctnc ctcttctcc ccnctttct 480
ctctctnct cttctctng tcatcctngt tcttctctt ncctanttc ctctancctt 540
ntcttatnct tctctatnct cctctcatct cacntctct cctctctnct tacttntct 600
nctcttccn ctccgtctc cctctctct tctnaccgc acccctcnn cntnctctct 660
ntctntct cactctctc tctccctnct tctcactnt ctcnctctc acntcctatn 720
ctcncttct ncttnactt tgtcacgct cctctctct ctctacgac ntttatctc 780
ttatctcnct catcncctc nttctnct nctattnact ctttctctc atactntatn 840
ctctntcnn cttnatnct cctctctct tnanccnct actgcn 886

```

<210> 112

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 13, 31, 36-37, 40, 45-48, 50, 53-54, 61, 63, 67-68, 70, 473, 512,  
523, 526, 535, 542-543, 545, 549, 558, 566, 571, 582, 589, 593-594, 603, 612-  
614, 616, 621, 623-624

<223> n = any nucleotide

<400> 112

```

gctgctcgag cgnccagcg tcggcagtg nagggnnatn tgccnnntn gcnnttagat 60
nanaggnntn agtatggggg tgaccacagt ggtacataac tgaggctgtt gcacttgagt 120
gtgagttgag ggtggcagca gaactaaggt acaccctag gattgcacca taaaataagg 180
agacaactga gaggtgagat gcacaggtgg aaaatgcctt gtacttcccc tgagctgatg 240
agattgcatg tatggaagaa attatcttag agtaagagta aaggatccca gtcaggggac 300
ctccaccag cagcgcaact gtaaaatata tcaccatgtg attaagaaag ctatcagaac 360
aagcaagttg gatgacctga ttaagttcac agaaaaagtg ggggatttct aaggctgtgc 420
agaaggacag cgtactacc attagattt gtagcaagga atacagagca ctnatggtcc 480
aggatgccag aaccagcagt cacagagggt gngggtttca tantgncct gtagnctcag 540
cnrcngacna gatggccnca aaccgntct nggcctcac gncctggna ggnngtttct 600
tantccacca cnnntnttct nannc 625

```

<210> 113

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 6-7, 30, 113, 128, 137, 142, 150, 157, 174, 297, 310, 313, 335, 354,  
356, 377, 382, 385, 389, 393, 421, 429, 431, 433, 435, 438, 440, 442-443,  
446, 455, 457, 465, 467, 477, 488, 491, 501-502, 504, 508-509, 515, 522, 525-  
526, 529-530, 542, 557-559, 561, 564, 565, 568, 577, 579-581, 584, 587-589,  
591, 596-603, 607-610, 612-613

<223> n = any nucleotide

<400> 113

```
catgcnnag caggctcgag cgccggcagn gtgagggata tctgcagaat tcgcccttcc 60
tatgtacttt ttcctgagcg tatacacaat cccatcatgt actggggaga agncagacca 120
tatcattnac aagctgnctt tngcagatgn actttgnttt ctcattaggc tgcncagagt 180
acttcctect ggcagccatg gcttatgacc gctgtcttgc catctgctat cctttacact 240
acggagccat catgagtagc ctgctctcag cgcagctggc cctgggctcc tgggtgngtg 300
gtttcgcgcn cantgcagcg cccacagccc tcagnagcgg tcttgcctct ctgngncccc 360
cgtgccatta accactnctt tngcngcant gncacctgca ttgtcttctc ctgcccacca 420
nacagcagna nancntgngn cnnttngatc gctgntnecg tctcngntct cactccnttc 480
caccttttnc ntcgattcc nntntccnnc tcgcnctect gncnntcnn tctcctcttc 540
tnaacgcgtc ctccgannng nctnnatgnt cgtctcntnn ntgngcnng ncagcnnnnn 600
nnccannnn tnngtgcgcc gctcc 625
```

<210> 114

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2, 12-13, 20, 23, 188, 375, 399, 402, 416, 443, 460, 472, 474-475, 480, 484, 487-488, 502, 505, 522-523, 529, 532, 537-538, 546, 553, 555, 557, 561, 564-565, 573, 575, 577, 581, 583, 586, 591, 594, 617, 634, 636, 643

<223> n = any nucleotide

<400> 114

```
gnttaagccc tnnccctctn gangcatgct cgagcggccg ccagtgtgat ggatatctgc 60
agaattcgcc cttgttccgc aaacaataga tgaaaggatt aagtgaagga gtgcccaccg 120
catagaagag accaaagaac ttgcccctcc cttgggcata cggatttttg ggctggaggt 180
agacagcnat gactgagctg tagaagaggg tgaccacagt gagatgggag gacaggtcc 240
caaaggcctt tctccatgct gtggcagagt taatcctcag cactgcctgg gcagtggctc 300
cataagaggc aaggatgagg ctgagaggca caaccacgaa gatgacactg gacacagcca 360
actggatttc attgnaggag gcatctccac aggagagtnc gnatcagaga tgggancctc 420
acataaaaaa gtcattctatc tgntgggtggg gacagaatgn ccatgtggag gntnnatgtn 480
cgtntcnac ctcttatttt tnttncctt ttctttcgct cnntccctnt tntccnct 540
cgccanttc atnncntct ntcnntttt ttntntnacc ntntntcat ntentctct 600
tattctctt ctcttgntc tccctctct ctentnttc canctctcc g 651
```

<210> 115

<211> 850

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 3, 15, 279, 288, 292, 295, 296, 299, 307, 309, 317-319, 322, 326-327, 329, 335, 340, 343, 345-346, 354, 362, 367-368, 377, 380-382, 386, 391, 394, 396, 399-400, 410, 412, 415-416, 418, 433, 436, 442, 444, 451, 455, 466, 468-469, 471, 474, 482, 488, 490, 500, 505, 514, 516, 522, 530, 537, 548, 550, 552, 559, 562-565, 569, 570, 571-573, 576, 581, 592, 597, 603, 605-606, 608, 617, 619, 624, 627, 630, 635-636, 643, 647, 653, 661-663, 667, 673-675, 678, 690, 697-698, 709-711, 720, 724, 727, 731, 736, 746, 760, 768, 771, 783-784, 789, 791, 794, 796, 797, 800-801, 808, 810, 816, 818, 821-822, 832, 836

<223> n = any nucleotide

<400> 115

```
ggntctcggt acaanacttg gccctctaga tgcattgctg agcggccgcc agtgtgatgg 60
```



```

atatctgcag aattcgccct tccaatgtat ttattcctgt tatttggaga cctggagagc 120
ttcctccttg tggccatggc ctatgaccgc tatgtggcca tctgcttccc cctgcactac 180
accgccatca tgagcccat gctctgtctc gccctgggtg cgctgacctg ggtgctgacc 240
accttccatg ccatgttaca cactttactc atggccagnt tgtgcttntg tncennacna 300
ttgttgntnc cccactnnnc tntgtntna gtctnctctn cctnnactg ctctcctct 360
tntccnnga gtccctcngn nncgtngtcg nttncngcnn tcaattgcan tncnncntc 420
atcctttctt tantntcca tntnttcaact nattnctctt tatccnncnt ntncnccctc 480
anctcctnnc tagcttactn tttctgtctc tccngngctc ancttttctn ccataatntc 540
ttctctcnnc tntctctcnc tnnncccn nntctctgt ntctctgtc cntcttnacg 600
tctnnncnt tatttantnt ctncnncntn tctcngctc cancgngta ccngccctat 660
nnctctctc gannntgntc atggcatctn cacattnngc cctactatnn ncgatctatn 720
ttcncgncat ntattncaca tccacntgca ctctactcnc ctctctance nccgtacatc 780
gennctacng ntgnncntcn nccgctctn cggcncnat nntccactt tntctnggtc 840
ccccctctcg                                     850

```

&lt;210&gt; 116

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 451, 479, 501, 533, 542, 550, 553, 561, 572, 582, 585, 600, 604-605

&lt;223&gt; n = any nucleotide

&lt;400&gt; 116

```

gatgcatgct cgagcgcccg cagtgtgatg gatatctgca gaattcgccc ttccaatgta 60
ctttttcctg aagaacctct ctgttttgga tctgtgctac atctcagtca ctgtgcctaa 120
atccatccgt aactccctga ctgcgagaag ctccatctct tatcttggct gtgtggctca 180
agcctatattt ttctctgcct ttgcatctgc tgagctggcc ttccttactg tcatgtctta 240
tgaccgctat gttgccattt gccacccct ccaatacaga gccgtgatga catcaggagg 300
gtgctatcag atggcagtc caccctggct aagctgcttt tctacgcag ccgtccacac 360
tggcaacatg tttcgggagc acgtttgcag atccaatgtg atccaccagt tcttccgtga 420
catccctcag gtgttggccc tggtttctct ngagggtttc tttgtagagc tttgaccnng 480
ccctgagcct caatgcttgg ntctgggatg ctttattccc atgatgatct ccnattttcc 540
anatctctn aanggggctc nagaatccct tnaggaccag antcnagcta aaagcctttn 600
cccnctgct tccccccacg                                     620

```

&lt;210&gt; 117

&lt;211&gt; 628

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 5, 9, 403, 505, 552

&lt;223&gt; n = any nucleotide

&lt;400&gt; 117

```

tggcnctcng atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta tttgttctct ttatttggag acctggagag ctctctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc ccctgacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt ggcgtgtcct ggggtgtgac caccttcac gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgtc tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgcac cccattccta ctnatccttg ggtcctatgc 420
aagaattgtc tctccatcc tcaaggtccc ttcttctaag ggtatctgca aggccttctc 480
tactgtggtc tcccaccctg tctgnggtgt cactggttct atggaaccgt tattggtctc 540
tacttatgct cntcagctaa tagttctact ctaaaggaca ctgcatggct atgatgtaca 600

```

ctgtggtgac ccccatgctg aaccctt

628

&lt;210&gt; 118

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 17, 25, 184, 187-188, 199, 202, 206, 212, 214-215, 223, 227-228, 232, 248, 250, 252-253, 255-256, 261-264, 266, 268, 271, 273, 276, 278, 284, 289, 292, 295-296, 298, 300-302, 306, 310, 315-316, 320-322, 325, 329, 333, 337, 340-341, 346, 349, 355, 369, 371, 373-374, 379-380, 383-384, 387-388, 391, 402, 407, 409, 417, 419-420, 436-437, 441-442, 445, 447-448, 450, 456-458, 461, 469, 472, 477-479, 486-487, 490, 493, 503, 510, 512, 517, 530, 540, 542, 544, 552-553, 565, 572, 587, 595, 597-598, 600, 611, 614, 617-618, 622-623, 625, 634-636, 639, 644-645, 646, 652-653, 663, 665, 668, 673-674, 679, 681, 683, 695-696, 699, 706, 710, 712, 716, 725-726, 731-732, 741, 745, 748-750, 763, 771, 774, 776, 772, 774-775, 777-778, 780, 782

&lt;223&gt; n = any nucleotide

&lt;400&gt; 118

gatgatgctc gagcggnegc agtgngatgg atatctgcag aattcgccct tcccatgtat 60  
 ttgttctga gcaacctctc cttcctggag atttggtata ccacagcagc agtgcccaaa 120  
 gcactggcca tcctactggg gagaagacag accatatcat ttacaagctg ccttttgag 180  
 atgnacnntg ttttctcant angccntaca gngnncatgt ttncgcnnngc cntgacttat 240  
 gagcgcntn cnnccntatc nnnntntnct ntacncnac ttentcatna tntgnncntn 300  
 nnttcnecntn tggcnnetcn nntcncggnc ttncctntgn negtntcnc ccttnggcct 360  
 gcatctctnc ntntccntn ccnncgnnet ntcttctctt cntacctntt ttctgtntnn 420  
 tccctccctt ctctgnntgc nntcnncnn catctnnntg ntctgatcnc tntctnnnt 480  
 ccactnngtn ctnttctctc gnttctctn cncgcncct gcatcactgn gcattatatn 540  
 cncngtctca tnnctatctt ccgtncctgt cnccttctct ctatgcncga cgtentntn 600  
 tactatcgtc ntentennat tnnngcctgt tccnnngcnc ccgncntcc anntactctc 660  
 cangntctc ctntctctnt ncctgtctta attcncntnt accgntctn gnetctctt 720  
 cgtenntccc ncttctctcc nctcncgnnn ccnttcagct ntcnanttct antnngnncn 780  
 cnc 783

&lt;210&gt; 119

&lt;211&gt; 674

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 1, 2, 114, 207, 212, 253, 261, 294, 316-317, 325, 327-329, 333-334, 340, 345, 352, 355, 364, 382, 384, 393-394, 397, 414, 418, 424, 426, 431, 440, 447, 449, 452, 455, 462, 467, 474, 482, 486, 492-493, 496, 500, 503, 509, 516, 519-520, 525, 532, 534, 539, 544, 550, 552, 555, 559, 564, 566, 573, 576, 586, 591, 594, 598, 605, 608, 610-611, 618, 626, 629, 635, 638, 644, 660-661, 666, 669

&lt;223&gt; n = any nucleotide

&lt;400&gt; 119

nntagatgca tgctcgagcg gcccgccagt gtgatggata tctgcagaat tcgcccttcc 60  
 tatgtatttc ttcttgcca acctgtcctt cttggagacc tggatcatct ctgngactgt 120  
 gcccaagtta ctgtttagtt tttggtctgc gaacaacagc atctctttca cactctgtat 180  
 gatacaactg tacttcttca ttgctcncat gngcacagaa tgcgtgcttc tggccgccat 240  
 ggccatgac cgntatgtgg ncatctggcg cccactccac taccacaacca taantgagcc 300  
 atgggctcct gctccnncct cgctntnnna tanngaaccn acagngtagc gncanctccc 360

```

tgtncgagaa tctacttcat cntnctgcct tannttntgt gggcccaatg tgcntaanca 420
cttngntctg nggacatttn ctccagnant tnaantctct tntctgnaca aganactgtt 480
cnttancttg annatntttn ggnacattnt tcttanggnn ttggnacgag cntntctanc 540
accngcactn cncantaant gctncngttc tantcngtgc cattcntgtg nctncccntt 600
tcatngcntn ncctccncg aaagcnaant aagtngngnt cttnactttc gcccccaacn 660
ncatcncant ggcc 674

```

&lt;210&gt; 120

&lt;211&gt; 643

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 359, 373, 439, 463, 506, 537, 564, 584, 594, 604, 610, 620, 633-634, 636

&lt;223&gt; n = any nucleotide

&lt;400&gt; 120

```

ggccctctag atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttcctatgta ttttttcctg ttatttggag acctggagag cctcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctggtg gcgctgtcct ggggtgctgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtng 360
atatttatca tgnagggcct cattcttgct atccattcc tactcatcct tgggtcctat 420
gcgagaattg tctcctcctt cctcaaaggc cccttcttct aangggatc tgcaaggcct 480
tctctacttg gtggctcccc ccctgncctgt ggtgtcactg ttcctattgg aaaccgntat 540
tgggactcta cttatgctca tcangctaag agttttactc ttangggaca ctgncaatgg 600
cctntgaagn tacccttggg gtggaccccc atnntngaac ccc 643

```

&lt;210&gt; 121

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 429, 447, 453, 484, 510, 519, 542, 544, 546, 549, 552, 561, 581, 587, 600-601, 613, 618, 620-621, 623, 632, 643, 655-656

&lt;223&gt; n = any nucleotide

&lt;400&gt; 121

```

ggccctctag atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta ctttttcctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctggtg gcgctgtcct ggggtgctgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggtc attcttgcat ccattccta ctcacccctt ggtcctatgc 420
aagaattgnc tccttccatc tcaaggncct ttnttctaaa gggatatctgc aaggccttct 480
ctanttggtg ctcccaccct gtcttggtgn tggcactgnt tctaattggga accggttaatt 540
gnancnctna cnttatgctc natcaactta aatagtttct nactttnaaa gggaccactn 600
ntcattggct tanggatngn ncnttggttt cntggaaatc ccnatcatc ttacnng 657

```

&lt;210&gt; 122

&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 9, 536, 543, 587, 609, 616, 619, 621-622

&lt;223&gt; n = any nucleotide

&lt;400&gt; 122

```

atgaccctna gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc 60
cttccaatgt atttgttcct gtccaacctg tcctttttgg atattggctt tatctctaca 120
ataattccca atatgctaga tcatatttagc tcaggaatta agctgatttc ttatggggag 180
tgtctgacac aactctatct ctctggccta tttgcagatc tggacaacaa ctttctcctg 240
gctgtgttgg cccttgaccg ctatgtggcc atcagccatc ctctccatta tggccctaacc 300
atgaactccc aacgctgtgt cctgttggtg gctgtgtcat gggatgatcac tattttacat 360
gccctagtgc ataccctcct agtgaccagg ctttccttct gtgggtccaaa tattatccct 420
cacttcttct gtgatctggc cccactcctg aagctggcct gctccagtac ttgtgtcaat 480
gatctgggtg tcatccttgt ggcaggaaca ctgctgaatg cgccctttgc tgcattctta 540
tgnccctact ttacattgca ttggccatcc tgagaattga ttccccnagg ggtatgcaaa 600
gggcccttnt ccagctcnc nn

```

&lt;210&gt; 123

&lt;211&gt; 610

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 4, 445, 568-569, 580, 587, 600, 607, 610

&lt;223&gt; n = any nucleotide

&lt;400&gt; 123

```

gcgncgcagt gtgatggata tctgcagaat tcgcccctcc aatgtatttg tttctgttat 60
ttggagacct ggagagcttc ctcttgttgg ccatggccta tgaccgctat tgggccatct 120
gttccccctt gcactacacc gccatcatga gccccatgct ctgtctcgcc ctgggtggcgc 180
tgtcctgggt gctgaccacc ttccatgcca tgttacacac tttactcatg gccagggtgt 240
gtttttgtgc agacaatgtg atccccact tttctgtga tatgtctgct ctgctgaagc 300
tggccttctc tgacactcga gttaatgaat gggatgatt tatcatggga gggctcattc 360
ttgtcatccc attcctactc atccttgggt cctatgcaag aattgtctcc tccatcctca 420
aggtcccttc ttctaagggt atctngcaag gccttctcta cttgcggctc cacctgcctg 480
tgggtgtcact gttctatgga accgttattg gtctctactt atgctcatca gccaataagt 540
tttactctaa aaggacactt gtcattggnnt atgatgtacn ctgtgngnac ccccatgctn 600
aaccctttn

```

&lt;210&gt; 124

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 469, 477, 482, 484, 493, 500, 509, 524, 527, 530, 536, 542, 549,  
553-555, 561, 571, 580, 581, 583, 591, 597, 602, 609, 617-619, 624-625, 627,  
636, 638, 642, 645-646

&lt;223&gt; n = any nucleotide

&lt;400&gt; 124

```

ccttgggccc tctagatgca tgctcgagcg gccgccagtg tgatggatat ctgcagaatt 60

```

```

cgcccttctt tattcctgag tgaatatatg aggggggttg cactgctgtt aagagtggac 120
aggaaaatgg aaactagacg aacgtgacaa atccacgtgg atccagaaaa ataggaatca 180
ctgaatgcc aagggcaggt cacagaggag gaagaccagc actctgagca ggatgggtcat 240
gtacagcctg gtcaaggga tcttccggga tccacaaagg atcctgacca gcagaaccgg 300
gctggaccgg cagagaacca cacataaaaa aatcagccat gtgactgtga tgaaatctga 360
tgtttcacac caaacagaat caagcaccac tagacaggaa gccacagaac atccattcca 420
ggatgctctg cagcagggac agggcccaga gcaggacaca cgactgctna ccaggtnntt 480
tngngtggct gcagctctn cttaggatng tccccaaagg ttgncnngn cggtnntt 540
gnttgcttnt cgnncccta nctatgcctt ngctcctgtt nangcttgac nattggncct 600
cnccacgng gcttaannnt ctcnngncgc atttanancg tnatnntact tccctgtgcg 660

```

<210> 125  
 <211> 632  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 2, 488, 505, 507, 586, 618  
 <223> n = any nucleotide

```

<400> 125
gnccctctag atgcatgctc gagcgggcgc cagtgtgatg gatattctgca gaattcgccc 60
ttcctatgta cttcttctctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc ccctgcacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgtgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgtc tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgtca tcccattcct actcctcctt gggtcctatg 420
caagaattgt ctctccatc ctcaaggctc cttcttctaa gggatctctg aaggccttct 480
ctacttgnng ctcccacctg tcttngngg cactgttcta tgggaaccgg tattggctctc 540
tacttaatgc tcatcaagct aatagttcta ctctaaagga cactgncatg gctatgatgt 600
acactgtggt gaccccnat gctgacccat tc 632

```

<210> 126  
 <211> 642  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 331, 422, 435, 441, 462, 467-468, 471, 479, 500, 502, 513, 521, 537,  
 543-545, 549, 551, 563, 565-566, 569, 577, 582-583, 586, 594, 596, 611, 614,  
 620, 624, 631, 639-640

<223> n = any nucleotide

```

<400> 126
tctagatgca tgctcgagcg gccgcagtgt gatggatata tgcagaattc gcccttccaa 60
tgtacttgtt cctggcagcc atggcttatg accgctgtct tgccatctgc taccctttac 120
actacggagc catcatgagt agcctgtctc cagcgcagct ggccctgggc tcctgggtgt 180
gtgggttctg ggccattgca gtgcccacag ccctcatcag tggcctgtcc ttctgtggcc 240
cccgtgccat caaccacttc ttctgtgaca ttgcaccctg gattgccctg gcctgcacca 300
acacacaggc agtagagctt gtggcctttg ngattgctgg tgtggttatc ctgagttcat 360
gcctcatcac ctttgtctcc tatgtggaca tcatcagcac cctccttcag gatccccctt 420
gncagtggcc ggagaaaaag ncttttccac gtgctcctcg cntctcnncg nggtgctcna 480
tttgggtatg gtccacaagn tntctttca cgnccgatt ntccattcaa aagatgncct 540
tgnnttttna ncaaaagctt ggnncnncgnc ctgaaanact gnnngtngact tcangnttta 600
aaactccttt natntcactn ttanggaac nagggcggnn ac 642

```

<210> 127  
 <211> 688  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 1, 4, 54, 154, 269, 284, 294, 327, 339, 342, 344, 360, 362, 366, 372-373, 379, 382, 390, 393, 395, 397, 402, 408, 410-411, 417, 425, 428, 433, 435, 442, 446-448, 456, 461, 468, 473, 476, 479, 485, 487, 489, 508-509, 514-515, 526, 532-533, 535, 537, 539, 547, 550-551, 553, 555, 559, 572, 578, 582, 587, 595, 597, 602-603, 609-613, 617, 619, 621, 630, 634, 636, 640, 650, 652, 660, 679, 681, 683-684  
 <223> n = any nucleotide

<400> 127  
 ntgngccctc tagatgcatg ctcgagcggc cgccagtgtg atggatatct gcangaattc 60  
 gcccttccca tgtatttatt ccttagcctg ttggattccc agctgcacag ctggattgtg 120  
 ttacacaact caccttcttc aagaatgtgg aaanctataa ttttttttct gtgacccatc 180  
 tcaacttctc aaccttgcct gttctgacag catcatcaat aacatattat gtattttaga 240  
 tatccctata tttggttttc tcccattnc agggatcctt ttgncttacc atanaattgt 300  
 cctcctccat tccaagaatt ccattgncag acgggacgna tnangccttc tctacctgt 360  
 cntctnacc gnnagtcgnt tntttatctn tgnantnccc tngggcgncn nccctgncct 420  
 cagccttngt cancttctc cncacnnntt cgtcgtgtt nccagtnct gtncctnctnc 480  
 tctctnctnc tttctgcctc cctccannng tctnncttctc tcagncctt tnnncnct 540  
 gccagncnc nangntccnc cctctccct cntgtctnct cnetcctntt cttctntctc 600  
 tnnctcatnn nnnccgncnc ncgtctccn ccctntctn tacgactccn gncgtctctn 660  
 cgcctacgac ctcctgtnc ncnncgg 688

<210> 128  
 <211> 619  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 10, 46, 60, 322, 365-366, 464, 472, 475, 482, 493, 498, 498, 504, 517, 535, 543, 547, 556, 564, 584, 590, 600, 602, 610  
 <223> n = any nucleotide

<400> 128  
 gcgtgctgcn agcggggcgg cagagtgagc ggatatctgc agaatncgcc cttccgatgn 60  
 atttctttct aagcaactta tctttcattg acatctgcta ctcttctgct gtggctccca 120  
 atatgctcac tgacttcttc tgggagcaga agaccatctc atttgtgggc tgtgctgctc 180  
 agtttttttt ctttgtcggc atgggtctgt ctgagtgcct cctcctgact gctatggcat 240  
 acgaccgata tgcagccatc tccagccccc ttctctaccc cactatcatg acccagggcc 300  
 tctgtacacg catggtggtt gnggcatatg ttggtggctt cctgagctcc ctgatccagg 360  
 ccagnnccat atttaggctt cacttttgcg gacccaacat catcaaccac ttcttctgct 420  
 acctccacca gtcctggctc tgtcttgctc tgacaccttc cttnagtcaa gncgncgaat 480  
 tntcccgtag tgntcacntg tcgngaggaa acatcgnttt cctccaaccc cttantctcc 540  
 cangggntac catagnctct gcgngtcctt gaagaatcct tttngccaan cgggcgaatn 600  
 gnaagccctn ccaccgcc 619

<210> 129  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 17, 223, 238, 260, 304, 310, 315, 317, 322, 325, 327, 329, 341, 345-347, 350, 351, 356, 361, 369, 373-374, 378, 386, 391, 394, 396, 403, 414, 416, 426, 447-448, 456, 459, 461-462, 469, 473, 475, 477, 482, 488, 493-495, 504, 508, 511, 515, 518, 523, 527, 532-533, 537, 543, 548, 555, 558, 561, 570-571, 578, 580, 587-588, 592, 598-599, 601-602, 606, 608, 613, 619, 622-623, 634-635, 645, 648, 656, 658, 661, 665, 674-675, 682, 685, 687, 694-695

&lt;223&gt; n = any nucleotide

&lt;400&gt; 129

```

gcggcgcagt gtgatgntat ctgacgaatt cgcccttccg atgtatttat ttctaagcaa 60
cttatctttc attgacatct gctactcttc tgctgtggct cccaatatgc tcaactgactt 120
cttctgggag cagaagacca tatcatttgt gggctgtgct gctcagtttt ttttctttgt 180
cggcattgggt ctgtctgagt gcctcctcct gactgctatg gcntacgacc gatatgengc 240
catctccagc ccccttctcn accccactat catgaccagc ggcctctgta cacgcatgga 300
ggtngeccn tatgntngtt gnetnctng agctcctga nccannnctn ntcacntatt 360
ntaggetcna ccnntcgngc tcccgntcca ncancnaacc ccttcgttc ctgnanactt 420
ctccancacg ttcctggctt ttctgcnntc gcctcncgnc nnccttatnc ttnangntca 480
cncctganct gcnntttctt ccangcngc ncgencancc cgnctctntct gngaancct 540
ttncatnct gctcnatnct nctctcatn ntctctantn ctctcnnct cncgctcnnt 600
nncctnct ctnaacctnt cnnatcctca cctnngatat cctcncgntc ttctgcnctc 660
nttctctgct cganntcctc anacnctcc ctanncg 697

```

&lt;210&gt; 130

&lt;211&gt; 625

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 473, 502, 524, 547, 550, 567, 572, 590, 596, 614-615, 619, 623

&lt;223&gt; n = any nucleotide

&lt;400&gt; 130

```

ctctagatgc atgctcgagc ggccgccagt gtgatggata tctgcagaat tcgcccttcc 60
tatgtattta ttccttagcc acttgccct cactgacatc tccttttcat ctgtcactgt 120
ccctaagatg ctgatgaaca tgcagactca gcacctagcc gtcttttaca agggatgcat 180
ttcacagaca tattttttca tattttttgc tgacttagac agtttcttta tcaacttcaat 240
ggcatataac aggtatgtgg ccatctgaca tcctctacat tatgccacca tcatgactca 300
gagccagtgt gtcattgtgg tggctgggtc ctgggtcatc gcttgtgctg gtgctctttt 360
gcgtaccctc ctcttgcccc agctttcctt ctgtgctgac cacatcatcc ctcaactactt 420
ctgtgacctt ggtgccctgc tcaagtggc ctgctcagac acctccctca atnagtttagc 480
aatctttaca ggagcattga cnggcattat gcttccattc ctgngcatcc tgggttctta 540
tgggcanatn tgggggtcac cattctncag anttcttcta ccagggcatn tgcaangcct 600
tggccacttg tggnnccnc tcncg 625

```

&lt;210&gt; 131

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 344, 419, 443, 464, 486, 521, 524, 535, 537-538, 545, 552, 564, 567, 572, 584, 586, 588, 601, 604, 608-609, 611-612, 616, 618, 620, 622, 626, 629-630, 633, 638-639, 643, 645, 655

&lt;223&gt; n = any nucleotide

&lt;400&gt; 131

```

ttggcctcta gatgcatgct cgagcgccgc cagtgtgatg gatatctgca gaattcgccc 60
ttgatacatg attgggttgc ggaaggaata aatcatcggg ttgcggaagg aataaataca 120
tcgggttgcg gaaggaataa atacatcggg ttgcggaagg aataaataca tcgggttgcg 180
gaaggaataa atcatcgggt tgcggaagga ataaatacat cgggttgcg aaggaataaa 240
tacatcgggt tgcgtaagga ataaatcatt ggggttgcgta aggaataaat cattgggttg 300
cgtaaggaat aaatcattgg gttgcgtaag gaataaatca ttgngttgcg taaggaataa 360
atctttgtgc tgggtaccgat ctatcatggg gttacgaaag ggaagaaata cattggaang 420
ggcgaattcc agcacactgc cgnccgctac tagtgggac cganctcgg accaagcttt 480
gatgcntagc ttgagtattt taacgcccgc aacctaaaat ngcnttggcc ttacncnntg 540
gaccnagctt gnttccttgc cgtnaanttt cnttatctct cctntntntc ttctccccc 600
ncanaatnnt nccccngntn ancacncann ttntatannc ctngngctcc cctantc 657

```

&lt;210&gt; 132

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 7, 27, 34, 39, 481, 484, 489, 493, 502, 520, 566, 614, 623-624

&lt;223&gt; n = any nucleotide

&lt;400&gt; 132

```

tggccncta gatgcatgct cgagcgnccg cagngtgang gatatctgca gaattcgccc 60
ttcctatgta tttattcctt aatgtcctct cgcttcttga tatttggtac tcttctgtgg 120
tcacacctaa gctcttggtc aacttccttg tctctgacaa gtccatctct tttgagggct 180
gtgtggtcca gctgccttc tttgtagtgc atgtgacagc tgagagcttc ctgctggcct 240
ccatggccta tgaccgcttc ctatccatct gtcaaccctt ccattatggg tctatcatga 300
ccagggggac ctgtctccag ctggtagctg tgtcctatgc atttggtgga gccaaactccg 360
ctatccagac tggaaatgtc tttgccctgc ctttctgtgg gcccaaccag ctaacacact 420
actactgtga cataccaccc cttctccacc tggcttgtgc caacacagcc acagcaagag 480
ngnccctcna tgncttttct gntctggcac ccttctggcn gctgcaggca ttctcacctc 540
taccggcttg ggcttggggg ccaatnggga ggatgcgcct caagaacagg gagggagaaa 600
ggactcccca cttntgcctc ccnn 624

```

&lt;210&gt; 133

&lt;211&gt; 590

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 161, 185, 190, 221, 278, 303, 320, 337, 348, 360, 371, 387-388, 390, 393, 395, 402, 407, 409, 413-414, 423, 437, 449, 455, 459, 461, 464, 466-467, 468, 471, 475, 482, 484, 487, 489, 491, 493-495, 499, 500, 503-504, 510, 515, 519-520, 528, 538, 540, 541, 543, 546, 548, 555-556, 558, 563, 566, 568, 572, 575, 584-586, 588

&lt;223&gt; n = any nucleotide

&lt;400&gt; 133

```

ggagttgata tgaacgggtt aagtgaagga gtgcccactg catagaagag accaaagaac 60
ttgcccctcc cttgggcata cggatttttg ggctggagggt agacagcaat gactgagctg 120
cagaagaggg tgaccacagt gagatgggag gagcagggtc naaaggcctt tctccatgct 180
gtggnagagn taattctcag cactgccttg gcagtcggct ncataagagg caaggatgag 240
gctgagaggc acaaccacga agatgacact ggacacangc caactgtatc cattgtagga 300
ggnatctcca caggagagtn gaatcagaga tgggacnttc acattaanaa gttatttatn 360
tgctggcggg nacagatgcc caagcggnan ggngntatgg tnctggncna ttnttctgctc 420

```



canacccatt atctcangcc acatgtatnt cagcncnttna ntcncnntnt nagtntagtc 480  
 tngntgntnt ncnnnattnn cncntctttn tccntcann tatcattntc attccttncn 540  
 ncnanantt atggncncnc cgnacncnct cngtnactcc cctnnngncg 590

<210> 134

<211> 655

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2-3, 5-11, 17485, 506, 512, 514, 518, 525, 543, 578, 590-592, 602, 609, 612, 616, 637, 646

<223> n = any nucleotide

<400> 134

gnntnnnnnn ntgttancct cgtccctcta gatgcatgct cgagcggccg ccagtgtgat 60  
 ggatatctgc agaattcgcc ctccgatgt atttatttct acacagacac agtgacaatc 120  
 tgatctctct tgcttttccc cacacactgc aacctctgcc tccacattca agtgattctc 180  
 ctgcctcagc ctcttgagta gctggaatta cagatgtgag ccaccatgcc tggcctgtcc 240  
 agatgttttt gaaacaaccc ccaccagcac tggagggagt caagggaaga caagccaggc 300  
 atctgagctc ctctgtctct gcctttcctt ctcactgtcc ccagggtaac ccgtcaccac 360  
 ccccatcacg aacccttca tctacacatt acgtaacaag ggcgaattcc agcacactgg 420  
 cgcccggttac tagtggatcc gagctcggtta ccaagcttga tgcatagctt gagtattcta 480  
 acgntcacc taaatagctt ggcgtnatca tngncccnag cttgntttct gtgtgaaatt 540  
 tgntatccgc tcacaaattc cacacaacat acgagccnga agcaataagn nntaaagcct 600  
 gnggtgccna angagngagc taactcacia ttaattncgt tggctnactt gcccc 655

<210> 135

<211> 639

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 4, 449, 480, 499, 510, 519, 524-525, 536, 543, 547, 550-551, 557-558, 564, 574, 581, 602, 615, 518, 621, 623, 627, 636, 639

<223> n = any nucleotide

<400> 135

ttngnccttc tagatgcatg ctcgagcggc cgccagtgtg atggatatct gcagaattcg 60  
 cccttcctat gtacttggtt ctaagcaacc tctccttctt ggagatttgg tataccacag 120  
 cagcagtgcc caaagcaccg gccatcttac tggggagaag tcagaccata tcatttacia 180  
 gctgtctttt gcagatgtac tttgttttct cattaggctg cacagagtac ttcctcctgg 240  
 cagccatggc ttatgaccgc tgtcttgcca tctgctatcc tttacactac ggagccatca 300  
 tgagtagcct gctctcagcg cagctggccc tgggctcctg ggtggtgtgg tttcgtggcc 360  
 attgcagtgc ccacagccct catcagtggc ctgtccttct gtggttcccg tgccatcaaa 420  
 cacttcttct gtgacattgc accctggant gccctggcct gcaccaaacac cacaggcagn 480  
 aagagcttgt ggcctttgng aatgccttgn tggggctanc cttngtcat gccctnatca 540  
 cctttntcn nctatgnngt acantcatta agncceaatc nctcatggga tccccttttg 600  
 cnagtggccc ggcgngcnaa ngncctnctc cccgtncen 639

<210> 136

<211> 654

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 3, 108, 186, 216, 221, 252, 322, 329, 339, 344, 346, 350, 370, 376, 379, 385, 388, 391, 398-400, 404, 409, 418, 422, 428-429, 433, 437, 455-456, 462, 465, 474-476, 493, 496, 498, 503, 506, 515, 521, 527, 538, 540, 542, 548, 554, 561, 563, 565, 586, 595, 598, 612, 628, 639, 646

&lt;223&gt; n = any nucleotide

&lt;400&gt; 136

```

tgnccctcta gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc 60
cttccgatgt atttgtttct agccaacctg tcattaactg atgcttgntt cacttctgcc 120
tccatcccca aaatgctggc caacattcat acccagagtc agatcatctc gtattctggg 180
tgtctngcac agctatattt cctccttatg tttggnggcc ntgacaactg cctgctggct 240
gtgatgccat angaccgta tgtggccatt tgccaaccac cccattacag cacatctatg 300
agtccccagc tctgtgcaact antgctgcnc gtgtgctgng tgcnanccan ttgtctgcct 360
gctgcacatn ctgttncnc cccnccngg nctctttnnn ccgnaccnc cctacaantc 420
cntatcannt tcnctnccc tttcttctcc cccnnttct tncnccttc ctcnnccta 480
ctttcttctc tcnccntnct canatnatca gtecnacctc nccttctttt cttcactnan 540
tntctcnct cccnctcacc ngntngtcta gtctgcegtc gcccctegc tatenctncc 600
cccctctccg cntccctga tcgtcctngt ctaccctcnc catctnatcc ctcc 654

```

&lt;210&gt; 137

&lt;211&gt; 658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 334, 346, 350, 352, 357, 360, 369, 376-379, 389, 394, 397, 400, 401-402, 411, 414, 421, 435, 438, 447-449, 460, 466-467, 474, 476, 480, 486, 500, 504, 510, 512-513, 515, 517, 521, 525, 528, 543, 551, 554-555, 557, 559, 569-570, 572-573, 585, 587, 591, 593-594, 600-601, 606-607, 612, 615, 617, 621, 623, 628-629, 631, 633, 636-637, 640, 655

&lt;223&gt; n = any nucleotide

&lt;400&gt; 137

```

ctctagatgc atgctcgagc ggccgccagt gtgatggata tctgcagaat tcgcccttcc 60
aatgtatttt tttctaagca acctctcctt cctggagatt tggataacca cagcagcagt 120
gccc aaagca ctggccatcc cactggggag aagtcagacc atatcattta caagctgtct 180
tttcagatg tactttgttt tctcattagg ctgcacagag tacttctctc tggcagccat 240
ggcttatgac cgctgtcttg ccattctgcta tcctttacac tacggagcca tcatgagtag 300
cctgctctca gcgcagctgg cctggggctc ctggncgtgn ggcttngtgn cnttgengcn 360
ctcctagcnc tcatgnnnnc cttgccttnt gggnccntgn nnatcaccct ntttctctgt 420
nacacttgta cctnccgnet tgccctnnnc tgcttetaan tccctnngtt gtantnccn 480
gccttntctc cccttegetn gttnatcttn anntnctgnc ntctntgncc ctctccttcc 540
ttngaccct ntannncnc tcttctctnn anntccctc tatencccg nttnccctcn 600
ntgtcnccg antangntac ntntcacnnt ntntcnctn ctctcctaac tcttnccg 658

```

&lt;210&gt; 138

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 342, 347, 358, 376, 383, 401, 403, 409, 448, 451, 455, 463, 470, 474, 478, 481-482, 484, 487, 489-490, 492, 499, 511, 514, 516, 518, 522, 525, 534,

536, 548, 556, 565, 577, 581, 585, 587, 589, 592, 598, 604, 607-609, 624-626,  
628, 636, 639, 645, 651, 655, 660, 661-663, 667-668

<223> n = any nucleotide

<400> 138

```
ggccccctag atgcatgctc gagcggggcgc cagcgtgatg gatatctgca gaattcgccc 60
ttcccatgta ttgttttcta agcaacctct ccttcttgga gatttggtat accacagcag 120
cagtgcceaa agcactggcc atcctactgg ggagaagtca gaccatatca ttacaagct 180
gtcttttgca gatgtacttt gttttctcat taggctgcac agagtacttc ctctggcag 240
ccatggctta tgaccgctgt cttgccatct gctatccttt aactacgga gccatcatga 300
gtagcctgct ctacgcgcag ctggccctgg gctcctgggt gngtggnttc gtggccantg 360
tagtgcceac agccentatc agnggcctgt ccttttggg ncnccegtnc catcaacccc 420
ttctttctgt gacatttgcc cccctgcntt nccntggcc ctncceaan cacngcagg 480
nngnttncnn gnetcggcnc cccctttgac ntantncntt gntgngcgt tatnctgcg 540
tttaatgncc ttaatnaaac tctcncctct catgttnttc nttntntng gnaccaantc 600
ttcnaannna cccttttttc catnnncng tctacntcnc tctcnccttc ntcgngtttn 660
nnngtcnccc 670
```

<210> 139

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 303, 314, 331, 339, 341, 360, 373, 379, 386, 395, 400, 406, 416, 419,  
423, 433, 435, 452, 456, 463, 473, 480-481, 487, 490, 493, 499, 501, 504-505,  
509, 511, 514, 517, 519, 522, 523, 534, 535, 543, 544, 554, 560, 563, 565,  
567, 579, 584, 593, 596-597, 599, 605-608, 611-612, 619-620, 624, 632, 634  
<223> n = any nucleotide

<400> 139

```
gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttccgatgt 60
atTTTTTct aagcaacctc tccttcttg agatttggtat taccacagca gcagtgcceca 120
aagcactggc catcctactg gggagaagtc agaccatatc atttacaagc tgtcttttgc 180
agatgtactt tgttttctca ttaggctgca cagagtactt cctcttgga gccatggctt 240
atgaccgctg cttgccatct gctatccttt aactacgga gccatcatga gtagcctgct 300
ctnagcgcag ctgncctggg ctcttggtg ngtggttcng ngccattcag cgccacagn 360
cttcatcagt ggncttgtnc ttctgngccc ccgncatcn aaccantttc ttctgngana 420
atngtacccc tgnanttgcc ctggccttg anccancaca tangetcgt tgngetctn 480
ntggcncnccn tgnctcgnt ngtnccgng ntancngnc tnnacgtcct ttcnnacact 540
ttnnctctat gttntcaacn tcncngncta ttcgtcang atanccactc ttcnancnt 600
cggannnnta ncttttcnn accntcttct cntnc 635
```

<210> 140

<211> 709

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 357, 369, 379, 382, 414, 430, 441, 458, 462, 468, 474, 481, 486, 494,  
505, 507-509, 514, 520, 533, 546, 551, 555-556, 563, 570, 574, 589, 600, 602,  
606, 613, 615-616, 622-623, 628, 638, 644, 653, 669, 671, 677, 679, 680-681,  
689, 691, 696-698

<223> n = any nucleotide

<400> 140

```
atgaccctct agatgcatgc tcgagcggcc gccagtgtga tggatatctg cagaattcgc 60
```

```

ccttcctatg tatttatttc taagcaacct ctcttctctg gagatttggg tataccacag 120
cagcagtgcc caaagcactg ggccatccta ctggggagaa gtcagaccat atcatttaca 180
agctgtcttt tgcagatgta ctttgttttc tcattaggct gcacagagta ctctctcctg 240
gcagccatgg cttatgaccg ctgtcttgcc atctgctatc ctttacacta cggagccatc 300
atgagttagc tgctctcagc gcaagctggc ctgggctcct ggggtgtgtg tttcggnggc 360
cattgcagng cccacagcnc tnatcagtgg gctgtccttt ctgtgggccc ccgngcccat 420
tcaacccaen tttctttttg nggatattgg caaccccntg gnatttgncc cctnggccct 480
ngcacncaaa ccancaccag ggtcngnnna caanctttgn cgggccccct ttntgaaatt 540
ggcctnggtg ngggnnntaat tcnctttggn tttnaatgcc cttccaatna acctttttgn 600
cnttctatg ggngnnccct tnnattcnag caccacance ttanggggaa ccnccttttt 660
gtcaagtngg nccggttnann naaaagccnt ntccnnntg cccccccc 709

```

&lt;210&gt; 141

&lt;211&gt; 671

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 1, 18, 368, 374, 375, 386, 392, 404, 405, 414-415, 420-422, 445-446, 449-450, 452, 460, 467-468, 471, 484, 488, 490, 512, 514, 531, 536-537, 541-542, 549, 562, 568, 572, 574-575, 577, 585, 588, 592-593, 595, 599, 617, 619, 627, 636, 639, 647, 658-659, 661-662, 665-667, 669

&lt;223&gt; n = any nucleotide

&lt;400&gt; 141

```

ntgggccctg agatgcangc tgcagcggcc gccagtgtga tggatatctg cagaattcgc 60
ccttcccatg tatttttttc taagcaacct ctcttctctg gagatttggg ataccacagc 120
agcagtcccc aaagcactgg ccatcctact ggggagaagt cagaccatat cattttacaag 180
ctgtcttttg cagatgtact ttgttttttc attaggctgc acagagtact tcctcctggc 240
agccatggct tatgatcgct gtcttgccat ctgctatcct ttacactacg gagccatcat 300
gagttagcctg ctctcagcgc agctggccct gggctcctgg gtctgtgggt tcgtggccat 360
tgaagtgncc acanngcctc atcagntggc cntgtccttc tgcnncccc cgtnncattn 420
nncacttctt tcgtgacatt gccannctnn tnttgccctn gtccttnncc natcatccat 480
ggcngttngn gctgttggcc ctttcgctca cncngtctgc gcccattctc nctgtnncaa 540
nngcctcent ctactctctg cnttctanct antnnncct ctttncctnc tnnantctnt 600
cctcgatctc ctttcangnc tccgctncac tgetcnctna acgtcctttt ctccctnnt 660
nntcnntnc g 671

```

&lt;210&gt; 142

&lt;211&gt; 739

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 5-6, 23, 232, 235, 349, 353, 358, 374, 397, 400, 406, 423-424, 427, 431, 434, 436-437, 440, 445, 448, 450, 452, 467, 471, 477, 488-489, 497-498, 506, 510-512, 518-520, 525, 528, 547, 550, 557-558, 560, 562-563, 566, 569, 590-591, 604-605, 613, 619, 631, 638-639, 642, 646, 649-650, 654, 660-661, 664, 670, 677, 679, 687, 690, 692, 694-695, 701, 714, 716, 722, 725, 731, 739

&lt;223&gt; n = any nucleotide

&lt;400&gt; 142

```

gggcnncttt gggatgcct tgncccttag atgcatgctc gagcggccgc cagtgtgatg 60
gatattctga gaattcgccc ttccaatgta cttatttcta gccaacctgt cattaactga 120
tgctgttttc acttctgcct ccattcccaa aatgctggcc aacattcata ccagagtca 180
gatcatctcg tattctgggt gtcttgca gctatatttc ctcttatgt tngnggcct 240

```

```

tgacaactgc ctgctggctg tgatggcata tgaccgctat gtggccatct gccaaaccact 300
ccattacagc acatctatga gtccccagct ctgtgcacta atgctgtgng tgnngctgngt 360
gctaaccaac tggngctgcc tgatgcacac actgttnctn atccnngcgc tttcttggtc 420
ccnntangcc nctnctnctn ttcnntnctn tntctctacc tctccnteg ngctctnccc 480
cttcccnnt ctctctnntg tactenctan nnetgttnnn cccntcntt ctctctctcc 540
ttctctnctn ctctcggnnc tnntnctnct tcttgtccct acctgtcccn ntcatacctt 600
ttcnnaatcg ctntctatcnc cgcctatagt ncaattcnc tncctnctnn attnctctacn 660
nccntcctcn ccatactnct taacctnctn cntnntctct ntctctgtcc tcanctctc 720
gnccnatttc nttttccn 739

```

&lt;210&gt; 143

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; 497, 528, 536, 540, 543, 551, 557, 563, 565, 570, 582, 589, 600, 605

&lt;223&gt; n = any nucleotide

&lt;400&gt; 143

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttgatagat 60
aattgggttc agcatggggg tcaccacagt gtacatcata gccatgacag tgtccttttag 120
agtagaacta ttagctgatg agcataagta gagaccaata acggttccat agaacagtga 180
caccacagac aggtggggagc cacaagtaga gaaggccttg cagataccct tagaagaagg 240
gaccttgagg atggaggaga caattcttgc ataggaccca aggatgagta ggaatgggat 300
gacaagaatg agccctccca tgataaatat caccattca ttaactcgag tgtcagagaa 360
ggccagcttc agcagagcag acatatcaca gaaaaagtgg gggatcacat tgtctgcaca 420
aaaacacaac ctggccatga gtaaagtgtg taacatggca tgggaagggtg tcagcaccga 480
ggacagcgcc accaggncca gacagagcat ggggctcatg atggcgnggt agtgcngggg 540
gangcagatg nccacantag tgntnatagn ccatggtcac angggaggna gctttcaggg 600
ctttnaataa c 611

```

&lt;210&gt; 144

&lt;211&gt; 641

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 242, 263, 289, 315, 353, 357, 360, 372, 376, 385, 392, 397, 407, 416, 420, 422, 425, 429, 431, 433, 439, 446-449, 454, 465-466, 471, 479, 485, 492, 499, 501, 512, 516, 524, 528-529, 532, 534, 539, 543, 545, 547, 549, 561, 563, 565, 572-573, 575, 578, 582, 584-586, 596, 602, 604, 613, 615, 617, 622, 627-628, 632, 636-637, 639

&lt;223&gt; n = any nucleotide

&lt;400&gt; 144

```

gcgtgctcga gcggccgcca gtgtgatgga tatctgcaga attcgccctt gttgcgcaaa 60
gagtacatga aggggttaag tgaaggagtg cccactgcat agaagagacc aaagaacttg 120
ccctccctt gggcatacgg atttttgggc tggaggtaga cagcaatgac tgagctgtag 180
aagaggggtga ccacagttag atgggaggag cagggtccaa aggcctttct ccatgctgtg 240
gnagagttaa tcctcagcac tgntgggca gtggctccat aagaggcang gatgaggctg 300
agaggcacia ccacngaaga tgacactgta cacagccaac tgtattttat tgnaggnggn 360
atctccacag gngagnccaa tcagntgatg gntccnccc atttcanaag tcaactnatn 420
tntntttgnc ngncacgang gtcctnnng agcngttctt gtcnntctt nactatcgt 480
taccntccct cntccctnt ntttcttct cncctnctc ttcnttttnc cntntccnt 540
gtncnctnt atcttcccta ntntcttct tnntnctnt tngnnnccct cctctntctt 600
tncntccctc tcnantat cnettggncc cncnntnct c 641

```

<210> 145  
 <211> 837  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> variation

<222> 8-9, 12, 330, 350, 364, 367, 387, 390-391, 393-395, 398, 399-400, 403, 406, 409, 411, 413, 416, 428-429, 438, 449, 454, 464-465, 475, 481, 486, 488, 492, 500-501, 504, 506-507, 515, 523, 532, 538, 548, 556, 562, 565, 567, 573-575, 578, 582-583, 589, 592, 598, 599-600, 604, 608, 612, 629, 637-639, 643, 645, 647, 652, 663, 666, 668, 672, 679, 686-687, 689-690, 693, 699, 710, 715, 717, 719, 721-722, 724, 732-734, 748-751, 763-764, 772-773, 780, 783, 791, 811, 818, 828, 834, 836

<223> n = any nucleotide

<400> 145

```

ggttgccnnc gnttaggcat tgggccctct agatgcatgc tcgagcggcc gccagtgtga 60
tggatatctg cagaattcgc ccttcgatg tatttgtttc taagcaacct ctccttcctg 120
gagatttggt ataccacagc agcagtgcc aaagcactgg ccatactact ggggagaagt 180
cagaccatat catttacaag ctgtcttttg cagatgtact ttgttttctc attaggctgc 240
acagagtact tctccttggc agccatggct tatgaccgct gtcttgccat cctgctatcc 300
tttacactac ggagccatca tgagtagccn tgctctcagc tgcagctggn cctgggctcc 360
tggntgngct ggtttctcgc cctattntn ncnnnacnnn cntantcng ncnctnctct 420
ctttcttntt tcccttttnc tcaactcatnc ctncctctct tttntgtgcc tcttnataac 480
nttgtnntnc gnttctccn ntentnntct ctctnttgct tcnctctcct cntttcgnat 540
ccctttgntc tctacnctct tncgnantca ctnnnatntc tnntcacng cntcctcnnn 600
gatnttcncc tncctactgc tactctctnc tatactnnnc ttntntncat anttcgtctg 660
ctnaccnanc tntcactcnt tccannncnn tcnctgtcnt ctgactctcn cctentntnt 720
nntnccctac cnnntacatg gtccctttnn ntccatctcg tcnntctctc cmtatacgn 780
ttncatactc nctaacttct ctccatcatc ntcacctntc tttctttntc cctngnc 837

```

<210> 146  
 <211> 639  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> variation

<222> 16, 340, 379, 394, 401, 425, 428, 433, 435, 437-438, 446, 457, 463-464, 487, 504-505, 508, 510-511, 517-518, 529, 542, 546-547, 549-550, 552-553, 555, 561, 567, 569, 573, 576, 582, 584-586, 590, 594, 597, 599-600, 604, 611, 618, 623, 631, 634, 636

<223> n = any nucleotide

<400> 146

```

gatgatgctc gagcgnccga gtgtgatgga tatctgcaga attcgccctt ccaatgtatt 60
tatttctagg caccactgac ttcttcctct tggccgcat gtctctggat cgttacctgg 120
caatctgccg accactccgc tatgagaccc tgatgaatgg ccatgtctgt tcccaactag 180
tgctggcctc ctggctagct ggattcctct gggctccttg cccactgtc ctcatggcca 240
gcctgccttt ctgtggcccc aatggtattg accattctt tcgtgacagt tggcccttgc 300
tcaggctttc ttgtggggac accacactgc tgaactggn ggctttcatg ctctctacgt 360
tgggtggtact gggccacng gctctgacct cagntttcta ngcccgcatt ctgcccactg 420
ttctnagngc ccncnanngc ttgcngagc gaagcanaag atnnttttca cattgcccac 480
tcggaantta aagggggtgg cgcnnancn nctgggmgc ttcatctnt ctttttactt 540
tnccanngnn tntnngctca ntccctntnc tentencaat cntnnnggcn ctentgntnn 600
gtanactgcc nttaattnga ccnctttccc nacnncac 639

```

&lt;210&gt; 147

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 347, 411, 415, 418, 435, 441-442, 445, 451, 466, 482, 506, 508, 513, 515-516, 526-527, 531-532, 534, 536, 552, 561, 564, 571, 574, 581, 583, 586-588, 591-592, 616

&lt;223&gt; n = any nucleotide

&lt;400&gt; 147

```

catagatgca tgctcgagcg gccgcagtgt gatggatatc tgcagaattc gcccttccga 60
tgtaagtctt tcttaggcac cactgacttc ttctcttgg ccgtcatgtc tctggatcgt 120
tacctggcaa tctgccgacc actccgctat gagaccctga tgaatggcca tgtctgttcc 180
caactagtgc tggcctcctg gctagctgga ttctcttggg tcctttgccc cactgtcctc 240
atggccagcc tgcctttctg tggccccaat ggtattgacc acttctttcg tgacagtggg 300
cccttgctca ggctttcttg tggggacacc cactgctga aactggnggc ttcatgtc 360
tctacgttgg tggtactggg ctactgggt ctgacctcag nttcntange ctgcattctt 420
gtcactgtct caggncctt nnagntgctg ngcgaaggaa agcgcntttc acttgcgcct 480
cnatcttaca ggggtggcat catctnangg ggngnntgca tccttnncta nntnncagg 540
tcccagctat antccaaagt nctnaaaaca ngancctcgg nangannnct nntattctac 600
ccttcttctg aacctncc                                     618

```

&lt;210&gt; 148

&lt;211&gt; 633

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

<222> 2, 11, 33-34, 36, 38, 346, 352, 370, 406, 412, 414, 417, 420, 423-424, 427, 434, 437, 440, 449, 452-453, 474-475, 477, 486-487, 491, 496, 499-500, 505-506, 515, 517-518, 533, 535, 537, 540, 543, 547, 549, 556, 558, 563, 568, 570, 571, 575, 577, 580, 588, 590, 593-594, 598, 607, 612, 623, 626

&lt;223&gt; n = any nucleotide

&lt;400&gt; 148

```

cntagatgca ngctcgagcg ggcgccagcg tgnngnanat ctgcagaatt cgcccttcca 60
atgtattttt tctcactaac ttgtctttcc tagatctctg cttcaccacc agttctatcc 120
cccagctgct ttcaaatcta ggcagcccag gcaagactat cagccacacg ggctgtgcca 180
tccagctctt catgttctct ggcctgggtg gcaagagtgt attctcttgg cagccgtggc 240
ctatgaccgc ttcatgcaa tctgcaagcc ccttcaactat tctgtcatta tgcacctca 300
gctgtgctgg aagtgggtgt ctgtggcccg ggggtgttgg actccncagt tntctaggta 360
tgcctcctgn gactatgaag cttgtcacga tgcggaagat gtaagnttgc ancnttncn 420
ttntngnat gccngcntcn tataaaaanc annctgggcg ggtcacagt cttngnata 480
gcattngtc nccttnatnn catcnnatnt gcctngnngt ccctcggtcc cantntnca 540
tcnttctnng gcttancntt ctncaccngn ncttncntan ctactcctn ttnnttctc 600
cttctancct tncatcttcc ttncntcca tcc                                     633

```

&lt;210&gt; 149

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> variation  
 <222> 433, 456, 511, 513, 516, 533, 541, 543-544, 557-558, 561-562, 567, 573, 582, 597, 604, 606, 609, 617, 619  
 <223> n = any nucleotide

<400> 149  
 gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttgttccta 60  
 agactataca tgaatgggtt tagcatcggg ttgaaagaac tgtaaaatag aaaaaggacc 120  
 ttctgtctgt cctcaggatg gcgggactta ggggccatgt acatgacgat ggcgctgcc 180  
 aagaagagtc ccactacgca gaggtgggag gagcagggtg agaaggcctt tctgcccgc 240  
 tcccagact ggatcctcag gatggccgcc aggatgtgtg agtaggagac cagcaccagg 300  
 cagagtggtc ccaccaggat gaacatgcag gctgcaaaga tgaccacctg gttgagccag 360  
 gtatcagcac aggccagcct gaggacagac aggatttcac aagaagaagt ggttgatttc 420  
 acgaggccca canaaagggc agtcttagga tgaggntcac atggaccata gccaggagg 480  
 agccacattg tcccaggaag ngntgnccag agtgatgcag acttttcagg tcntgatgat 540  
 ngntttattc ggagagnntg nnagacnggt cancgttccc gntcgttaga caattancac 600  
 ccancngng ccttcantna tgtc 624

<210> 150  
 <211> 611  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 449, 480, 506, 555, 578-579, 601, 608, 610-611  
 <223> n = any nucleotide

<400> 150  
 gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttccaatgt 60  
 atttatttct ctctgacctc tcttcttgg acctctgctt taccacaagt tgtgtccccc 120  
 agatgctggc caacctctgg ggcacaaaga agaccatcag cttcctggga tgctctgtcc 180  
 agctcttcat ctctctgtcc ctggggacca ctgagtgcac cctcctgaca gtgatggcct 240  
 ttgaccgata cgtggctgtc tgccagcccc tccactatgc caccatcatc ccccccgcc 300  
 tgtgtggca gctggcatct gtggcctggg ttatgagtct ggttcaatcg atagtccaga 360  
 catcatccac cctccacttg cccttctgtc cccaccagca gatagatgac tttttatgtg 420  
 aggtcccatc tctgattcga ctctcctgng gagatacctc ctacaatgaa atccagttgn 480  
 ctgtgtccag tgtcatcttt ggtggntgtg cctctcagcc tcctccttgc ctcttatgga 540  
 gccactgcc aggcnggggc tgaggattaa ctttgccnna gccatggaag aaaggtcttt 600  
 nggacctngn n 611

<210> 151  
 <211> 619  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> variation  
 <222> 415, 417, 427, 516, 524, 536, 544-545, 558, 561, 575, 580, 582, 584, 590, 607, 610, 615  
 <223> n = any nucleotide

<400> 151  
 gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc ctttctttat 60  
 ttcgaagagt atacactagt ggattgaaga gaaacaaata cataggaagg gcgaattcca 120  
 gcactctggc ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg 180  
 agtattctaa cgcgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttctgtg 240  
 tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300



```
gcctggggtg cctaagtagt gagctaactc acattaattg cgttgcgctc actgtccgct 360
ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcgngnaga 420
ggccggnttg cgtattgggc gctcttccgc ttctcgctca ctgactcgct gcgctcggga 480
cgtccggctg cggcgagcgg tatcagctta ctcaanggcc gtantacggt tattcncagg 540
aatnnggggt taacgccngg naaagaacat tgtgngccan angncaagcn taatgcccgag 600
gaaccgntan aacgntccc 619
```

&lt;210&gt; 152

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variation

```
<222> 139, 203, 209, 211-213, 216, 221, 225, 234, 243, 245, 248, 253, 255,
261, 277-279, 287, 296, 302, 311, 318, 321, 344, 348, 350, 353, 376, 379,
381, 383, 395, 397, 402, 406-407, 414, 420, 429, 436, 438, 448, 450, 452,
463, 476, 481, 483, 496, 499, 502, 517, 520, 523, 527, 530, 535, 537, 539,
542, 549, 550, 558, 570, 571, 579, 580, 584, 587, 596, 605, 609, 634-635,
637-638, 640, 644, 648-649, 663, 665-666, 671, 675, 677, 681, 692, 699, 705,
715, 718, 721, 736, 745, 750, 758, 766, 778-779, 791, 793, 797, 811, 816,
821, 829, 831, 832, 837, 839, 840, 843, 846, 846, 851, 858, 883, 889, 892,
895, 897, 898, 917, 923, 928, 935, 945, 956
```

&lt;223&gt; n = any nucleotide

&lt;400&gt; 152

```
ctcgagcggc gcagtgtgat ggatatctgc agaattcgcc cttcctatgt attattttctc 60
cataatztat ctattgccga tatctgcttc tcttccatca cagcgcccaa ggttctggcg 120
gaccttctgt ctgaaagana gaccatctcc ttcaatcatt gctccactca gatgtttcta 180
ttccacctta ttggaggggc gngtgtatnt nnnccntggt ncccnatgcg cctncttttc 240
ccntntcttt tcnantcttt nccctctctc tcatgcnnnc ccttccntct tattcntgtc 300
gnaatacgct ntctccgnet nctgtctgct catccttgcg gttncgtntn canctcatcg 360
ctgtctgtcg tacctnttnc ntctgtgtgc tgcgngntca tncacnntct caancgtctn 420
ccctcaactnc tcttntctng ctctctctnn cncctgtgtc tancctcttg ccctgntacg 480
nncgcgcgct catatnccng tncgtggtat ccctctnatn ttnttctctn cctctnttnc 540
cntctcacnn acttctctng ctctctccan ncttcgacnn ctctctnctc tccacnacgc 600
actntctnt ctatatccgc tcttaccgct ctctnnnnan cacncttnc tctgcatac 660
agntntcttc ncacnccat nttcttctca cncctctcnc tgtcncacag atctntctct 720
nctctgtctc cgttgntccc cctgncactn cgcaatcnca catatnctgc tctctctnnt 780
cgccacttat ntngcanctt tctctgcggt nctctnegat ntccctcnc nntctcncnn 840
ctnatnatcg nttattcnaa tcatactccg tactgtttct gtntctctnt cntgncnct 900
agcttctctc tattcantct acnttctntt cgctntctat ccacnctctt cactcncct 959
```

&lt;210&gt; 153

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g1 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 153

```
ttggcctgtg ctgacacatc cttagcccag aggggtgagct tccccgacgt tggcctcata 60
tctcttgtct gctttctgct aattctttta tcctacacta gaatcacaat atctatctta 120
agcattcgta caactgaggg ccgtcgccgt gccttctcca cctgcagtgct tcacctcatt 180
gccatcctct gtgcctatgg gccatcctc actgtctacc tgcagccac acccaacccc 240
atgtctggaa ccgtgtgata aattctcatg aatctggtag gaccaatgct gaaccctttg 300
atctatacct tgaggaataa ggaagtaaaa acagccctga aaacaatatt gcacaggaca 360
ggccatgttc ctgag 375
```

<210> 154  
 <211> 965  
 <212> DNA  
 <213> Unknown (H38g2 nucleotide)

<220>  
 <223> Synthetic construct

<400> 154  
 cacacagagc cacggaatct cacagatgtc tgagaattcc tcctcctggg actctcagag 60  
 gatccagaac tgcaaccggg cctcgttttg ctctccctgt ccctgtccat gtatctgggc 120  
 acggtgatga ggaacctgct cagcatcctg actgtcagct ctgtctctcc cctccacacc 180  
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcggtttcac ctcgccacg 240  
 gttcccacga tgattgtgga catgcagtcg catagcagag tcatccctca tgcgggctgc 300  
 ctgacgcaga tgtatttctt ggtctttttt gcatgtatag aaggcatgct cctgactgtg 360  
 atggcctatg actgctttgt agccatctgt cgccctctgc actaccagct catcgtgaat 420  
 cctcacctct gtgtcttctt cgttttgggt tccttttttc ttagcctgtt ggattcccag 480  
 ctgcacagtt gaattgtgtt acaattcaac atcatcaaga atgtggaaat ctctaatttt 540  
 gtctgtgacc cctctcaact tctcaactt gctgttctg acagcgtcat caatatcatt 600  
 ttcataatatt tcgatagtag tatgtttgct tttcttccca tttcaggat cctatggctt 660  
 actataaaat cgtccctctc attctaagga tttcatcgtc agatgggaag tataaatcct 720  
 tctccacctg tgccctctac ctacgagttg tttgctgatt tgatggaaac ggcatgggca 780  
 tgtacctgac ttcagctgtg tcaccacccc ccaggaatgg tgtgggtggc tcagtgatgt 840  
 acgctgtggg ccccccatg ctgaaccttt tcatctatag cctgagaaac aggaacatac 900  
 aaagtgcctt gcggaggctg cgcagcagaa cagtcgaatc tcatgatctg ttccatcgtt 960  
 tttct 965

<210> 155  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g3 nucleotide)

<220>  
 <223> Synthetic construct

<400> 155  
 atggatggag ataaccagag tgagaactca cagttccttc tcctggggat ctacagagagt 60  
 cctgagcagc agcggatcct gttttggatg ttctgtcca tgtacctggt cacggtgctg 120  
 ggaaatgtgc tcatcatcct ggccatcagc tctgattccc acctgcacac ccccatgtac 180  
 ttcttctctg ccaacctctc ctctactgac ctcttctttg tcaccaacac aatccccaag 240  
 atgctggtga acttcagtc ccagaacaaa gccatctcct atgcagggtg tctgacacag 300  
 ctctacttcc tgggtctcct ggtgacctg gacaacctca tcctggccgt gatggcgtat 360  
 gatcgtatg tggccacctg ctgccccctc cactatgtca cagccatgag ccctgggctc 420  
 tgtgtcttgc tcctctcctt gtgttggggg ctgtctgttc tctatggcct cctctcacc 480  
 ttctcctga ccagggtgac cttctgtggg cctcagaga tccactacct cttctgtgac 540  
 atgtacatcc tgcgtgggct ggcattgtcc aacaccaca tcattcacac agcgttgatt 600  
 gccactggct gcttcatctt cctcaccccc ttaggggttc tgaccacatc ctatgtacgt 660  
 attgtcagaa ccactcttca aatgccctcg gcctctaaga aatacaaaac cttctctacc 720  
 tgtgcctccc atttgggtgt ggtctccctc ttttatggga cgcttgctat ggtgtacctg 780  
 cagccctcc atactactc catgaaggac tcagttagcca cagtgtgta tgcgtgtctg 840  
 acacctatga tgaaccttt catctacagg ctgaggaaca aagacatgca tggggctccc 900  
 ggaagagtcc tatggagacc ctttcagagg cctaaa 936

<210> 156  
 <211> 914  
 <212> DNA  
 <213> Unknown (H38g4 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 156

atgaggaatc	acacattgct	gaatgaattc	attctacggg	gaatacctca	gacagagggg	60
ctggaggctg	tactctgtgc	tgtcttctca	ttcatctacc	tcttcaccct	acttggaat	120
ttactcatcc	ttatagcgat	tgtttcttca	cactcctatg	tatttcttct	tgggacgcct	180
gtctactttt	gacatattgt	tcccatctgt	aacatgtccc	aagatgctat	tgtatctctc	240
tggccagagc	ccagtcattt	cttttaaggg	atgtgcttca	cagctcttct	tctatcagtt	300
gctgggttct	gctgaaggct	gcctctattc	tgtgatgtct	tatgatcgct	ttgttgccat	360
acatcacaca	ctgagatata	tgctcatcat	gaagcctgga	gtctgtgtcg	gcttggtcgt	420
gggtgccggg	tgggtgggtg	tcttcacgcc	accattctga	cctcctttac	ctttcagttg	480
tcctactgtg	gccccaatca	ggtggactac	ttcttctgtg	acattcctgc	tgttttacct	540
ctggcttgta	ctgacagtgc	cctggcccag	agggtgggtt	ccataaatgt	tggctttctg	600
gctttaacac	ttttgatcag	tgtctgtgtc	tgctacacta	gcattgggat	tgccatcttg	660
agaatccgct	catcagaggg	caggcagaaa	gccttctcca	cctgcagtgc	tcaccttggt	720
gcaatcctct	gtgcctatgg	acctgtaatc	atcatctatc	tgaagtccac	acccaacccc	780
ttgcttggtg	ccagggtcaa	atattaaata	atgttgtctc	acccatgctg	aactcgtaa	840
tctattcctt	aaggacaacg	gaagtgaata	ggtccctgaa	aagagtattc	tgaatgttt	900
tacttactgt	ttgt					914

&lt;210&gt; 157

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g5 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 157

atgggaacag	ataaccagac	ttgggtgagt	gaatttatcc	tcctcggcct	gtccagtgc	60
tgggacactc	gggtctccct	gtttgtcctg	ttcttgggtc	tgtatgtggg	gaccgtgctg	120
gggaactgtc	tcattgtcct	tctgatcaga	ctggacagcc	gactccacac	tcccatgtat	180
ttctttctca	ccaacctctc	ccttgctgat	gtctcctatg	ccacaagtgt	agtccctcag	240
ctgctggcac	attttcttgc	agaacataaa	gccatcccat	tccagagctg	tgcagcccag	300
ttatttttct	ccctggcctt	gggtgggatt	gagtttggtc	tcctggcggg	gatggcctat	360
gaccgctatg	tggctgtgtg	tgatgccctg	cgatactcgg	ccatcatgca	tggagggctg	420
tgtgctaggt	tggccatcac	atcctgggtc	agtggcttca	tcagctctcc	tgtgcagact	480
gctatcacct	ttcagctgcc	catgtgcaga	aacaagttta	ttgatcacat	atcctgtgaa	540
ctcctagctg	tggtcaggct	ggcttgtgtg	gacacctcct	ccaatgaggt	caccatcatg	600
gtgtctagca	ttgttcttct	gatgacaccc	ttctgcctgg	ttcttttgtc	ctacatccag	660
atcatctcca	ccatcctaaa	gatccagtc	agagaaggaa	gaaagaaagc	tttccacacg	720
tgtgcctctc	acctcacagt	ggttgccctg	tgctatgggt	tggccatttt	cacttacatc	780
cagccccact	ccagtccttc	tgtccttcag	gagaagttgt	tctctgtctt	ttatgccatt	840
ttaacaccaa	tgctgaaccc	catgatttac	agcctaagga	ataaagaggt	gaagggggcc	900
tggcagaaac	tattatggaa	attctctggg	ttaacatcaa	agctggcaac	t	951

&lt;210&gt; 158

&lt;211&gt; 1025

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g6 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 158

gatacagacc	cacagagtct	aacagatgtc	tctatattcc	tcctcctcga	actctcagag	60
gatccagaac	tgcagccggg	catcgctggg	ctgttccctg	ccatgtgcct	ggtcacgggtg	120
ctggagaaac	tgctcatcat	catggcagtc	agccctgact	tccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	acgggtcccca	240
agatgattgt	ggacatccag	tctcacagca	gagtcattct	ctatgcaggc	tgcctgactc	300
agatgtctct	ctttgcccatt	tttggaggca	tgggaagagag	acatgtctct	gagcgtgatg	360
gcctacgacc	agtttgtagc	catctgtcac	cctcccatat	cgttcagcca	tcttgaaccc	420

gtgtttctgt	ggcttccaag	atttgttgtc	cctgtttttt	tttctttttt	tttttttttc	480
ctcaggcttt	tagactccca	gctgcataac	ttgattgcct	tacaaatgac	ctgcttcaag	540
gatgtggaaa	tttctaagt	cttctgggaa	ccttctcaac	tcccccatct	tgcattgtgt	600
gacaccttca	ccaggaacat	caacctgtat	ttccctgctg	ccgtattggg	ttttcttccc	660
atctcgggga	cgctttttct	ttactgtaaa	attgtttcct	ccattctgag	ggtttcatca	720
tcagggtggga	agtataaacc	ttctccacct	gtgggtctca	cctgtctgct	gtttgctgat	780
tttatggaac	agggcttggg	gggtatctcg	gttcagatgt	gtcatcttcc	ccgagaaaga	840
gtgcagtggc	ctcagtgatg	tatacgggtg	tcaccccat	gctgaacccc	ttcatctaca	900
gcctgagaaa	cagggatatg	aaaagtgtcc	tgcggcggcc	gcacagcagc	acggtctaata	960
ctcaatatct	tcttatctgt	tccattcctt	ttgtaggggtg	ggttaaaaaa	ggcagcaagg	1020
tcaaa						1025

&lt;210&gt; 159

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g7 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 159

atggtaaaag	gaaatcattc	cacgggtgact	gaatttaatc	tcgctgggct	aacagacaaa	60
ccagagctcc	agctgcctct	tttctctctc	ttcctgggaa	tctatgtggt	cacagtgggtg	120
ggcaacctga	gcatgatcac	tctaataagg	ttcagttctc	acctgcacac	ccccatgtac	180
catttctcca	gcagtctgtc	cttcattgat	ctctgccagt	cttctgtcat	taccccaaaa	240
atgctgggtg	attttgtgtc	agagaggaat	attatctcct	accagcatg	catgactcag	300
ctctacttct	tccttgttct	tgtcatatct	gaatgtcaca	tgttggctgc	aatggcttat	360
gaccactaca	ttgccatatg	taacccactg	ctttaccatg	tcgccatgtc	ttatcagggtc	420
tgctcctgga	tggtagttga	ggtgtatatt	atgggcttta	ttgggtgctac	gtgctcacac	480
agtctgcatg	ctaagagtgc	ttttctgtaa	ggctgatgta	atcaaccatt	acttctgtga	540
tcttttccca	ctactggagc	tctcccgcct	cagtatttct	atcaatgaaa	tagtagtttg	600
tgcttcagtg	catttaatat	ccttttccgc	agcctcacca	tccttagctc	ttacatcttc	660
atcgttgcca	gcactctctg	cattcgctcc	actgagggca	ggtccaaaac	cttcagcact	720
tgcagctccc	acatctcggc	tgtttctggt	ttctttgggt	ctgcagcatt	catgtacctg	780
cagccatcat	ccgtcagctc	catggaccag	gggagtgtct	tctgtgtttt	atgctactgt	840
tgtgcccatt	ctgaaccccc	aatctacagc	ctgaggaata	aagatgtcaa	agttgcctta	900
attaagttcc	ttgaaaaaag	aagtttctct	tgaagg			936

&lt;210&gt; 160

&lt;211&gt; 985

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g8 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 160

atgggtcagg	aaaataaaaa	ccagacatgg	gtgagtgagt	tcattctgct	ggggatttcc	60
agtgattggg	gcattcaggt	atccctcttc	gccctgatcc	tggccatgta	tttgggtgact	120
attttaggaa	acaccctcat	tcttcttctg	atcagactgg	acaacaggct	tcataacccc	180
atgtacttct	cccttagtgt	tctgtcattt	gtggactttt	gttatacaaa	gagtattgtc	240
ccacaaatgc	tgtcccactt	gctctcagcc	cgaaagtcca	tccattctta	cagttgtgtg	300
ctccagctct	atgtttctct	ggcatttgtt	gggtctgagt	tcttctgct	gggggcatg	360
gcctatgacc	gctacgtggc	cgtgtgccac	ccactgcact	acacggtcac	catgcatgga	420
gggctgtgcc	tggggctggc	ggccagccgc	ctgggtggctg	gcttctcaaa	ttccctgatg	480
gaaacaatta	tcaccttcca	gcttctctgt	tcacgggtgt	atcaatcact	ttgtctgtga	540
gaccttagca	gtgctacagc	tagcctgtgt	ggatgtcccc	ttcaacaagg	tcatgggtggc	600
catctcaggg	tttctgggtg	tcttgccttc	ctgttccctg	gttctattct	cctatgcttg	660
catagttgcc	accattttgt	gcattcgctt	taccaggta	cgctgcaaag	cctttgggac	720
ctgtgcctct	cacctcattg	tggtttgcac	gtgctttggg	gctaccatct	gcacctacct	780
ggggccacag	ttggcctcct	cagcagagga	agagaagatg	attgctctct	tctatggagt	840

gggtgtacccc atgttgaacc ccttgatcta cagcttgagg aataaggaag ttacggctgc	900
tgtccggaaa gttttagaaa gatgcagata aagggtcaag actctaagaa cctcttgta	960
tctatcatca aaacaaaaa ggaga	985

&lt;210&gt; 161

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g9 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 161

atggacaaa gcaattatag ttctttacat ggttttatc tgcttggtt ctctaaccat	60
ccaaaaatgg agatgatcct gtcaggagtt gtcgccatct tctacttaat tacattgggtg	120
ggtaacacag ccattcattct tgcatctctc ctggattccc agcttcatac accaatgtac	180
tttttcctca gaaatttate ttccctagat ctatgtttca caaccagcat catccctcag	240
atgctgggtca acttggtggg accatcagct atgtgggttg tatcatccaa	300
ctctatgttt acatgtggtt gggctcagtt gagtgccttc tcctggctgt tatgtcctat	360
gatcggttta cagctatatg taagcccttg cattattttg tagtcatgaa cccacatcta	420
tgtctaaaga tgattatcat gatctggagt attagtttgg ccaattctgt agtattatgt	480
acactcactc tgaatttgcc cacatgtgga aacaacattc tggatcattt cttgtgtgag	540
ttgccagctc tggtaagat agcttgtgta gacaccacaa cagttgaaat gtctgttttc	600
gctttaggca ttataattgt cctcacacct ctcatcctta ttcttatatc ctatggctac	660
attgccaaag ctgtgctgag aacgaagtc aaagcaagcc agcgaaaagc aatgaatacc	720
tgtggatctc atcttactgt agtgtctatg ttctatggaa ctattatcta catgtacctg	780
caaccaggta acagggcttc caaagaccag ggcaagttcc tcacctctt ttacaccgtc	840
atcactccaa gtctcaaccc gtcattttac accttaagaa ataaggacat gaaggatgcc	900
ctgaagaaac tgatgagatt tcaccacaaa tctacaaaaa taaagaggaa ttgc	954

&lt;210&gt; 162

&lt;211&gt; 970

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g10 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 162

cacacagagc cacggaatct cacaggtgtc tgagaattcc tcctcctggg actttcagag	60
gatccagagc tgcagtcggt cctcgctttg ctgtccctgt ccctgtccac gtatctggcc	120
acgggtgctga ggaacgtgct caacatcctg gctgtcagct ctgactcccc cctccacacc	180
cccatgtact tcttcctctc caacctgtgc tgggctgaca tcgggtttcac ctcgccacg	240
gttcccaaga tgattgtgga catgcagtcg tatagtagag tcattctctca tgagggtgc	300
ctcacacaga tgtctttctt ggtccttttt gcattgtatag aaggcatgat cctgactgtg	360
atggcctatg actgctttgt agccatctgt cgccctctgc attaccagat catcgtgaat	420
cctcacctct gtgtcttttt cgttttgggt tcctttttcc ttagcctgtt ggattcccag	480
ctgcacagtt gaattgtgtt acaattcaac atcatcaaga atgtggaaat ctctaatttt	540
gtctgtgacc cctctcaatt tctcaaactt gcctgttctg acagcgtcat caatagcata	600
ttcacgtatt tccatagtac tatgtttggt ttctctccca ttccagggtat ccttttttct	660
taatttaaaa tcgtcacctt cattctctgg atttcatctt cagatgggaa gtataaagcc	720
ttctccacct gtgactctca cctagcagtt gtttgctgat tttatggaac aggcattggc	780
atgtacctga cttcagctgt gtcaccaccc ccaggaatgg tgtagtggcg tcaatgatgt	840
acgctgtggg caccctcatg ctgaaccttt tcatctacag cctgagaaac agggacatac	900
aaagtgcctt gcggaggctg ctccagcagaa cagtcgaatc tcatgatctg ttccatcgtt	960
tttcttgtgt	970

&lt;210&gt; 163

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g11 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 163

atggagttgg	agaaccagac	acgagtcacc	aagttcattc	tggtgggatt	ccctgggagc	60
ttgagtatgc	gggcagccat	gtttctgata	ttccttgtag	cctatattct	gacagtggct	120
gaaaacgtga	tcatcatcct	attggtgctg	caaaatcggc	cactgcacaa	gcctatgtac	180
ttcttcctgg	ccaacctgtc	cttcttgtag	acctggtaga	tctctgtgac	tgtgcccag	240
ttactgttta	gtttttgggc	tgtgaacaac	agcatctctt	tcacactctg	tatgatacaa	300
ctgtacttct	tcattgctct	catgtgcaca	gaatgtgtgc	ttctggccgc	catggcctat	360
gaccggtagt	tggccatctg	tcgcccactc	cactacccaa	ccataatgag	ccatgggctc	420
tgcttcggcc	tcgctcttgg	ttcctggggc	attggctttg	gcactctccct	ggcgaagatc	480
tacttcatct	cctgcctcag	cttctgtggt	cccaatgtca	tcaaccactt	cttctgtgac	540
atctctccag	tacttaatct	ctcctgcaca	gacatgtcca	taactgagtt	ggtagacttt	600
atcctggcac	tggtcatctt	cctattccca	ctctttatta	ctgtcctgtc	ctacggatgc	660
attctggcca	ccatattatg	catgcccaca	ggaaagcaga	aagcgttctc	cacttgtgcc	720
tcccatcttg	tggtgggtcac	cattttctat	tcagccatta	ttttcatgta	tgtctgacct	780
cgagttatcc	atgccttcaa	catgaacaaa	attatttcca	tcttctatgc	cattgtcact	840
ccttctctca	accctttcat	ttattgccta	agaaaccgag	aggtcaagga	agctctgaag	900
aaactggcat	attgccaggc	cagcagatct	gac			933

&lt;210&gt; 164

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g12 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 164

atggagcaag	tcaataagac	tgtgggtgaga	gagttcgtcg	tcctcggtt	ctcatccctg	60
gccaggctgc	agcagctgct	ctttgttatc	ttcctgctcc	tctacctgtt	cactctgggc	120
accaatgcaa	tcatcatttc	caccattgtg	ctggacagag	cccttcatac	tcccatgtac	180
ttcttccttg	ccatcctttc	ttgctctgag	atttgctata	cctttgtcat	tgtacccaag	240
atgctgggtg	acctgctgtc	ccagaagaag	accatttctt	tcctgggctg	tgccatccaa	300
atgttttctt	tcctcttctt	tggtctctct	cactccttcc	tgctggcagc	catgggctat	360
gatcgctata	tggccatctg	taaccactg	cgctactcag	tgctcatggg	acatgggggtg	420
tgtatgggac	taatggctgc	tgctgtgtgc	tgtggcttca	ctgtctccct	ggtcaccacc	480
tccttagtat	ttcatctgcc	cttccactcc	tccaaccage	tccatcactt	cttctgtgac	540
atctccctcg	tccttaaaact	ggcatctcag	cactccggct	tcagtcagct	ggtcataatc	600
atgcttgggtg	tatttgcctt	ggtcattcct	ctgtacttta	tcctagtctc	ctacatccgc	660
atcatctctg	ccattctaaa	aatcccttcc	tccgttggaa	gatacaagac	cttctccacc	720
tgtgcctccc	atctcattgt	ggtaactggt	cactacagtt	gtgcctcttt	catctactta	780
aggcccaaga	ctaattacac	ttcaagccaa	gacaccctaa	tatctgtgtc	atacaccatc	840
cttacccecat	tgttcaatcc	aatgatttat	agtctgagaa	ataaggaatt	caaatcagcc	900
ctacgaagaa	caatcggccca	aactttctat	cctcttagt			939

&lt;210&gt; 165

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g13 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 165

tgtgtcgatt	cttctttaaa	atgagaaatc	acacagtgat	gtctgagttt	gttactgtga	60
atggctgagg	gctggagatt	gtatttcatt	atcctgatta	tatcttataa	attttgtacc	120
cttttgggaa	atgttatatt	caggaccctt	gtttgttctt	tgggatttca	cacatcatgc	180
atgtattttt	ttccttgaaa	aatatcattg	tgattggcat	gagtttgtct	tcaattattg	240

```

ctttaccttc aacgcagaaa tgagccatca atgttcaggg tgctgctgtc catgttttct 300
cctttccttg cctgtactgc cccgagatct tcttgcatte actgacacag tgccaccctt 360
ttattgccat tggatatcca ctgcaaggta tgcacaccat tacacacaaa ctgtatatac 420
tgctcaccac agggccctgg agaggctgct agctacatgt caatctcctg atgctatatt 480
aggcagctac cctaatacctg tgccaacgaa gttatggctg tcattcccat cacattcctg 540
aagtcaaact gtgacctatg caagcatata ctaagcccta tgccggtctc tctctctgtc 600
tctctcttag tctctctctc tctttctctc tcttttccat tatttccata tcttatactt 660
gcaatgaaat tgacatacca aaaattatct ctgcagacag tgtgcatgga gctttctcaa 720
cctgccttgc tcacctcttt gcttttcaa cctgcattgc tcaacctgca gtctgcaact 780
ctttgtggcc atggacagaa gctcagaccg agagctctct gcgattctgt gattcagaga 840
ccgaacttgt gtgtgaccat ctcttgaac tccttgattt ctacgctgag aaatgaaagt 900
gtgaaacaag cttcacataa aatatttaaa gaacaaactt tattcatgaa aata 954

```

&lt;210&gt; 166

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g14 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 166

```

atggatggag agaatcactc agtggatatct gagtttttgt ttctgggact cactcattca 60
tgggagatcc agctcctcct cctagtgttt tctctgtgac tctatgtggc aagcattact 120
ggaacatcc tcattgtgtt ttctgtgacc actgaccctc acttacctc ccccatgtac 180
tttctactgg ccagtctctc cttcattgac ttaggagcct gctctgtcac ttctcccaag 240
atgatttatg acctgttcag aaagcgcaaa gtcatctcct ttggaggctg catcgctcaa 300
atcttcttca tccacgtcat tgggtgtgtg gagatgggtg tgctcatagc catggccttt 360
gacagttatg tggccctatt aagcccctcc actatctgac cattatgagc ccaagaatgt 420
gcctttcatt tctggtgtgt gcctggaccc ttggtgtcag tcaactccctg ttccaactgg 480
catttcttgt taatttacct ttctgtggcc ctaatgtgtt ggacagcttc tactgtgacc 540
ttcctcagct tctcagacta gcctgtaccg acacctacag attgcagttc atgggtcactg 600
ttaacagtgg gtttatctgt gtgggtactt tcttcatact tctaactctc tacatcttca 660
tcctgtttac tgtttgga aa cattcctcag gtggttcac caaggccctt tccactcttt 720
cagctcacag cacagcggtc cttttgttct ttggtccacc catgtttgtg tatacatggc 780
cacaccctaa ttcacagatg gacaagtttc tggctatatt tgatgcagtt ctcaactcct 840
ttctgaatcc agttgtctat acattcagga ataaggagat gaaggcagca ataaagagag 900
tatgcaaaca gctagtgtt tacaagaaga tctcataaat gatacaataa gcccttctcg 960
ttaaacatga tatggcctta tgtttcttct tttgatat 998

```

&lt;210&gt; 167

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g15 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 167

```

cacacagggc cacggaatct cacagatgtc tgagaattcc tcctcctggg actctcagag 60
gatccagaac tgcagccact cctcactttg ctgtccctgt cctgtccat gtatctggtc 120
acgggtgctga ggaacctgct cagcatcctg gctgtcagct ctgactcccc cctccacacc 180
cccatgtact tcttctctc caacctgtgc tgggctgaca tgggtttcac ctaggccaca 240
gtccccaaga tgattgtgga catgcagtcg catagcagag tcactctctc tgcggtctgc 300
ctgatacaga tgtctttatt agtccttttt gcatgtatag aaggcatgct cctgactgtg 360
atggcctatg actgctttgt agccatctgt tgccctctgc actaccagat catcgtgaat 420
cctcacctct gtgtcttctt cgttttggtg tcctttctcc ttagcttgtt ggattcccag 480
ctgcacagtt ggattgtgtt acaattcacc atcatcaaga atgtggaaat ctctaattct 540
gtctgtgacc cctctcatct tctcaaaact gcttggtctg acagcgtcat caatagcata 600
ttcatatatt tcgatagtac tatgtttggt tttcttccca tttcagggat cctatggtct 660
tactataaaa tcgtccctc cattctcagg atttcatcgt cagatgggaa gtataaagcc 720

```

ttctccacct	gtgcctctca	cctagcagtt	gtttgctgat	tttatggaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaatg	gtgtgggtggc	gtcagtgatg	840
tacgctgtgg	tcacccccc	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgcgagggt	acgcagcaga	acagtcgaat	ctcatgatct	gttccatcgt	960
ttttct						966

&lt;210&gt; 168

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g16 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 168

atgtacctgg	ccactgtcct	ggggaacctg	ctcatcatcc	tggccataag	catagactcc	60
cgctgcaca	ccccatgta	cttcttcctc	agcaacatgt	cctttgtgga	caactgcttc	120
tccaccaccg	tccccaagat	gctggccaat	cacatactca	ggactcaaac	catctccttc	180
tctggctgtc	tcatgcagat	gtattttatc	agtgaagctt	ctgacatgga	caatttcctc	240
ctggctgtga	tggcctatga	ccgctttgtc	gccgtgtgcc	gccccttaca	ttacacagca	300
aagatgaccc	atcagctctg	tgccctgctg	gtcactggat	catgggtggg	tgccaactcg	360
aatgctctgc	tgcacaccct	gctgatggct	cgactctcat	tctgtgcaga	caacaccatc	420
ccccacatct	tctgcgatgt	gactccccct	ctgaaactct	cctgttcaga	cacacacctc	480
agtgaagtga	tgattcttac	tgagggtgcc	ctagtcaaga	tcacccatt	tctttgcctc	540
ctggcttcct	atatgcacat	cacctgcgtt	gtcctgaggg	tcccatccac	aaagggaga	600
tggaaagcct	tctccacctg	tggtccccc	ctggctgtgg	ttctctctct	ctatggcacc	660
atcatgtctc	catatttcag	aacttcaccc	tcccactcag	ctcagagaga	tatagcagct	720
gctgtgaggt	tcacagtggg	gactccccgt	atgaatcctt	tgatctacag	cctgaggaac	780
aaggacataa	aaggggctct	tgtaaaagtg	gttgctgtga	aatttttttc	tgttcaa	837

&lt;210&gt; 169

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g17 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 169

ttcattctct	ggggtttctt	tgaccacccc	tagccggaaa	tgtttctctt	cataatgggg	60
cttggtgctt	atctctgcat	actgggtggac	aacatctcaa	ttattgtggt	acccagggga	120
tattttaggg	gagcaccaaa	tgcattcatt	tagctgtgac	gtctttggat	ccttacattg	180
ccatctgcaa	acacttgagg	taccagcta	tcatgcatca	gcaactctgt	gtcctcctag	240
tggccatggc	atggctaagc	agtttggcca	actctacttc	agtcattcct	tgccgtccag	300
ctgccactag	gcggttaaaa	gggtggacgac	tttctgtgtg	aggtctcagc	gatgatcaag	360
atatcacgtt	ttgacaccac	attcaatgta	tctatgtctt	ccattgtgag	gatatttttag	420
tccctcgttc	tctaataaat	tatctttgct	tactgtggat	tcattgtagc	tactgtgctg	480
aggattcagt	cctcaggggg	aaagaaggag	gtcttcaaca	catgtggttc	tcattattgta	540
tctctctctt	atgggcctgt	aattagcatg	tatgtacagc	cctctgccaa	ctcccaggac	600
aaaaacaaat	tcattgtccct	gttctacagt	ttggtgactc	ctatgcttaa	cccttttctc	660
tacactttga	gcaacagggg	cataaaaagg	gcaatgagga	ggcttcttgt	ctttttgtat	720
caccaggaag	agaacaaaag	taattatttt	tatactccac	attcttcata		770

&lt;210&gt; 170

&lt;211&gt; 1003

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g18 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 170

tctacagacc	cacagaatgt	aacggatgtc	tctcgattcc	tcctcctcaa	actctcagag	60
gatccagaac	tgcagccggg	ccttgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggccgct	agccctgact	cccacctcca	cacttccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcccctccc	cacggtcccc	240
aagatgggtg	tggacatcca	atctcacagc	agtcacatcc	tatgcaggct	gcctgactca	300
gatgtctctc	tttgccattt	ttggaggcat	ggaagagaca	catgctcctg	aatgtgatgg	360
cctatgtccg	gtttgtagcc	atctgtcacc	ctctatatca	ttcagccatc	atgaaccctg	420
gtttctgtgg	cttcttactt	ttgttgctt	ttttttttct	cggctcttta	gacgcccagc	480
tgcacaacat	gattgcctta	caaatgacct	gcttcaagga	tgtggaaatt	cctaatttct	540
tctgtgatcc	ttctcaactc	ccccatcttg	catgttggtg	caccttcacc	aataacatca	600
tcatgtattt	ccctgctgcc	gtatttggtt	tccttcccat	ctcggggacc	cttttctctt	660
actctaaaat	tgtttcctcc	attctgaggg	tttcgtcatc	aggtgggaag	tataaacctt	720
ctccacctgt	gggtctcacc	tgctcagttt	ttgtcgattt	tatggaacag	gcattggagg	780
gtacctcagt	tcagatgtgt	catcttcctt	gagaagggtc	gcagtggcct	cactgatgta	840
caagatgggtc	acccccatgc	tgaacccctc	catctacagc	ctgagaaaca	gggatattaa	900
aagtgtcctg	cggcagccgc	acggcagcac	ggtctaattc	caagaccttc	ttatctgttc	960
cattcctttt	gtagtgtggg	ttaaaaaagg	cagcaagggtc	aaa		1003

&lt;210&gt; 171

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g19 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 171

atggatggag	agaatcactc	agtggatatc	gagtttttgt	ttctgggact	cactcattca	60
tgggagatec	agctccctcc	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaacatcc	tcattgtatt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
ttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtggtgt	gagatgggtc	tgctcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccccctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttggtgtcag	tcactccctg	ttccaactgg	480
catttcttgt	taattttacc	ttctgtggcc	ctaattgtgt	ggacagcttc	tactgtgacc	540
ttcctcggtt	tctcagacta	gcctgtaccg	acacctacag	attgcagttc	atggctactg	600
ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tgtaatctcc	tacatcttca	660
tcctgtttac	tgtttgga	catctctcag	gtgggtcacc	caaggccctt	tccactcttt	720
cagctcacag	cacagcggtc	cttttggtct	ttggtccacc	catgtttgtg	tatacatggc	780
cacaccctaa	ttcacagatg	gacaagtctt	tggctatttt	tgatgcagtt	ctcactcctt	840
ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaa	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttcttg	960
ttaaacatga	tatggcttta	tgtttctttc	tttgatat			998

&lt;210&gt; 172

&lt;211&gt; 1018

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g20 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 172

gatacagacc	cacagagtct	aacagatgtc	tctatattcc	tcctcctcga	actctcagag	60
gatccagaac	tgcagccggg	cctcgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctcaggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtcctttcct	gacagtctgt	tcacctccac	cacagtcctc	240
aagatgattg	tggacatcca	gtctcacagc	agagtcacat	cctatgcagg	ctgcctgact	300
cagatgtctc	tctttgccat	ttttggagac	atggaagaga	gacatgttcc	tgagtgtggg	360

ggcctatgac	cggtttgtag	ccatctgtca	ccctttat	cgttcagcca	tcttaaacc	420
ctgtttctgt	ggcttcttag	attcggtgtc	cttggttttt	ttttttttt	tttctcagtc	480
tttttagactc	ccagctgcac	aacttgattg	ccttacaaat	gacctgcttc	aaggatgtgg	540
aaattcctaa	tttcttctgg	gaacctctc	aactccccca	tcttgcatgt	tgtgacatct	600
tcaccaggaa	catcaacctg	tatttccctg	ctgccatatt	tgggtttctt	cccatctcgg	660
ggacgctttt	ctcttactat	aaaattgttt	ccttcattct	gagggtttca	tcacaggtg	720
ggaagtataa	accttctccg	cctgtgggtc	tcacatgtca	gttggttact	gagtttatgg	780
aacaggcttt	ggagggtacc	tcagttcaga	tgtgtcatct	tccccgagaa	agggtgcagt	840
ggcctcagtg	atgtacacgg	tggtcacccc	catgctgaac	cccttcattct	acagcctgag	900
aaacggggat	attaaaagt	tcttgcggca	gccgcacggc	agcacagtct	aatctcaata	960
tcttcttctc	tgttccattc	ctttttagt	gtgggttaaa	aaaggcagca	aggtcaaa	1018

&lt;210&gt; 173

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g21 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 173

atggagacaa	gaaaatactc	tgccatgact	gaattctttc	tgggtgggct	ttcccaatat	60
ccagagctcc	agctttttct	gttcctgtct	tgccatcatc	tgtacatgat	aatcctcctg	120
ggaaatagcc	tcctcattat	catcaccatc	ttggattctc	gcctccatac	tcccatgtat	180
ttctttcttg	gaaacctctc	attcttggac	atctgttaca	catcctcatc	cattcctcca	240
atgcttatta	tatttatgtc	tgagagaaaa	tccatctcct	tcattggctg	tgctctgcag	300
atggttgtgt	cccttggctt	gggtccact	gagtgtgtcc	tcctggctgt	gatggcctat	360
gaccactatg	tggccatctg	caacccactg	aggtactcca	tcacatgaa	cggagtgtg	420
tatgtgcaaa	tggctgcatg	gtcctggatc	ataggctgtc	tgacctccct	attgcaaaac	480
gttctgacaa	tgatgttgcc	tttctgtggg	aataatgtca	ttgatcatat	tacctgtgaa	540
attttggccc	ttctaaaact	tgtttgttca	gatatacaca	tcaatgtgct	tatcatgaca	600
gtgacaaata	ttgtttcact	gtgtattctt	ctactgttaa	tttcatctc	ctatgtgttt	660
attctctctt	ccatcctgag	aattaattgt	gctgagggaa	gaaagaaagc	cttctctacc	720
tgttcagcgc	actcgattgt	ggtcatctta	ttctacgggt	cagccctttt	tatgtacatg	780
aaacccaagt	caaagaacac	taatacatct	gatgagatta	ttgggctgtc	ttatggagtg	840
gtaagcccaa	tgttaaatcc	catcatctat	agcctcagga	ataaagaggt	caaagagggt	900
gtaaagaaag	tcctgagcag	acatctgcat	ttattgaaaa	tg		942

&lt;210&gt; 174

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g22 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 174

atgaagaata	aaaggaatgt	gactgaattc	gttttaacag	gtcttacaca	gaaccctaaa	60
atggagaaaag	tcatgtttgc	agtatttttg	gttctttaca	tgataaacact	ttcaggcaac	120
ctgctccttg	tggttacaat	taccaccagc	caggctctta	gctcccccat	gtacttcttc	180
ctgagccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtcgattccc	ttcatgagaa	gaaaatcatc	tcctttaatg	ggtgtatggc	tcaagcctat	300
gaagaacaca	tttttgggtc	tactgagatc	atcctgctga	cagtgtatggc	ctgtgacaac	360
tatgtggcca	tctgcaaac	tctgcactac	acaaccatca	tgagccacag	cctgtgcatt	420
ctcctagtgg	tagtggcctg	gataggagga	tttctccatg	caaataattca	gattctattt	480
acagtatggc	tgcccttctg	tggccccaat	gtcatagacc	acttcatgtg	tgacttgtgc	540
cctttgttaa	aacttgtttg	cctggacact	catacccttg	gtctctttgt	tgtgccaac	600
agtgggttca	tctgcttatt	aaacttcctt	ctctaggtgg	tatcctatgt	gatcatcttg	660
agatgtttaa	agaactatat	cttggagggg	aggggtaaaag	ccctctccac	ctgtatttct	720
cacatcataa	tagttgtctt	attctttgtg	ccttgtatat	ttgtgtatct	gcaccagtg	780
acaaactctg	cccattgata	aagctgctgc	tgtattttat	actatggtgg	tcccaatgtt	840

aaatcctttg atctacacac tcagaaatgc tgaggtaaaa agtgcaataa ggaagctttg 900  
 gagaataaaa gttatttcag ataatgacta aataagacca ttgagcactc atcataga 958

<210> 175

<211> 933

<212> DNA

<213> Unknown (H38g23 nucleotide)

<220>

<223> Synthetic construct

<400> 175

atgaggaatt tctcgggtgt gtccgaattc atcctgctgg gcatccctca cacggagggt	60
ctggagacta ttctgttggt cctgtttttg tccttctaca tcttcacct tatggggaac	120
ctgctcatct tgctggctat tgtctcctct gctcggcttc acacgcccac gtacttcttc	180
ctgtgcaagc tgtctgtttt tgacctatct ttcccttctg tgagttcccc taagatgctg	240
tgctatcttt caggggaacag ccgagccatc tcctatgcag gctgtgcac ccagctcttc	300
ttctaccatt tcctgggctg cactgagtgt ttccctgtaca cggatgagg ctacgaccgc	360
tttgttgcca tttgtcacc tctacgctac accataatca tgagccacag agcatgtatc	420
atcctagcca tggggacctc attctttggc tgcattcagg ccacctttct gacctctc	480
accttccaat tgccttactg tgtccccaat gaggtggact attatttctg tgatatccca	540
gtcatgctga agctggcttg tgcagatacc tcagccctgg agatgggtgg gttcatcagt	600
gtgggacctc tggccctcag ctgtttcctt ctcacctca cctcctacag tggcatcgtc	660
ttctccatct tgtagatctg ctctgcccag ggccgacgcc gtgccttctc cacctgcagc	720
gcccacctca ccgccatcct gcttttttac attgccagtg tctcattta cctgaggcct	780
acccacagcc tgtggttgga tgcaactgtt caaattctga ataacctggt caccctcatg	840
ctgaaccctc taatctacag tctcaggaat aaggaggtga aattatcact aaggaaggtc	900
ttatatcagc tgggcttcct tcctgagcag ttg	933

<210> 176

<211> 906

<212> DNA

<213> Unknown (H38g24 nucleotide)

<220>

<223> Synthetic construct

<400> 176

atggacatac cacaaaaatc cacagaattt ttcattgctgg ggctctcaca gaactcagag	60
gtacagagag ttctctttgt ggtctttttg ctgatctatg tggtcacggg ttgtggcaac	120
atgctcattg tggctactat cacctccagc cccacgctgg cttccctctg gtattttttc	180
ctggccaacc tatcctttat tgacaccttt tattcttctt ctatggctcc taaactcatt	240
gctgactcat tgtatgaggg gagaaccatc tcttatgagt gctgcatggc tcagctcttt	300
ggagctcatt ttttgggagg tgttgagatc attctgctca cagtgatggc ttatgaccgc	360
tatgtggcca tctgtaagcc cctgcacaat actaccatca tgaccaggca tctctgtgcc	420
atgctttagg ggggtggctg gcttgggggc ttcttgcatc cattgggttc gctcctctg	480
gtcctttggg tgcccttctg tgggccaat gtgatcaatc actttgcctg tgacttgtac	540
cctttgctgg aagttgcctg caccaatacg tatgtcattg gtctgctggg ggttgccaac	600
agtggtttaa tctgcctggt gaacttcctc atgctggctg cctcctacat tgtcatcctg	660
tactccttga ggtccacag tgcagatggg agatgcaag ccctctccac ctgtggagcc	720
cacttcattg ttgttgccct gttctttgtg ccctgtatat ttacttatgt gcatccattt	780
tctactttac ctatagacaa aaatatggca ttattttatg gtattctgac acctatgttg	840
aatccactca tttataccct gagaaatgaa gaggtaaaaa atgccatgag aaagctcttt	900
acatgg	906

<210> 177

<211> 798

<212> DNA

<213> Unknown (H38g25 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 177

atgatcacac	tgattgggct	cagttctcac	ctgcacacac	ctatgtacta	tttcctcagc	60
agtctgtcct	tcattgactt	ctgccattcc	actgtcatta	cccctaagat	gctgggtgaac	120
tttgcgacag	agaagaacat	catctcctac	cctgaatgca	tggtcagct	ctattttatc	180
agtatttttg	ctattgcaga	gtgtcacatg	ttggctgcaa	tggtgatga	ctgttatgtt	240
gccatctgca	gccccttgct	gtacaatgtc	atcatgtcct	atcaccactg	cttctggctc	300
acagtgggag	tttacatttt	aggcatcctt	ggatctacaa	ttcataccag	ttttatgttg	360
agactctttt	tgtgcaagac	taatgtgatt	aaccattatt	tttgtgatct	tttccctctc	420
ttggggctct	cctgctccag	cacctacatc	aatgaattac	tggttctggg	cttgagtgcg	480
tttaacatcc	tgatgcctgc	cttaaccatc	cttgcttctt	acatctttat	cattgccagc	540
atcctccgca	ttcactccac	tgagggcagg	tccaaagcct	tcagcacttg	cagctcccac	600
atcttggctg	ttgctgtttt	ctttggatct	gcagcattca	tgtacctgca	gccatcatct	660
gtcagctcca	tggaccagag	gaaagtgtcg	tctgtgtttt	atactactat	tgtgcccatt	720
ctgaaccccc	tgatctacag	cctgaggaat	aaagatgtca	aacttgccgt	gaagaaaatt	780
ctgcatcaga	cagcatgt					798

## &lt;210&gt; 178

## &lt;211&gt; 954

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g26 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 178

atgggaaact	ctaatacagtc	tttcatgaca	gaatttgtcc	tgctggggct	ttctggctac	60
ccagagctag	aggccattta	ctttgtgctg	gtcctatgta	tgtatttggg	gatcctgttg	120
ggaaatggag	tcatacatcat	tgtgagtgtt	tatgacaccc	acttgcacac	ccccatgtac	180
ttttctctca	gtaacttata	attcttggac	atctgtctaca	ctagttcatc	tattccacta	240
tttctcagca	gcttcttaac	gtcaaagaaa	actatttctc	tctctgggtg	tggagtgcga	300
atgtttctct	cttttgcctat	gggagcaaca	gagtgtgtcc	ttctaagtat	gatggcggtt	360
gactgctatg	tggccatctg	taaccctcta	tgatacccta	tcatacatgag	caaggcttca	420
tacatgtcca	tggctgcggg	gtcctggatt	ggaggaggca	tcaattctgt	gttgcaaac	480
tcccttgcaa	tgcggcttcc	tttctgtgga	gataacgtca	ttaatcattt	tacttgtgaa	540
atcttggctg	tcttaaaatt	ggcctgtgct	aatatctcca	taaataattat	tagcatgggt	600
gttgctagta	tgatttttct	tgtagggcca	gtacttttta	ttttgtttac	atatgttttt	660
attctctcca	ccatcctgag	aattccttct	gcagaaggaa	ggcacaaaagc	ctcctccacc	720
tgtctgtccc	acctaacagt	ggtgattata	ttctacagaa	ccatcctttt	catgtatgca	780
aagcccaagg	ctaaagactc	ttctggtgca	gacaaagaac	aagtcacaga	caaaatcatc	840
tccctgttct	atggagtggg	gacacctatg	cttaatcctc	ttatctatag	tttgaggaa	900
aaagacgtga	aggcagctgt	gaagagtata	ctgtgacaaa	aatgcttctt	ggaa	954

## &lt;210&gt; 179

## &lt;211&gt; 984

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g27 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 179

aaatctatga	aaaagatgaa	caatgtaata	gaattcatac	tgctggggct	cactcacaat	60
ccagaactgc	agaaattctt	gtttgttatg	tttttaatac	cctacttgat	cacattggca	120
ggtaacctgt	tcatactcagt	catcatcttc	atcagcccag	ccctgggttc	ccccatgtac	180
tcttttccgt	cctatttgtt	cattatagac	attttctgct	cttcttccat	agccccataa	240
atgaactttg	acttgatctc	tgaaaagaac	accataatct	tcaatggctg	catgactcag	300
ctcttcacag	aacatttctt	tacagaacat	ttctttgagg	cagctgagat	catcttatta	360
agtgtcatgg	cctatgacca	ctatgtggcc	atccgtaagc	ccttgcaacta	tgcaaccatc	420
atgagccaac	ctatgtgtgg	attcctgatg	gtggtggctg	ggattctggg	atttgtgcat	480

ggagggatcc	agactttgtt	catagcccag	ttaccattct	gtggcccaa	tgtcatcaac	540
cactttatgt	gtgatttagt	acctcttctg	gagctggcct	gcacagacac	tcacaccttg	600
gggaccttga	ttgctgccaa	cagtgggtca	ctgtgttccc	tcattttttc	catgctgggt	660
gcttcctatg	tcatactcct	gtgcttccctg	aggactcata	gctctgaagg	gcgtcgcaaa	720
gctctgtcta	gttgtgcctc	tcatactctc	attgtcatct	tattctttgt	ccctttttca	780
tacctgtatc	taagacctaa	cctccttccc	cactgacaaa	gctgtgactg	tgttttgac	840
cctatttaca	cctatgttga	accctttaat	ctacacctc	aaaaataaag	aagtgaaaaa	900
tgtcattaag	aagctctgga	agcaaataat	gacaactgat	gataaataag	tcttgtgaca	960
caaacattta	ggcaagaata	tctg				984

&lt;210&gt; 180

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g28 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 180

atggaatggg	aaaaccacac	cattctgggtg	gaattttttc	tgaagggact	ttctggtcac	60
ccaagacttg	agttactctt	ttttgtgctc	atcttcataa	tgtatgtggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcatc	ttggacctc	accttcacac	ccctatgtac	180
ttctttcttg	ggaacctctc	cttcttggac	atctgtctaca	ccaccacctc	tattccctcc	240
acgttagtga	gcttcctttc	agaaagaaag	accatttccc	ttcttggctg	tgcagtgcag	300
atgttcctcg	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcat	gatggccttt	360
gaccgctatg	tggctatctg	caacctctg	agatatccca	tcatcatgag	taaggatgcc	420
tatgtacca	tggcagctgg	gtcctggatc	ataggagctg	tcaattctgc	agtacaatca	480
gtgtttgtgg	tacaattgcc	ttcttgcagg	aataacatca	tcaatcattt	cacctgtgaa	540
attctggctg	tcatgaaact	ggcctgtgct	gacatctcag	acaatgagtt	catcatgctt	600
gtggccacaa	cattgttcat	attgacacct	ttgttattaa	tcattgtctc	ttacacgtta	660
atcattgtga	gcatcttcaa	aattagctct	tccgagggga	gaagcaaagc	ttcctctacc	720
tgttcagccc	atctgactgt	ggtcataata	ttctatggga	ccatcctctt	catgtacatg	780
aagcccaagt	ctaaagagac	acttaattcg	gatgacttgg	atgctaccga	caaaattata	840
tccatgttct	atgggggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaac	900
aaggatgtga	aagaggcagt	aaaacacctc	ctgaacagaa	ggttctttag	caag	954

&lt;210&gt; 181

&lt;211&gt; 792

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g29 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 181

atggtagaca	acctaatacat	tgtgggtgaca	atcaccacca	gcccagccct	ggactccccc	60
gtgtattttt	ttctgtcttt	cttttccttc	atagatggct	gctcctcttc	taccatggcc	120
cccaaaatga	tatttgactt	actcactgaa	aagaaaacta	tttccttcag	tgggtgcatg	180
accagctct	ttgtagaaca	tttctttggg	ggagttgaga	tcattctgct	cgtgggtgatg	240
gcctatgact	gctatgtggc	catctgcaag	cccctgtact	acctgatcac	aatgaacagg	300
caggatgtg	gcctcctggg	ggccatggca	tgggtcgggg	gatttcttca	cgctctgatt	360
caaatgcttt	taatagtctg	gctgcccttc	tgtggcccca	atgtcattga	ccatttcac	420
tgtgaccttt	tcctctgct	aaaactctcc	tgcactgaca	ctcacgtctt	tggactcttt	480
gttgccgcca	acagtgggct	gatgtgtatg	ctcatttttt	ctattcttat	tacctcttac	540
gtcctaatac	tctgtccaca	gcggaaggct	ctctctacct	gcgccttcca	tatcactgta	600
gtcgtcctat	tctttgttcc	ctgtatattg	gtgtaccttc	gacctatgat	caccttccct	660
attgataaag	ctgtgtctgt	gttttatact	gtggtaacac	ccatgttaaa	ccctttaate	720
tacacctca	gaacacacaga	ggtgaaaaat	gccatgaagc	agctctggag	ccaaataate	780
tggggtgaaca	at					792

&lt;210&gt; 182

<211> 936  
 <212> DNA  
 <213> Unknown (H38g30 nucleotide)

<220>  
 <223> Synthetic construct

<400> 182  
 atgtggccca atattactgc agcccccttt ttgctgactg gttttccagg gctggaggca 60  
 gctcatcact ggatctccat ccccttcttt gctgtttatg tgtgcatcct tctgggcaat 120  
 ggcattgctcc tctacctcat caagcatgac cacagtcttc atgagcccat gtactacttc 180  
 ctcaccatgc tggcaggcac agacctcatg gtgacattga ccacgatgcc tactgtaatg 240  
 ggcattcctat gggatgaatca cagggagatt agcagtgtgg gctgcttcct acaggcttac 300  
 tttattcact ccttttctgt tgtggaatca ggttccctcc tggcaatggc atatgatcgt 360  
 ttcattgccca tccgcaatcc tttgagatat gcttccattt tcaccaatac tagagtcata 420  
 gcgttaggag tgggagtgtt tctaaggggt tttgtatcca tcctgcctgt aattttgcgt 480  
 cttttttcat tttcatattg caaatctcat gttatcacac gtgctttctg cctccaccaa 540  
 gaaatcatga gactggcttg tgcagacata actttcaata gactttaccg tgaattttg 600  
 atctctttta caatcttct agactctctg atcatcctct tctcctatat tctaattctt 660  
 aatactgtca taggcattgc ctctggtgaa gagagagcca aagccctcaa tacctgtatc 720  
 tcccacatta gttgtgttct tatcttctat gttacggtga tgggtttgac attcatttac 780  
 agatttggga agaattgtgc agaggtgtgc cacattatca tgagttacat ctacttcctc 840  
 tttctcctt taatgaaccc tgtcatctac agcatcaaaa ccaagcaaat acaatatggc 900  
 attatccgcc ttttatctaa acataggttt agtagg 936

<210> 183  
 <211> 854  
 <212> DNA  
 <213> Unknown (H38g31 nucleotide)

<220>  
 <223> Synthetic construct

<400> 183  
 gacacagagc cacagaatct cacagctgtc tcagaattcc tcctcctggg actctcagag 60  
 gatccagaac tgcagcccat cctcgctggg ctcttctctg ccatgtacct ggtcacgggtg 120  
 ctgggggaac tgcctcattat cctggccatc ggctctgact cccacctcga ccccccatg 180  
 tacttcttcc tctccaacct gtccttgctt gacatcggtt tcacctcggc cagggtcccc 240  
 aagatgattg aggagatgca atcgcatagc agagtcatct accatgggga ctgctgacac 300  
 agatgtcttt ctttgtcctt tttgcatgta aggatgacat gatcctgact gtgatggcct 360  
 atgactgggt tgtggccatc tgtcaccccc tgaactaccc aggcattcat aatcctcacc 420  
 tctgtgtctt attagttttg gtgccttttt tccttagcct gttggattcc cagctgcaca 480  
 atttgattgt gttacaattc atctgcttca agaattgtga aatctctaatt tttttctgtg 540  
 acccgtttca acgtctcaac cttgcctggt ctgacagtga catcaataac atatacatat 600  
 atttagatag tactatattt ggttttcttc gcatttcagg gatccttttg tgttactata 660  
 cagttgtctt ccccatctta agaattccat cctcagatgg gaattataaa gccttctcca 720  
 cctgaggctc tcgcctggca gttgtttgct tattttatgg aacaggcatt ggcgtgtacc 780  
 tgacttcctc tgtgtcatca tccccagga atgatgtggt ggcgtcagta atgtacgctg 840  
 tggtgggtcac cccc 854

<210> 184  
 <211> 951  
 <212> DNA  
 <213> Unknown (H38g32 nucleotide)

<220>  
 <223> Synthetic construct

<400> 184  
 atgggtgaga ttaaccagac acttgtgtca gaatttcttc ttctgggtct ttctgggatac 60  
 ccaagattg agattgttta ctttgctctc attctagtta tgtacctagt gattctaatt 120

ggcaatggtg	ttctaatacat	agccagcatc	tttgattctc	attttcacac	accaatgtac	180
ttcttcctgg	gcaacctctc	tttcttgat	atctgctata	catcctctc	tggtccctca	240
acattggtga	gcttaatactc	aaagaaaaga	aacatttcct	tctctggatg	tgcatgtcag	300
atgttctttg	ggtttgcaat	ggggtcaaca	gaatgtctgc	ttcttggcat	gatggcattt	360
gatcggtatg	tggccatctg	caaccactg	agatacccca	tcacccctgag	caaggtggcg	420
tatgtattga	tggcttctgt	gtcctggctg	tccggtggaa	taaattcagc	tgtgcaaaca	480
ttacttgcca	tgagactgcc	tttctgtggg	aataatatta	tcaatcattt	cgcatgtgaa	540
atattagctg	tcctcaagct	ggcctgtgct	gatatatccc	tcaatattat	caccatgggtg	600
atatcaaata	tggccttcct	ggttcttcca	ctgatgggtca	tttttttctc	ctatatgttc	660
atcctctaca	ccatcttgca	aatgaattca	gccacaggaa	gacgcaaggc	attttccacg	720
tgctcagctc	acctgactgt	ggtgatcata	ttttacggta	ccatcttctt	tatgtatgcg	780
aaaccgaagt	ctcaagacct	gattggggaa	gaaaaattgc	aagcattaga	caagctcatt	840
tctctgtttt	atggggtagt	gacacccatg	ctgaatccta	tactctatag	cttgagaaat	900
aaggatgtaa	aagctgctgt	aaaatatttg	ctgaacaaaa	aaccaattca	c	951

&lt;210&gt; 185

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g33 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 185

atgggtgcca	agaacaatgt	gactgagttt	gttttatttg	gcctttttga	gagcagagag	60
atgcagcata	catgctttgt	ggtattcttc	ctctttcatg	tgctcactgt	cctggggaac	120
cttctgggtca	tcatacccat	caatgctaga	aagaccctga	agtctcccat	gtatttcttc	180
ctgagccagt	tgtcttttgc	tgacatatgt	tatccatcca	ctaccatacc	caagatgatt	240
gctgacactt	ttgtggagca	taagatcatc	tccttcaatg	gctgcatgac	ccagctcttt	300
tctgcccact	tctttgggtg	cactgagatc	ttcctcetta	cagccatggc	ctatgaccgc	360
tatgtggcca	tctgtaggcc	cctgcactac	acagccatca	tggattgccc	gaagtgtggc	420
ctgctagcgg	gggctctctg	gttagctggc	ttcctgcatt	ccatcctgca	gaccctcttc	480
acgggttcagc	tgcctttttg	tggggccaat	gagatagaca	acttcttctg	tgatgttcat	540
cccctgctca	agttggcctg	tgcagacacc	tacatggtag	gtctcatcgt	gggtggccaac	600
agcgggtatga	tttcttttagc	atcctttttt	atccttatca	tttctatgt	tatcatctta	660
ctgaacctaa	gaagccagtc	atctgaggac	cggcgtaagg	ctgtctccac	atgtgggtca	720
cacgtaatca	ctgtcctttt	ggttctcatg	ccccccatgt	tcatgtacat	tcgtccctcc	780
accaccctgg	ctgctgacaa	acttatcatc	ctctttaaca	ttgtgatgcc	acctttgctg	840
aaccctttga	tctatacact	aaggaacaac	gatgtgaaaa	atgccatgag	gaagctgttt	900
agggtcaaga	ggagcttagg	ggagaag				927

&lt;210&gt; 186

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g34 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 186

gctacttgcc	acttgatgaac	acacaatgcg	gctccttttt	tgctgcctgg	cttttcagta	60
ctggaggcaa	cttatcactc	gatctccatc	cccttctttg	ctgtttatgt	gtgcgtcctt	120
cttggcaatg	gcaagctcct	ctacctcatc	aagcatgacc	acagtcttca	cgaaccatg	180
tactgtttcc	ttgccacact	gaggcaagac	ctcatggtga	aattgaccat	gatgccact	240
gtaatgggcg	tcttgtggat	gaatcacaaa	gaggttatcc	atggggcctg	cttcttgacg	300
gtttacatta	tccactccca	ttatccactt	gcagaatcag	gtattctcct	gtcaatggcc	360
tatgaccgtt	tcattatcat	ccacatgctt	ctcaggtata	actctatttc	tactaaatct	420
tgggtgaaga	tagaactgtg	gctatttatg	agggactttt	tatccctcgt	gcctccaatt	480
ctgccactcc	attgcttccc	atattgtcat	tcccatgttc	tcttccacac	cttttttctc	540
catcaagatg	tcctgaaact	tgccgtgct	gatattacat	tcaatcactt	ataccagct	600
attctgggtg	ctttgatatt	cttcttagac	gctctgatca	ttgtcttttc	ttatatcctg	660

atccttaaaa	cagttatagg	tattgcctcc	agaaaagagc	aagccaaagc	tctcaacatg	720
tgtgtctccc	atatcagctg	tgtcttggtg	tttcacatca	ccgtgatcag	tgagactttc	780
attcacaggt	tgggaaaca	tgaccacat	gtggtgcaca	ttaccgtgag	ctaagtactc	840
atttcttttt	ctccattca	tgaaccctat	tatatacagc	atcaaaacca	gcagatccaa	900
agaagcattg	ttgcctatt	ttctgggcac	agaatggctt	gagccctttt	ttcagaattt	960
tgtgatcttc	atgatttctg	ggccttt				987

&lt;210&gt; 187

&lt;211&gt; 887

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g35 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(887)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 187

ctgctgctcc	tgggtgctct	gctgcccacg	ttcctgctga	gtcttntggg	gaacntgctc	60
atcatctcca	ctgctgctgc	ctgctcccgc	ctccacaccc	ccatgacttc	ttcttgtgca	120
acctctctat	cctggacatc	ctcttcacct	cagtcattct	tccaaaagtg	ttggccaact	180
taggatctag	ggataaaacc	atctcctttg	cggatgtat	caccagtg	tatttctact	240
ttttcttggg	cacagttgag	ttcctcctgc	tgacggtcac	gtcctatgac	tgctatgccg	300
ccatctgctg	ccccctgagg	tacaccacca	tcagagacc	ttatgtctgc	attgggaccg	360
ttgtgttctc	ttgggtggga	ggcttcctgt	ctgtgctctt	tccaaccatc	ctcatctccc	420
agctgccctt	ctgtggctcc	aatatcatta	accacttctt	ctgtgacagt	ggacccttgc	480
tggccctggc	ctgtgcagac	accactgcca	tcgagctgat	ggattttatg	ctttcttcca	540
tggtcacctt	ctgctgcata	gtcctcgtgg	cctatttcta	tacgtacatc	atcttgacca	600
taatgctcat	tccttctgca	agtgaagga	agaaggcctt	taatacctgt	gcttcccacc	660
tgaccatagt	catcatttct	agtggcatga	ctgtgtttat	ctatgtgact	ccctcccaga	720
aagaatatct	ggagatcaac	aagatccctt	cgttcttgag	cagtttgggtg	actccatttc	780
tcaaccctt	tatatatact	ctgaggaatg	acacagtgc	gggagtcctc	agggatgtgt	840
gggtcagggt	tcgaggaggt	ttcgaaga	ggatgagggc	agtgtctg		887

&lt;210&gt; 188

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g36 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 188

atgtggtata	acaacagtgc	tggcccttcc	ttgtgactg	gcttcttggg	ctcagaggca	60
gttcaactacc	ggatctctat	gtccttcttt	gtcatctact	tctccgtcct	ttttggaaat	120
ggcactcttc	ttgtcctcat	ttggaatgat	cacagcctcc	atgagcccat	gtactacttc	180
ctggctatgc	tggcagacac	ggaccttggg	atgacattca	ctacaatgcc	cacagtcctg	240
ggtgtcctgc	tgctagacca	gagggagatt	gcccatgctg	cctgtttcac	ccaatccttc	300
attcattcac	tggccattgt	agaatcaggt	atcttgcttg	ttttggccta	tgactgtttc	360
attgccatcc	gcacaccact	gaggtacaac	tgcattctta	ccaattcccg	agtgatgaac	420
ataggactgg	gggtactgat	gagaggtttt	atgtccattt	tgcccataat	tctttcactc	480
tactgtctacc	catattgtgg	tcccgtgccc	ctcttgacac	cattttgcct	ccatcaagat	540
gtcataaaac	tcgcctgtgc	tgatatcacg	tttaatcaca	tatatccaat	tattcagact	600
tctttgactg	tctttttaga	tgctctaate	atcatctttt	cttatatact	aatccttaag	660
acagtgatgg	gcattgcgtc	tggacaagag	gaagctaaat	ctctcaacac	ttgtgtctcc	720
catattagct	gtgtcctagt	atttcacatc	actgtgatgg	gactgtcatt	cattcacagg	780
tttgggaaac	atgcacctca	tgtgggtccc	attaccatga	gctatgtcca	ttttctcttt	840
cctccattcg	tgaatcctat	catttatagc	atcaagacca	agcagattca	aagaagcatt	900
attcgcctat	tttctgggca	gagttaggct				930



<210> 189  
 <211> 996  
 <212> DNA  
 <213> Unknown (H38g37 nucleotide)

<220>  
 <223> Synthetic construct

<400> 189  
 cacacagagc cacggaatct cacaggtgtc tgagaattcc tcctccttgg actcccagag 60  
 gatccagaac tgcagccggg tctcgttttg ctctccctgt cctgtgccat gtatctgggc 120  
 acggtgctga ggaacctgct catcatcctg gctgtcagct ctgtctctcc cctccacacc 180  
 cccatgtact tcttctcttc caacctgtgc tgggctgaca tcggtttcac ctcgccacg 240  
 gttcccaaga tgattgtgga catgcagtcg catagcagag ccatctctca tgcgggctgt 300  
 ctgacgcaga tgtctttctt gttccttttt gcatgtatag aaggcatgct cctgactgtg 360  
 atggcctatg actgctttgt agccatctgt cgccctctgc actaccagc catcgtgaat 420  
 cctcacttct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt ggattcccag 480  
 ctgcacagtt ggtattgtgt acaattcacc atcttcaaga atgtggaaat ctctaatttt 540  
 gtctgtgacc cctctcaact tctcaaactt gcctgttctg acggcgctcat caatagcata 600  
 ttcatatatt ttgatagtac tatgtttggt ttccttccca tttcagggat cctatggtct 660  
 tactataaaa tcgtcccttc cattctaagg atttcacgt cagatgggaa gtataaagcc 720  
 ttctccacct gtggtcttca ccaggcagtt gtttgctgat tttatagaac aggcattggc 780  
 atgtacctga cttcagctgt gtcaccaccc cccaggaatg gtgtggtggc atcattgata 840  
 tacgctgttg tcactcccat gctgaacctt ttcactaca gcctgagaaa caggacata 900  
 caaagtgcc tgcggaggct gctcagcaga acagtcgaat ctcatgatct gttccatcct 960  
 ttttcttggg gggtagagaa gggcaaccac attaaa 996

<210> 190  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g38 nucleotide)

<220>  
 <223> Synthetic construct

<400> 190  
 atgggagaca atataacatc catcagagag ttcctcctac tgggatttcc cgttgggcca 60  
 aggattcaga tgcctctctt tgggctcttc tccctgttct acgtcttcac cctgctgggg 120  
 aacgggacca tactggggct catctcactg gactccagac tgcacgcccc catgtacttc 180  
 ttcctctcac acctggcggg cgtcgacatc gcctacgcct gcaacacggg gccccggatg 240  
 ctggtgaacc tcctgcatcc agccaagccc atctcctttg cgggcccgcg gatgcagacc 300  
 tttctgtttt ccacttttgc tgtcacagaa tgtctctcc tgggtggtgat gtcctatgat 360  
 ctgtacgtgg ccatctgcca cccctccga tatttgacca tcatgacctg gagagtctgc 420  
 atcaccctcg cggtgacttc ctggaccact ggagtccttt tatccttgat tcatcttggt 480  
 ttacttctac ctttaccctt ctgtaggccc cagaaaattt atcacttttt ttgtgaaatc 540  
 ttggctgttc tcaaacttgc ctgtgcagat acccacatca atgagaacat ggtcttggcc 600  
 ggagcaattt ctgggctggg gggacccttg tccacaattg tagtttcata tatgtgcac 660  
 ctctgtgcta tccttcagat ccaatcaagg gaagttcaga ggaaagcctt ccgcacctgc 720  
 ttctcccacc tctgtgtgat tggactcgtt tatggcacag ccattatcat gtatgttggg 780  
 cccagatatg ggaaccccaa ggagcagaag aaatatctcc tgctgtttca cagcctcttt 840  
 aatcccatgc tcaatcccct tatctgtagt cttaggaact cagaagtga gaatactttg 900  
 aagagagtgc tgggagtaga aagggcttta 930

<210> 191  
 <211> 968  
 <212> DNA  
 <213> Unknown (H38g39 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 191

cacacagagc	cacggaatct	cacgggtgtc	tgagaattcc	tcctcctggg	aatctcagag	60
gatccagaac	tgagcccgt	cctcgctggg	ctgaccctgt	ccatgtacct	ggtcacgggtg	120
ctgaggaacc	tgctcatcat	cctggctgtc	agctctgact	cccacctcca	cacctccatg	180
tacttcgtcc	tctccaacct	gcgctgggtt	gacatcggtt	tcacctcggc	cacgggtccc	240
aagatgattg	tgacatgca	gtcgcatagc	agagtcacct	cttatgcggg	ctgcctgaca	300
cagatgtctt	tcttggtctt	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatgtcc	360
tatgaccaat	ttttggccat	ctgtcacccc	ctgcactacc	cagtcacgt	gaatcctcac	420
ttctgtgtct	tcttagtttt	ggtgtccttt	ttccttagcc	tgttggattc	ccagctgcat	480
agatggattg	tgttacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttctcaa	ccttgctgt	tctgacagcg	tcataaatat	catattcata	600
tatttagata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaattgtcc	cctccattct	aaggatgtca	ttgtcagatg	tgaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttttttgc	ttattttacg	gagcaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	accttccggc	aatgggtgtg	tggcttcagt	gatgtacact	840
gtggtcacc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacaggga	cattcaaagt	900
gccccgtgga	ggctgcgag	cacaacagtt	gaatctcatg	atctcttcca	tcctttttct	960
tgtgtctg						968

&lt;210&gt; 192

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g40 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 192

cacacagagc	cacagaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgagcccat	cctggctggg	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgaggaacc	tgctcatcat	cctggctgtc	agctctgacc	cccacctcca	cacccccatg	180
tgcttcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcaccttggc	cacgggtcct	240
aagatgattg	tgacatgca	gtctcatacc	agagtcacct	cttatgaggg	ctgcctgaca	300
cggatatctt	tcttggtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcacgt	gaatcctcac	420
ctctgtgtct	tcttcttttt	ggtatacttt	ttccttagct	tgttggattc	ccagctgcac	480
agttggattg	tgttacaatt	caccatcatc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gacccctctc	aacttctcaa	acttgctgt	tctgacagcg	tcataaatag	catattcatg	600
tatttccata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaatcgtcc	cctccattct	aaggatttca	tcacagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacttggc	agttgtttgc	tgattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	acccccagg	aatgggtgtg	tagcgtcagt	gatgtacgct	840
gtggtcacc	ccatgctgaa	ccttttcatc	tacagcctga	gaaacaggga	catacaaagt	900
gcctgcgga	ggctgctcag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

&lt;210&gt; 193

&lt;211&gt; 980

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g41 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 193

tctacagact	gacagagtct	aacaggtgtc	tctatattcc	tcctcctaga	actctcagag	60
gatccagaac	tgagccggg	cctcgctggg	ctgttcctgt	ccatgtgcct	ggtaaggtg	120
ctggggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	catgggtccc	240
aagatgattg	tggaaatccaa	tctcacagca	gagtcattctc	ctatgcaggc	tgctgtactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaaagagag	acatgtctct	gagtgtgatg	360

gcctatgacc	ggtttgtagc	catctgtcac	cctctatata	attcagccat	catgaacccg	420
tgtttctgtg	gcttcctagt	tttgetgtct	tttttttctt	tctttttctc	agctgcacaa	480
cttgattgcc	ttaaaaatga	cctgcttcaa	gaatgtggga	attcctaatt	tcctctgtga	540
cccttctcaa	ctcccccatc	tcacatgttg	tgacaccttc	accaatcaca	taatcatgta	600
tttccccgct	gccatatttg	gtttttcttc	catctcgggg	acccttttct	cttaccatgt	660
aattgtttcc	tccattctga	gggtttcatc	atctgtggga	ggtgtaaagc	cttccccatc	720
tgtgagttgt	ttgctgatat	tatggaacag	gctttggagg	gtacctcagt	tcagatgtgt	780
catcttccct	gagaaaggct	gcagtggcct	cagtgatgta	catggtggtc	acacccatgc	840
tgaacccctt	catctacagc	ctgagaaaca	gggatattaa	aagtgtcgtg	cagcggccgc	900
atggcagcac	ggtctaattc	caatatcttc	ttatctgttc	cattcctttt	gtagtgtggg	960
ttaaaaaagg	cagcaaggtc					980

&lt;210&gt; 194

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g42 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 194

atgggaaact	ggagcactgt	gactgaaatc	accctaattg	ccttcccagc	tctcctggag	60
attcgaatat	ctctcttcgt	ggttcttgtg	gtaacttaca	cattaacagc	aacaggaaac	120
atcaccatca	tctccctgat	atggattgat	catcgccctg	aaactccaat	gtacttcttc	180
ctcagtaatt	tgtcctttct	ggatatctta	tacaccactg	tcattacccc	aaagtgtgtg	240
gcctgcctcc	taggagaaga	gaaaaccata	tcttttctgt	gttgcatgat	ccaaacatat	300
ttctacttct	ttctggggac	gggtggagttt	atcctcttgg	cgggtgatgtc	ctttgaccgc	360
tacatggcta	tctgcgaccc	actgcactac	acggtcatca	tgaacagcag	ggcctgcctt	420
ctgctgggtc	tgggatgctg	gggtgggagcc	ttcctgtctg	tgttgtttcc	aaccattgta	480
gtgacaaggc	tacccttactg	taggaaagaa	attaatcatt	tcttctgtga	cattgcccct	540
cttcttcagg	tggcctgtat	aaatactcac	ctcattgaga	agataaaact	tctcctctct	600
gcccttgcta	tcctgagctc	cctggcattc	actactgggt	cctacgtgta	cataatttct	660
accatcctgc	gtatccccctc	cacccagggc	cgtcagaaag	ctttttctac	ctgtgcttct	720
cacatcactg	ttgtctccat	tgccacggg	agcaacatct	ttgtgtatgt	gagacccaat	780
cagaactcct	cactggatta	tgacaagggtg	gccgctgtcc	tcacacagct	ggtgaccctt	840
ctcctgaacc	cttttatcta	cagcttgagg	aatgagaagg	tacaggaagt	gttgagagag	900
acagtgaaca	gaatcatgac	cttgatacaa	aggaaaaact			939

&lt;210&gt; 195

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g43 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 195

atgggaaata	tcaacataag	tcttgaaaat	tactttattc	tactgggtct	ttctaattga	60
cctcctctgg	aaatagttat	ttttgtagtt	ctcttgatat	tctgcttcat	gacactgata	120
ggcaagctgt	tcagcatcat	tctgtcatac	ctggactccc	atccccacac	tctcggtaet	180
tattctcttt	tctggatttc	tgtacacca	tcagttccat	cttttaatta	cagtacaatc	240
tctggggccc	acagaagaac	atctcttatg	ccagtgggtat	gattcaaatt	tattttgttc	300
tcacactggg	aacctgggat	tgcgctctac	tgggtgggtg	gtccaggact	gtgatgcagc	360
tggacacaga	cacttgccct	atactgttgt	tatggctgtg	gctttttggg	taagttagctt	420
taccaactca	gcatttgatt	ccttttttac	cttctgggta	accctgtgtg	gacatcacta	480
ttatgcttac	atctttatat	ttacatcatt	gttagtataa	agatggttca	ttaacagaaa	540
gaaacagtct	gtgttctcac	tgaatcatgc	agctttatta	acattatctt	ttccattata	600
aaatgactgc	ttccaggaga	ttgaaaagaa	catgttaaga	aaagcacagc	attggagaaat	660
ctgaaagcat	gtgatcttgt	tcaattaaac	caagtatcaa	aaacatgcat	ttttatgaga	720
ctatttttagg	aaattca					737

<210> 196  
 <211> 949  
 <212> DNA  
 <213> Unknown (H38g44 nucleotide)

<220>  
 <223> Synthetic construct

<400> 196  
 gacatccaaa atcagaccac agtgactgag tttaccctga cggcctttcc ggttcttcag 60  
 cagcttcaaa tttccctttt ggcagtcctc tgggttactt atatgcttac tctaacagga 120  
 aacggttgcca tcatctccct aacatgtgag aatcatcgcc tccaaacccc aatgtacttc 180  
 ttcctcagta attggtcaat ttgggacatt tttttcacca cctcagttat cccaaagcta 240  
 ttagcctgtc tcctgcagga caagaagacc atatctttgg ctgggtgcat caccctaaact 300  
 tatttccttg gttttctggg ggacagtggg gtttatcctc tgggcagtga tgccttttga 360  
 ctgctacgtg gccatctgtg acccctgca ctacaccatt atcatgaaca gcagggcctg 420  
 cctcctacta gttctgggct gctgggttgg agccttcctg tctgtgttgt gcccaccat 480  
 tgtggtgtcc agattgcctt tctgttaciaa ggaaattagt cacttcttct gtgacatcac 540  
 cctctgcta catgtgtcct gtatagacac tcatttcac gagatgataa acttcctctt 600  
 atcttccctc atcctcctga cctcactggt gctcaccact gtgtcctaca tctacatcat 660  
 ttctaccatc ctgcacatcc cctcagccca aggacgtcgg aaggcctttt ccacgtgcgc 720  
 tccccacatc accgtcattt ccatcgctta tataagcaac atcttcaggt atgtgaggcc 780  
 cagccagagt cattcaatgg gttttgacaa ggtgacagct gtccccacaa tgggtgacccc 840  
 tcttctgaat cccttcactt atagtctaag aaatgaaaag gtaaaggcag tcttgaaaga 900  
 agcagtcagc aaaattatgt cctcatggca caggagaact taaaacttt 949

<210> 197  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g45 nucleotide)

<220>  
 <223> Synthetic construct

<400> 197  
 atggaaccac agaaccacac acaggtatca atgtttgtcc tcttaggggtt ttcacagacc 60  
 caagagctcc agaaattcct gttccttctg ttcctgttag tctatgttac caccattgtg 120  
 ggaacacctc ttatcatggt cacagtgaact tttgactgcc ggctccacac acccatgtat 180  
 tttctgtccc gaaatctagc tctcatagac ctctgtctatt ccacagtcac ctctccaaag 240  
 atgctggtgg acttctctca tgagaccaag acgatctcct accagggctg catggcccag 300  
 atcttcttct tccacctttt gggaggtggg actgtctttt ttctctcagt catggcctat 360  
 gaccgtaca tagccatctc ccagcccctc cggatgtgca ccatcatgaa cactcaattg 420  
 tgtgtgggcc tggtagtagc cgcctgggtg gggggctttg tccactccat tgtccaactg 480  
 gctctgatac ttccactgcc ctctctgtgac cccaatatca tagataactt ctactgtgat 540  
 gttccccaag tactgagact tgcctgcact gatacctccc tcctggagtt cctcatgac 600  
 ttcaacagtg ggctgctagt tatcatctgg ttctcctccc ttctgatctc ttatactgtc 660  
 atcctggtga tgcctgaggtc ccactcggga aaggcaagga ggaaggcagc ttccacctgc 720  
 accaccaca tcacgtggtg gtccatgac ttcatctcct gtatctatat ctatacctgg 780  
 cccttaccac cattcctcat ggacaaggct gtgtccatca gctacacagt catgacccc 840  
 atgctcaacc ccatgatcta caccctgaga aaccaggaca tgaaagcagc catgaggaga 900  
 ttaggcaagt gcctagtaat ttgcagggag 930

<210> 198  
 <211> 932  
 <212> DNA  
 <213> Unknown (H38g46 nucleotide)

<220>  
 <223> Synthetic construct

<400> 198

gaccaagaaa atcagacttc tgaagtcacc ttcacccctc tgggcttctc agaatatcca	60
gaccttcaga cgcctctgtt cctgggtgtc ctgacctatc acacagtcac tgtgctgggg	120
aatctgggca tgatcatagt catcaggatc agcccaaac tccacacccc catgtgcttt	180
tcctcagcc acttgctctt tgttgattc tgttattcca ccacaattac acccaaaactg	240
ctggagaact tgggtgtgga agatagaact atctccttca caggatgcac catgcagtta	300
ttctttgtct gcatatttgt agtaacagaa acattcatgc tggcagtgat ggcctatgac	360
cgatatgtgg cgggtgtgta ccctcttctc tacacagttg caatgtacca gaggctttgc	420
tccttggttag tggtacatc atactgttg gggatagtct gttccctgac acttacctag	480
tttctactgg aattatcctt cagaggaaat aatatcatta ataactttgt ctgtgagcac	540
gctgccattg ttgctgtgtc ttgctctgac cctctgtgtg gccaggagat cactttagtt	600
ttggccacat tcaatgaaat aagcagcctg ctctctatgc tttcattttt atcactgtca	660
tgaagacgcc ttccactggg gggcgcaaga aagcgttctc cagctctgcc tcccacttga	720
cggccattac cattttccat gggactatcc ttttctcta ctgtgttctt aactccaaa	780
gttcgtggct catggccaag gtggcctctg tcttttacac agtggtcatt cccatgtgta	840
accccttgat ctatagctc aggaacaaag atgtaaaaga gacagttagg aggttactca	900
ttaccaaatt attatgtctc atattataaa at	932

&lt;210&gt; 199

&lt;211&gt; 1000

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g47 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 199

tatgcagacc cacagaatct aacagatgtc tctatatctc tcctcctaga agtctcaggg	60
gatccagaac tgcagccagt ccttgctggg ctgttctctg ccatgtgcct ggtcacgggtg	120
ctggggaacc tgctcatcat cctggccatc agccctgact cccacctcca caccctcatg	180
tacttcttcc tctccaacct gtccttgctt gacatcgggt tcacctccac cacggtcccc	240
aagatgattg tggacatcca gtctcacagc agagtcactc cctatgcagg ctgcctgact	300
cagatgtctc tctttgccc atgttgagga gacatgctcc tgagtgtgat	360
ggcctatgac tggttttagt ccatctgtca cccgctatat cattcaccat catgaaccgg	420
tgtttctgtg cctttctagt tttgttgtct ttttttttct cagtctttta gactcccagc	480
tgcacaactt gattgcctta caagtgaact gcttcaagga tgtggaaatt cctaatttct	540
tctgtgaccc tctcaactc tcccatcttg catgttgtga caccttcacc attaacataa	600
tcatgtattt cctgtctgcc atatttggtt ttcttcccat cttggggacc cttttctctt	660
tctctaaaat tgttctctc attctgaggg ttcttctatc aggtgggaag tataaagccc	720
tctccacctg tgggtctcgc ctgtcagttg tttgtcaggt ttatggaaca ggcgttgag	780
ggtacctcag ttcagatgtg tcatcttccc ccagaaaggg tgcagtgagg tcagtgtatg	840
acacactggt caccctcatg ctgacccctt tcatctacag cctgagaaac agggatatga	900
aagggtgctt gcggcagcgg cacggcagca cagtctaate tcaatatctt atctgttcca	960
ttcctttgta gtgtgggttc aaaaaggcag caaggtcaaa	1000

&lt;210&gt; 200

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g48 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 200

atggaaacag ggaacctcac gtgggtatca gactttgtct tcctggggct ctgcagact	60
cgggagctcc agcgtttcct gtttctaatt ttctgtttg tctacatcac cactgttatg	120
ggaaacatcc ttatcatcat cacagtgaac tctgattccc agctccacac acccatgtac	180
tttctgtctc gaaacctggc tgctcctagac ctctgtttct ctccagtcac tgctcccaaa	240
atgctagtgg acctcctctc tgagaagaaa accatctctt accagggtcg catgggtcag	300
atcttcttct tccacttttt gggaggtgcc atggctttct tcctctcagt gatggccttt	360
gaccgctca ttgccatctc cgggcccctc cgctatgtca ccgtcatgaa cactcagctc	420
tgggtggggc tgggtggtag cacctgggtg ggaggctttg tccactctat tgtccagctg	480

gctctgatgc	tcccactgcc	cttctgtggc	cccaacattt	tggataactt	ctactgtgat	540
gttccccaag	tactgagact	tgctgcact	gacacctcac	tgctggagtt	cctcaagatc	600
tccaacagtg	ggctgctgga	tgtcgtctgg	ttcttcctcc	tcctgatgtc	ctacttattc	660
atcctggtga	tgctgaggtc	acatccaggg	gaggcaagaa	ggaaggcagc	ttccacctgc	720
accaccaca	tcctcgtggt	ttcatgata	ttcgttccaa	gcatttacct	ctatgcccgg	780
cccttcaact	cattccctat	ggacaagctt	gtgtccatcg	gccacacagt	catgaccccc	840
atgctcaacc	ccatgatcta	taccctgagg	aaccaggaca	tgcaggcagc	agtgagaaga	900
ttaggagagc	accggctggt	t				921

&lt;210&gt; 201

&lt;211&gt; 947

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g49 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 201

cacacagagc	cacagaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgacagccgt	cctcgctttg	ctctccctgt	ccctgtccat	gtatctgggc	120
atgggtgctg	ggaacctgct	cagcctcctg	gctgtcagct	ctgtctctcc	cctccacacc	180
cccacctgtg	ctgggctgac	atcgggtttca	ccttggccac	ggttcccaag	atgattgtgg	240
acatgcagtc	gcatagcaga	gtcatctctc	atgcgggctg	tctgacgcag	atgtctttct	300
tcctcctttt	tgcatgtata	gaaggcatgc	tcctgactgt	gatggcctat	gactgctttg	360
tagccatctg	tcgcccctctg	cactaccctg	tcctcgtgaa	tcctcacctc	tgtgtcttct	420
tcgttttggg	gtcctttttc	cttagcctgt	tggattccca	gctgcacagt	tgaattgtgt	480
tacaattcac	catcatcaag	aatgtggaaa	tctctcattt	tttctgtgac	ccctctcaac	540
ttctcaaact	tgctgtttct	gacagcgtca	tcaatagcat	attcatatat	ttcgatagta	600
ctatgtttgg	ttttcttccc	atttcaggga	tcctatgggc	ttactataaa	atcatcccct	660
ccattctaag	gatttcatca	tcatatggga	agtataaagc	cttctccaca	tgtgcctctc	720
acctagcagt	tggtttgctg	ttttatgtaa	caggcattgg	catgtacctg	acttcagctg	780
tgtcaccacc	ccccagcaat	ggtgtagtgg	cgtcagtgat	gtatgtgcg	gtcactccca	840
tgctgaaccc	tttcatctac	agcctgagaa	acagggacat	acaaagtgcc	ctgcggaggg	900
tgctcagcag	aacagtcgaa	tttcatgata	tggtccatcc	tttttct		947

&lt;210&gt; 202

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g50 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 202

atgtctggct	cccccaactca	actgacagca	ggccccagga	cagccagtgg	ctgtgtcatc	60
atgatctgct	ttgcccctcac	tgtcctctct	tacatccgca	tcttggccac	agtggttcag	120
atccgttcag	cagccagccg	ccggaaggcc	ttctccacct	gttcttccca	cctgggcatg	180
gtgctcctgt	tctatggcac	cggcagctcc	acctacatgc	gacccaccac	ccgctactcc	240
ccgctggaag	ggcgcttggc	tgtgtcttct	tactccatcc	tcataccac	cctgaatccg	300
ctcatctaca	gcctgaggaa	ccaggacatg	aagagagccc	tgtggaagct	ctatctccag	360
gtgccatac						369

&lt;210&gt; 203

&lt;211&gt; 1068

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g51 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 203

atgatcaatg atagccactt cagtgggtttt atactccttg gattcacagg gcagcctcag	60
cttcagatga tgatctcttg ggttgctctt ttcttctaca ctattgcctt catgggaaat	120
atggccatca tectattgtc ttctctagat gaccatctcc aagtcccat gtactttctt	180
cttagaaatt tggccatctt ggatctctgt tataccacaa atatagtccc acaaatgttg	240
gtcagtatct ggggcaaaga caaaagaatt acctttgggtg ggtgtgcctt tcaacttttc	300
attgatgtgg cactgtactc agttgaatgc atccttctgt ccatgatgtc atatgatcga	360
ctcaatgcta tctgcaagcc tctgcatcat atgaccataa tgaacctcca actctgccag	420
ggccttggtg tcatctcctg ggtagttggt gtgattaatt gcatcatacc ttccccctat	480
gccacgagtc ttctcctgat taggaaccac cacctagacc acttttttgt gtgtgtgaaa	540
tgcttgcaat gatcaagatt caagattgca tgtgtggaca ccacagccat ggaggttaacc	600
acatttgcca tgtgcctgat tatagttctt gttcctcttc ttcttattct tgtgtcatat	660
ggtttcattg ctgtggctgt actcaagatc aagtctgcag caggaagaca aaaagcattt	720
gggacctgtt cctcccatct cgttgtggta tccatcttct gtgggacagt tacatacatg	780
tatatacagc caggaaacag tccaaatcag aatgagggca aacttctcag tatattttac	840
tccattgtta ctcccagctt gaacccatta atttatacgg taaggaataa ggagttcaag	900
ggggccatga agaggctaac tggaaaagaa aaagattgca tggaaaaaag aggacattga	960
ttcttctctc cagcaatttc taatatggca attgatcttc ccaatctaaa atgtagacaa	1020
tttattttgt aaataaattg tctacacctg agataaagat aatatcca	1068

&lt;210&gt; 204

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g52 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 204

atgatcaatg atagttactt tggttggctt atgctccttg ggttccctgg gaagcctcag	60
ctggagatga tcatctcttg ggttgctctt ttcttctatg caatttcttt gatgggaaat	120
atggctctta tctgctgcc attactggat aaacatctcc aaaccccat atatttcttt	180
cttagaaatc tggctatctt ggatctttgt tacaccacaa atatagtccc acagatgttg	240
gtcaatgcct ggggtaaaga caagaaaatc acttttgggtg gctgtgcttt tcaacttttc	300
actaatgtga cgctatgcac ggttgaatgt atgcttcttg ctgtgatgtc atatgacca	360
ttcaatgctg tctgcaagcc tctggactat atgaccataa tgaaccccca actctgtcaa	420
ggcctgggtg ccatgacctg gtttaattggt gtcactaatt gcatgatact ttccccctgt	480
cctgtgagtc ttctcctgat cggagaccac cacctggatc actatttttg tgaatatct	540
gcaatggta aaattgcatg tggggctacc acagtcatgg aggaaaaacc ttatttgcac	600
tgtgtgtgtg ttgttgtttt catttctctt gcatcacttc ttctcattct tgtgtcatat	660
ggcttcattg ctgtggctgt actcaagatc aagtctgcag caggaagaca aaaagcattt	720
gggacctgtt tctcccatct cattgtggta tccatcttct atgggactgt tagatatatg	780
tatatagagc caggaaacag tccatctcag gatgagggca aacttctcca tatattttac	840
tccattgtta ctcccacctt gaacccatcc cactaaggaa taaggagttc aagtgggcca	900
tgaaaaggct tattggaaaa gaaaaagggt ctggagacac aataggtca	949

&lt;210&gt; 205

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g53 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 205

atgggttaacc aaagctccac accgggcttc ctcttcttg gcttctctga acaccaggg	60
ctggaaagga ctctctctgt ggttgctctt acttctctacc tcctaaccct agtgggcaac	120
acactcatca tctgctgtc tgcgctggac cccaagctcc actctccaat gtactttttc	180
ctctccaacc tctcttctt ggacctctgt ttccaccaga gttgtgttcc ccaaatgctg	240
gtcaacctct ggggcccaaa gaagaccatc agcttcttg actgctctgt ccagatcttc	300
atcttctgt ccctggggac aactgagtgc atcctcttga cagtgatggc ttttgatcgc	360
tacgtggctg tctgccagcc cctccactat gccaccatca tccacccccg cctgtgctgg	420

cagctggcat	ctgtggcctg	ggtcattggg	ctagtggagt	cagtgggtcca	gacaccatcc	480
accctgcacc	tgcccttctg	ccccgatcgg	cagggtggatg	atthttgtctg	tgagggtccca	540
gctctaattc	gactctcctg	tgaagacacc	tcctacaatg	agatccagggt	ggctgttgcc	600
agtgtcttca	tcttggttgt	gcctctcagc	ctcatccttg	tctcttacgg	agccattacc	660
tgggcagtg	tgaggattaa	ctctgcaaaa	gggcggagga	aagcttttgg	gacctgctcc	720
tcccatctca	ctgtgggtcac	cctcttctac	agctcagtca	ttgtgtgcta	cctccagccc	780
aaaaatccct	atgcccaga	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcaact	840
ccttcactta	accctctcat	atacaccctg	aggaacaagg	aggttaaccag	ggcattcagg	900
agattgctgg	ggaaggaaat	ggggctcaca	caaagc			936

&lt;210&gt; 206

&lt;211&gt; 1030

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g54 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 206

atggttaacc	aaagctccgc	accaggcttt	ctccttctgg	gcttctctga	acacccagca	60
ctggaaagga	ctctctttgt	agttgtcttc	acttctacc	tcctaaccct	ggtggactca	120
tcactctgct	gtctgtgctg	gaccccaggc	tcactctcc	aatgtacttt	ttcctctcca	180
acctctcctt	cttggaacctc	tgtttcacca	taagttgtgt	ccccgggatg	ctggtcaacc	240
tctgggagcc	aaagaagacc	atcatcttac	tgggctgctc	tgtccagttc	ttcatcttcc	300
tgtccctggg	gaccactgag	tgcatcctcc	tgacggtgat	ggcctttgac	cgctacatgg	360
ctatcttcaa	gcccctgcgc	catgccacca	tcgtccacct	ctgcctgtgc	tggcagctgg	420
catctgtggc	ctgggtcatt	gggctggtag	agtcagtggg	ccagacacca	tccaccctgc	480
gcctgccttt	ctgcccccat	cagcagggtg	atgattttgt	ctgtgagggtc	ccagctctaa	540
ttcgactctc	ctgtgaagac	acctcctaca	atgagatcca	gatggctgtt	gccagtgtct	600
tcactctggc	tgtgcctcag	cctcatcctt	gtctcttatg	gagccattgc	ctgggcagtg	660
ctaaggacta	actgcaaaag	ggcagaggaa	agcttttggg	acctgtcct	cccactctac	720
tgtggtcacc	ctcttctaca	gtcagtcatt	tgctgtctac	ctccagccca	aaaatcccta	780
tgcccaagag	aggggcaagt	tctttgggtc	cttctatgca	gtgggcactc	cttcaactaa	840
ccctctcata	tacaccctga	ggaacaagga	ggtaaccagg	gcattcagga	gattgctggc	900
gaaggaaatg	gggctcatat	aaagttgagg	gagagctgtt	taatgtgctt	tctaaattaa	960
gaagaaatta	tttatccttt	tgtgaacaag	tttgaagctc	caagtatact	acctttcata	1020
caccatcac						1030

&lt;210&gt; 207

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g55 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 207

atgttcgccc	cccttgctct	cctgtgctac	ctcctgacct	tgacgggcaa	ctcggcgctg	60
gtgctgctgg	cgggtgcgca	cccgcgcctg	cacacgccc	tgtactactt	cctctgccac	120
ctggccttgg	tagacgcggg	cttcaactact	agcgtgggtc	cgccgctgct	ggccaacctg	180
cgcgaccag	cgctctggct	gcccgcagc	cactgcacgg	cccagctgtg	cgcatcgctg	240
gctctgggtt	cgcccgaaatg	cgctcctctg	gcgtgtgatg	ctctggaccg	cgcgcccaag	300
aaagtgaagg	gggcagcgag	gaggctgctg	cggagtctgg	ggagaggcca	ggctgggcag	360
agcgctcct	ggctaagcgg	cctcaccaac	tcggttgctc	aaaccgcgct	cctggctgag	420
cgccgctgt	gcgcgcccc	cctgctggac	cacttcatct	gtgagctgcc	ggcgttgctc	480
aagctggcct	gcggaggcga	cggagacact	accgagaacc	agatgttcgc	cgcccgctg	540
gtcatcctgc	tgtgcctgtt	tgcgctcctc	ctggcctcct	acggtgcctg	ggcccgagct	600
gtctgttgca	tgcggttcag	cggaggccgg	aggagggcgg	tgggcacgtg	tgggtcccac	660
ctgacacccg	tctgcctgtt	ctacggctcg	gccatctaca	cctacctgca	gcccgcgcag	720
cgctacaacc	aggcacgggg	caagttcgta	tcgctcttct	acaccgtggg	cacacctgct	780
ctcaaccgcg	tcactctac	cctcaggaat	aagaaagtga	agggggcagc	gaggaggctg	840



ctgcggagtc tggggagagg ccaggctggg cag

873

&lt;210&gt; 208

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g56 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 208

gagctgatta	cgaattcgag	ctcggtagcc	tcttgtagc	ggacaattca	gatcttcctc	60
ttctcactca	taactacaat	atatgcactg	actataacag	gtaatggagc	cattgctttt	120
gccctgtggt	gtgaccggcg	acttcacact	ccatgtaca	tgctcctggg	agatttctcc	180
tttttagaga	tatggtatgt	cttttctaca	gttccaaga	tggttggtcaa	cttcctttca	240
gagaaaacaa	acatctcctt	tgctggattg	ctttctccag	atctatttct	tcttctcttt	300
gatacatcag	aatgcttgct	tttgactgtg	atggcctttg	atcagaacct	tgctatctgc	360
cggcccttgc	actatcctaa	tatcatgact	gggcattctt	gtgccaaact	ggccatactg	420
tgctgggttt	gtggctttct	gtggttctcg	atccccattt	tctcatctct	cagatgccct	480
tctgtgcccc	aaacattatt	gacatgttg	tgtgtgacct	agggccacta	tttgcatggg	540
attgtgtttc	tgccccaga	atccaactgt	tttgctacac	tctaagctca	ttagttattt	600
ttggttaactt	cctctttatt	attggatcct	atactattgt	cctgaaagtt	gtgttgggtg	660
cgccttcaag	cactgggaga	cataaggcct	tctctacctg	tggttctcat	ttggctgtgg	720
tatcactgtg	ctatggctct	cttatgggtc	tgtatgtgag	cccaggactc	ggacattcta	780
cggagatgca	gaaaattgta	actttgttct	atgctatggt	gacctcactc	ttcaatcccc	840
ttatctatag	gcctccagaa	taaggagata	aaggcagcct	tgaggaaagt	tctggtgagt	900
tccaacataa	tctaaggcat	a				921

&lt;210&gt; 209

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g57 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 209

gcatgtaagc	atgcatgata	ctgactgtga	tgccctatga	ctgcttagta	gccatctgtc	60
gccctctgca	ttaccagtc	atcgtgaatc	ctcacctctg	tgtcttcttc	gttttggtgt	120
ccttctcatt	agcatgtagg	ttcccagctg	cacagttgaa	ttgtgttaca	attcaccatc	180
atcaagaatg	tggaatctc	taattttgtc	tgtgaccctc	ctcaatttct	caaacttgcc	240
tgctctgaca	gcgtcatcaa	tagcatattc	acgtatttcc	atagtactat	gtttgggttt	300
cttcccattt	cagggatcct	tttgtcttac	tttaaaatcg	tcaccttcat	tctctggatt	360
tcactctcag	atgggaagta	taaagccttc	tccacctgtg	actctcacct	agcagttggt	420
tgctgatttt	atgggaacagg	cattggcgtg	tacttgactt	cagctctgtc	accacccccc	480
aggaatgggtg	tgatggcgtc	agtgatgtac	gctgtgggtc	cccccatgct	gaaccttttc	540
atctacagcc	tgagaaacag	ggacatacaa	agtgcctgtg	ggaggctgct	cagcagaaca	600
gtcgaatctc	atgatctgtt	ccatcctttt	tcttgtgtgg	gtaaggggcaa	ccacattaaa	660

&lt;210&gt; 210

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g58 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 210

atggccaaga	ataatctcac	cagagtaacc	gaattcattc	tcattgggctt	tatggaccac	60
cccaaattgg	agattcccct	ctttctgggtg	tttctgagtt	tctacctagt	cacccttctt	120
gggaatgtgg	ggatgattat	gttaatccaa	gtagatgtca	aactctacac	cccaatgtac	180

ttcttctga gccacctctc cctgctggat gcctgttaca cctcagtcac caccctcag	240
atcctagcca cattggccac aggcaaacg gtcactctct acggccactg tgctgccag	300
ttctttttat tcaccatctg tgcaggcaca gactgctttc tgctggcagt gatggcctat	360
gacgctatg ctgccattcg caaccactg ctctataccg tggccatgaa tcccaggctc	420
tgctggagcc tgggtgtagg agcctatgtc tgtgggggtg caggagccat cctgcgtacc	480
acttgacact tcacctctc cttctgtaag gacaatcaaa taaacttctt cttctgtgac	540
ctccaccctc tgctgaagct tgcctgcagt gacacagcaa acatcgagat tgcacatc	600
ttctttggca attttgtgat tttggccaat gcctccgtca tcctgatttc ctatctgctc	660
atcatcaaga ccattttgaa agtgaagtct tcagggtggca gggccaagac tttctccaca	720
tgtgcctctc acatcactgc tgtggccctt ttctttggag cccttatctt catgtatctg	780
caaagtggct caggcaaatc tctggaggaa gacaaagtcg tgtctgtctt ctatacagt	840
gtcatcccca tgctgaacct tctgatctac agcttaagaa acaaagatgt aaaagacgcc	900
ttcagaaagg tcgctaggag actccagggt tccctgagca tg	942

&lt;210&gt; 211

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g59 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 211

atgggtgggc taaaaagaga caatgcctct gagatgactg aactcatcct tgttggattt	60
gcccaacacc ctgaaatcca gactgccttc ttcttggaac tactgttttt ctactagtca	120
cagcgtttga gaacatcctt atcggtgctg tagtgagatg agattctcga cttcatactc	180
ctatgggatt tttttttcct cagtaccta tcctcccttg aaatgtgta ctccatcagc	240
tgggagctat aagtcttggc tcaatgcac aaggacttcc ccaccatctc ctataacagc	300
tgttctgttc agatgatcac acacctctt ctggggatga cagtgtctcc tccttgcctg	360
catggcttac aacagggttg ttgaaatctc ttatctctc cattacacta ttattatgag	420
caatcgggtc tgtatacagt tggccttggg aatctggacc catgccttct tagtagcagt	480
cacactaatc attgcaattc ctgctagtta ttatggacac aatgtcatca accattttac	540
cttgagatcc aggcctgct gaagctcgtc tgctcagaca cccttgctcag cctgattcag	600
ggtctggtta tcagtgtggt cacactgccc ctgccttca cattcatcct catctcctaa	660
ttttgcattt ttgttgtgct gtggaggcta ggcgtgaagc tttctccacc tgtggatctc	720
atctgactgg agtcaccata ttttatgggg cagccatctg catgtacttg aaacctcagt	780
caaaggggaa ccagggaagag gataaagttg tctcaaaact ttatggagca gttactccca	840
tgtaaatcc cccaatttac attcagagaa ataaggatat aaaagggtgca cttagaaagt	900
tagccaaagg aaatgaaaaa tcctaacagt tctctttaa c	941

&lt;210&gt; 212

&lt;211&gt; 1049

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g61 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 212

atggatattc tggttattga taatggcagt gaagtgcacag agttcatcct ggtgggtttg	60
tacaaccatc caaaatttca gattgccttt tatcgacca tggtagtggt ctacctgatc	120
acatttgttg gtagcagtct cattattggt gtggttaaag ttgatgggtg gcttcacact	180
cctatgtgtt ttttctaag caacctgtcc ttcttgata tctgtactc cagcaattca	240
gtaccttttt tgttgttcaa tggcttaaga gactaccca ccatttcta taacagctgt	300
tatgccaga tgaccagtgc tttttttctg gggatgcacag ggtgtcttct ccttgcctgc	360
atggcttatg agagatttgt tgtgatctcc aatccctgc gctacatcat cattatgaac	420
aataaggctc gcatacagtt ggccatgggt acctgggcca gtgccttctt tatgtcatta	480
atacaataat tgcaataata cattgcaata atacattaat tgcaatgatt gcattgcaat	540
tcctgcccac ttttgtggac acaatgtcat caaccatttt acctgtgagg tgcaggaatt	600
gttgaagctt gtcgtcag acatcccagg cagcctcatc ctgggtctag tcatcggcat	660
attcaccttg tccctgcctc tcacctgccc cctgccttc accctcatcc tcttcgccta	720

tgctcacatt	gtggttgctg	tgctgaggat	caactctgca	gaggccagac	tcaaagcttt	780
ctccacctgt	ggatcccatc	tgactgtgat	catcatat	tatgggacag	ccacctacat	840
gtacttgaaa	cctcagtcaa	gggaatccca	agatgagggt	aaagtcattc	ctgtattttt	900
tttgaaagta	gagaagcaac	atcaaaatga	tagcatctct	gtattttatg	gtgttgtagc	960
ccctatgttg	aacccccctc	tttacacctt	gagagacaag	gatgcgaaaa	tgctctaaga	1020
aaaataatta	ggaagaaaga	gtcctaaaa				1049

&lt;210&gt; 213

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g62 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 213

atggacaaga	taaaccagac	atttgtgaga	gaattcattc	ttctgggact	ctctgggttac	60
cccaaaacttg	agatcat	ctttgctctg	attctagtta	tgtacgtagt	gattctaatt	120
ggcaatgggtg	ttctgatcat	agcaagcatc	ttggattctc	gtcttcacat	gccccgttac	180
ttcttctctgg	gcaacctctc	tttcttggtg	atctgctata	caacctcctc	cattccctca	240
acactgggtga	gcttaattctc	aaagaaaaga	aacatttcct	tctctggatg	tgcatgtcag	300
atgttcttttg	ggtttgcaat	gggttcaaca	gaatgtttcc	tccttggcat	gatggcattt	360
gatecgttatg	tggccatctg	taacctctctg	agatacccca	tcacatgaa	caagggtggg	420
tatgtactgc	tgacttctgt	atcatggctt	tctgggtggaa	tcaattcaac	tgtgcaaaaca	480
tcacttgcca	tgcatggcc	tttctgtggg	aacaatatta	ttaacattt	cttatgagag	540
atcttagctg	tcctaaaatt	agcttggtct	gatatactctg	tcaatattgt	taccctagca	600
gtgtcaaaata	ttgctttcct	agttcttctc	ctgctcgtga	tttttttctc	ctatatgttc	660
atcctctaca	ccatcttgcg	aacgaactcg	gccacaggaa	gacacaaggc	attttctaca	720
tgctcagctc	acctgactgt	ggtgatcata	ttttatggta	ccatcttctt	tatgtatgca	780
aaacctaagt	cccaggacct	ccttgggaaa	gacaacttgc	aagctacaga	ggggcttggt	840
tcctatgtttt	atgggggttg	gacccccatg	ttaaaccca	taatctatag	cttgagaaat	900
aaagatgtaa	aagctgctat	aaaatatttg	ctgagcagga	aagctattaa	ccag	954

&lt;210&gt; 214

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g63 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 214

atgttccccg	caaattggac	atctgtaaaa	gtatttttct	tcctgggatt	ttttcactac	60
cccaaagttc	aggtcatcat	atttgcggtg	tgcttgctga	tgtacctgat	caccttgctg	120
ggcaacattt	ttctgatctc	catcaccatt	ctagattccc	acctgcacac	ccctatgtac	180
ctcttctctca	gcaatctctc	ctttctggac	atctgggtact	cctcttctgc	cctctctcca	240
atgctggcaa	actttgtttc	agggagaaac	actatttcat	tctcaggggtg	cgccactcag	300
atgtacctct	cccttgccat	gggtccact	gagtgtgtgc	tcctgcccat	gatggcatat	360
gaccgggtatg	tggccatctg	caacccccctg	agataccctg	tcacatgaa	taggagaacc	420
tgtgtgcaga	ttgcagctgg	ctcctggatg	acaggctgtc	tactgccat	ggtggaaatg	480
atgtctgtgc	tgccactgtc	tctctgtggt	aatagcatca	tcaatcattt	cacttgtgaa	540
attcttgcca	tcttgaaatt	ggtttgtgtg	gacacctccc	tgggtgcagtt	aatcatgctg	600
gtgatcagtg	tacttcttct	ccccatgcca	atgctactca	tttgtatctc	ttatgcattt	660
atcctcgcca	gtatcctgag	aatcagctca	gtggaagggtc	gaagtaaagc	cttttcaacg	720
tgacagccc	acctgatggt	ggtagttttg	ttctatggga	cggctctctc	catgcacctg	780
aagccctccg	ctgtagattc	acaggaaata	gacaaattta	tggcttttgg	gtatgccgga	840
caaaccccca	tgttgaaatc	tatcatctat	agtctacgga	acaaagaggt	gaaagtggcc	900
ttgaaaaaat	tgtctgattg	aatcattttt	aatactgcct	tcatttccat	cctcaaa	957

&lt;210&gt; 215

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g64 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 215

atggcagaga tgaacctcac cttggtgacc gagttcctcc ttattgcatt cactgaatat	60
cctgaatggg cactccctct cttcctcttg tttttattta tgtatctcat caccgtattg	120
gggaacttag agatgattat tctgatcctc atggatcacc agctccacgc tccaatgtat	180
ttccttctga gtcacctcgc tttcatggac gtctgtact catctatcac tgtccccag	240
atgctggcag tgctgtgga gcatgggga gctttatctt acacacgctg tgctgtcag	300
ttctttctgt tcaccttctt tgggtccatc gactgtacc tcttggccct catggcctat	360
gaccgtact tggctgtgtg ccagccctg ctttatgtca ccatcctgac acagcaggcc	420
cgcttgagtc ttgtgctgg ggcttacgtt gctggtctca tcagtgcctt ggtgcggaca	480
gtctcagcct tcactctctc cttctgtgga accagtga ttagctttat tttctgtgac	540
ctccctctc tgttaaagtt gacctgtgg gagagtaca ctcaagaagt gctgattatt	600
atgtttgcca tttttgtcat ccctgcttcc atggtggtga tcttgggtgc ctacctgtt	660
atcatcgtgg ccatcatggg gatccctgct ggaagccagg ccaagacctt ctccacctgc	720
acctcccacc tcactgtgt gtcactctt tttggtacc tcacttctat gtacttgaga	780
ggtaactcag atcagtcttc ggagaagaat cgggtagtgt ctgtgcttta cacagaggtc	840
atccccatgt tgaatccct catctacagc ctgaggaaca aggaagtga ggaggccctg	900
agaaaaattc tcaatagagc caagttgtcc	930

&lt;210&gt; 216

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g65 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 216

atgggcatgg aggtcttct ccagaactcc actaacttcg tcctcacagg cctcatcacc	60
catcctgcct tccccgggt tctctttgca atagtcttct ccatctttgt ggtggctata	120
acagccaact tggatcatgat tctgtctatc cacatggact cccgcctcca cacacccatg	180
tacttcttgc tcagccagct ctccatcatg gataccatct acatctgtat cactgtcccc	240
aagatgctcc aggacctcct gtccaaggac aagaccattt ccttcttggg ctgtgcagtt	300
cagatcttcc tctacctgac cctgattgga ggggaattct tcctgctggg tctcatggcc	360
tatgaccgct atgtggctgt gtgcaacct ctacgggtacc ctctcctcat gaaccgcagg	420
gtttgcttat tcatgggtgt cggtccttgg gttggtggtt ccttggatgg gttcatgctg	480
actcctgtca ctatgagttt ccccttctgt agatcccag agatcaatca ctttttctgt	540
gagatcccag ccgtgctgaa gttgtcttgc acagacacgt cactctatga gacctgatg	600
tatgctgtct gctgtctgat cgctgcttat cctctatct gtcactctctg tctctacac	660
gcacatcttc ctgactgtcc acaggatgaa ctctgctgag ggccggcgca aagcctttgc	720
tacgtgttcc tcccacatta tggcgggtgag cgttttctac ggggcagcct tctacacaa	780
cgtgctgcc cactcctacc acactccaga gaaagataaa gtggtgtctg ccttctacac	840
catcctcacc cccatgctca accactcat ctacagcttg aggaataaag atgtggctgc	900
agctctgagg aaagtactag ggagatgtgg ttcctcccag agcatcaggg tggcgactgt	960
gac	964

&lt;210&gt; 217

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g66 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 217

atggctcaca caaatgaatc gatgggtgtct gagttgtac ttttgggact ctctaattcc	60
---	----

tggggacttc	aacttttctt	tttcgccatc	ttctctatag	tctatgtgac	atcagtgcta	120
ggcaatgtct	taattattgt	cattatttct	tttgactccc	atttgaactc	tcctatgtac	180
ttcttgctca	gtaatcttct	tttcattgat	atctgtcagt	ctaactttgc	cacccccaag	240
atgcttgtag	acttttttat	tgagcgcaag	actatctcct	ttgagggttg	catggcccag	300
atattcgttc	ttcacagttt	tggtgggagt	gagatgatgt	tgcttgtagc	tatggcatat	360
gacagattta	tagccatag	taagcctctg	cactacagta	caattatgaa	cgggaggctc	420
tggtgaattt	ttgtgtctat	ttcctgggcg	gtgggcgttc	ttcattctgt	gagccacttg	480
gcttttacag	tggacctgcc	attctgtggt	cccaatgagg	tggatagctt	cttttgtagc	540
cttcccttg	tgatagagct	ggcttgcatg	gatacatatg	aaatggaaat	tatgacccta	600
acgaacagtg	gcctgatatc	attgagctgt	ttcctggcct	taattatttc	ctacaccatc	660
attttgatcg	gtgtccgatg	caggtcctcc	agtgggtcat	ctaaggctct	ttctacatta	720
actgccacac	tcacagtggg	cattcttttc	ttcgggcctt	gcatttattt	ctatatatgg	780
ccttttagca	gacttcctgt	ggacaaattt	ctttctgtgt	tctacactgt	ttgtactccc	840
ttgttgaaac	ccatcatcta	ctctctgagg	aatgaagatg	ttaaagcagc	catgtggaag	900
ctgagaaacc	gtcatgtgaa	ctcctggaaa	aac			933

&lt;210&gt; 218

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g67 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 218

atggatcaga	aaaatggaag	ttctttcact	ggatttatcc	tactgggttt	ctctgacagg	60
cctcagctgg	agctagtcct	ctttgtgggt	cttttgatct	tctatatctt	cactttgtctg	120
gggaacaaaa	ccatcattgt	attatctcac	ttggaccac	atcttcacac	tcctatgtat	180
tttttcttct	ccaacctaa	ctttttggat	ctgtgttaca	caaccggcat	tgttccacag	240
ctcctgggta	atctcagggg	agcagacaaa	tcaatctcct	atggtgggtg	tgtagttcag	300
ctgtacatct	ctctaggctt	gggatctaca	gaatgcgttc	tcttaggagt	gatgggtattt	360
gaccgctatg	cagctgtttg	caggcccctc	cactacacag	tagtcatgca	cccttgctctg	420
tatgtgctga	tggcttctac	ttcatgggtc	attggttttg	ccaactccct	attgcagacg	480
gtgctcatct	tgcttttaac	actttgtgga	agaaataaat	tagaacactt	tctttgtgag	540
gttcctccat	tgctcaagct	tgctgtgtgt	gacactacta	tgaatgaatc	tgaactcttc	600
tttgtcagtg	tcattattct	tcttgtagct	gttgcatata	tcatattctc	ctatagtcag	660
attgtcaggg	cagtcagtag	gataaagtta	gcaacagggc	agagaaaagt	gtttgggaca	720
tgtggctccc	acctcacagt	ggtttccctg	ttctacggca	cagctatcta	tgcttacctc	780
cagccccgca	acaactactc	tcaggatcag	ggcaagttca	tctctctctt	ctacaccatc	840
attacacca	tgatcaaccc	cctcatatat	acactgagga	acaaggatgt	gaaaggagca	900
cttaagaagg	tgctctggaa	gaactacgac	tccaga			936

&lt;210&gt; 219

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g68 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 219

atgtgctcag	ggaatcagac	ttctcagaat	caaacagcaa	gcactgattt	caccctcacg	60
ggactctttg	ctgagagcaa	gcatgctgcc	ctcctctaca	ccgtgacctt	ccttcttttc	120
ttgatggccc	tactgggaa	tgccctctc	atcctctca	tccactcaga	gccccgcctc	180
cacacccccca	tgtacttctt	catcagccag	ctcgcgctca	tggatctcat	gtacctatgc	240
gtgactgtgc	ccaagatgct	tgtgggcccag	gtcactggag	atgataccat	ttccccgtca	300
ggctgtggga	tccagatgtt	cttcacactg	accctggctg	gagctgaggt	tttctctctg	360
gctgccatgg	cctatgaccg	atatgctgct	gtttgcagac	ctctccatta	cccactgctg	420
atgaaccaga	gggtgtgcca	gtcctgtgtg	tcagcctgct	gggttttggg	aatgggtgat	480
ggtttgttgc	tcacccccat	taccatgagc	ttcccccttt	gccagtctag	gaaaatcctg	540
agttttttct	gtgagactcc	tgccctgctg	aagctctcct	gctctgacgt	ctccctctat	600

aagatgctca	cgtacctgtg	ctgcatcctc	atgctttctca	cccccatcat	ggatcatctcc	660
agctcataca	ccctcatcct	gcatctcatc	cacaggatga	attctgccgc	cggccgcagg	720
aaggccttgg	ccacctgctc	ctcccacatg	atcatagtgc	tgctgctctt	cgggtgcttcc	780
ttctacacct	acatgctccc	gagttcctac	cacacagctg	agcaggacat	gatgggtgtct	840
gccttttaca	ccatcttcac	tcctgtgctg	aacccctca	tttacagtct	ccgcaacaaa	900
gatgtcacca	gggctatgag	gagcatgatg	cagtcaaga			939

&lt;210&gt; 220

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g69 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 220

atggatgtgg	gcaataagtc	taccatgtct	gaatttggtt	tgctggggct	ctctaattcc	60
tgggaactac	agatgttttt	ctttatgggtg	ttttcattgc	tttatgtggc	aacaatgggtg	120
ggtaacagcc	tcatagtcat	cacagttata	gtggaccttc	acctacactc	tcctatgtat	180
ttcctgctta	ccaatctttc	aatcattgat	atgtctcttg	cttctttcgc	caccccaaag	240
atgattacag	attacctaac	aggtcacaaa	accatctctt	ttgatggctg	ccttaccag	300
atattctttc	tccacctttt	cactggaact	gagatcatct	tactcatggc	catgtccttt	360
gataggtata	ttgcaatatg	caagcccttg	cactatgctt	ctgtcattag	tccccagggtg	420
tgtgttgctc	tcgtgggtgg	ttcctggatt	atgggagtta	tgcatccaat	gagtcaggtc	480
atatttgccc	tcacgttacc	attctgtggt	ccctatgagg	tagacagctt	ttctgtgac	540
cttctgtggg	tgttccagtt	ggcttgtgtg	gatacttatg	ttctgggcct	ctttatgatc	600
tcaacaagtg	gcataattgc	gttgctctgt	tttattgttt	tatttaattc	atatgttatt	660
gtcctgggtta	ctgtgaagca	tcattcttcc	agaggatcat	ctaaggccct	ttctacttgt	720
acagctcatt	tcattgttgt	cttcttgttc	tttgggccat	gcattctcat	ctacatgtgg	780
ccactaagca	gctttctcac	agacaagatt	ctgtctgtgt	tttataccat	ctttactccc	840
actctgaacc	caataatcta	tactttgagg	aatcaagaag	taaagatagc	catgaggaaa	900
ctgaaaaata	ggtttctaaa	ttttaataag	gcaatgcctt	ca		942

&lt;210&gt; 221

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g70 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 221

atgggagaca	atataacatc	catcagagag	ttcctcctac	tgggatttcc	cgttggtccc	60
aggattcaga	tgctcctctt	tgggctcttc	tccctgttct	acgtcttcac	cctgctgggg	120
aacgggacca	tactggggct	catctcactg	gactccagac	tgacgcgcc	catgtacttc	180
ttcctctcac	acctggcggt	cgctgacatc	gcctacgcct	gcaacacggg	gccccggatg	240
ctgggtgaacc	tcctgcatcc	agccaagccc	atctcctttg	cgggcccgc	gatgcagacc	300
tttctgtttt	ccacttttgc	tgtcacagaa	tgtctcctcc	tggtggtgat	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttggtcca	tcatgacctg	gagagtctgc	420
atcaccctcg	cggtgacttc	ctggaccact	ggagtccctt	tatccttgat	tcattctgtg	480
ttacttctac	ctttaccctt	ctgtaggccc	cagaaaattt	atcacttttt	ttgtgaaatc	540
ttggctgttc	tcaaaacttg	ctgtgcagat	acccacatca	atgagaacat	ggctcttgcc	600
ggagcaattt	ctgggctggg	gggacccttg	tccacaattg	tagtttcata	tatgtgcac	660
ctctgtgcta	tccttcagat	ccaatcaagg	gaagttcaga	ggaaagcctt	ccgcacctgc	720
ttctcccacc	tctgtgtgat	tggactcggt	tatggcacag	ccattatcat	gtatgttggg	780
cccagatatg	ggaaccccaa	ggagcagaag	aaatatctcc	tgctgtttca	cagcctcttt	840
aatcccatgc	tcaatccctt	tatctgtagt	cttaggaact	cagaagtga	gaatactttg	900
aagagagtgc	tgggagtaga	aagggtttta				930

&lt;210&gt; 222

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g71 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 222

cacacggagc	cacggaatct	cacagggtgc	tgagaattcc	tcttcctggg	actctcagag	60
gatccagaac	tgctgccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
atgggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	tccacacccc	180
cgtgtacttc	tccctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cgcccacggt	240
tcccaaatg	attgtggaca	tgcaagtcga	tagcagagtc	atctctcatg	cgggctgcct	300
ggcacagatg	tctttcttgg	tcttttttgc	atgtatagaa	gacatgctcc	tgactgtgat	360
ggcctatgac	agctttgtag	ccatctgtca	ccctctgcac	taccagtcga	tcatgaatcc	420
tcacctctgt	gtcttctctg	ttttggtgtc	ctttttcctt	agcctgttgg	attcccagct	480
gcacggttgg	attgtgttac	aattcaccat	catcaagaat	gtggaaatct	ctaattttct	540
ctgtgacccc	tctcaacttc	tcaaacttgc	ctgttctgac	agcgtcacca	atagcatatt	600
catatatatt	gatatgacta	tgtttggttt	tcttcccatc	tcagggatcc	ttttgtctta	660
gtataaaatt	gtcccctcca	ttctaaggat	gtcatcgtca	gatgggaagt	ataaagcctt	720
caccacctgt	ggctctcacc	tagcagttgt	ttgctgattt	gatggaacag	gcattggcat	780
gtacctgact	tcagctctgt	caccaccccc	caggaatggg	gtggcggcgt	cagtgatgta	840
cgctgtgggc	accccatgc	tgaacctttt	catctacagc	ctgagaaaca	gggacataca	900
aagtgcctcg	cggaggctgc	gcagcagaac	agtggaaatct	catgatctgt	tccatccttt	960
ttcttgtgt						969

&lt;210&gt; 223

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g72 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 223

atggcctgga	gcaatcagtc	tgcggttaacc	gaattcatac	tacggggtct	gtccagttct	60
ttagaactcc	agattttcta	cttcctggtt	ttctccatag	tctatgcagc	cactgtgctg	120
gggaaccttc	ttattgtggg	caccattgca	tcagagccac	accttcattc	ccctacgtac	180
ttctgtctgg	gcaatctctc	cttcattgac	atgtccctgg	cctcatttgc	cacccccaaa	240
atgattgcag	acttccttag	agaacacaaa	gccatctctt	ttgaaggctg	catgacccag	300
atgttcttcc	tacatctctt	agggggtgct	gagattgtac	tgctgatctc	catgtccttt	360
gataggtagc	tggtatctg	taagcctcta	cattacctaa	caatcatgag	ccgaagaatg	420
tgtgttgggc	ttgtgatact	ttctgggatt	gtcggcatct	tccatgctct	gagtcatgta	480
gcattttacag	tgaatctgcc	cttctgtgga	cccaatgaag	tagacagttt	cttttgtgac	540
ctcccttttg	tgattaaact	tgcttgtgtc	gacacatata	ttctgggggt	gttcatgac	600
tcaaccagtg	gcatgattgc	cctgggtgtc	ttcatcctct	tggtgatctc	ttacactatc	660
atcctggtea	ccgttcggca	gcgttccctc	ggtggatcct	ccaaagccct	ctccacgtgc	720
agtgccact	ttactgttgt	gacccttttc	tttggcccat	gcactttcat	ttatgtgtgg	780
cctttcacaa	atttcccaat	agacaaagta	ctctcagtat	tttataccat	atacactccc	840
ctcttgaatc	cagtgatcta	taccgtagg	aataaagatg	tcaagtattc	catgaggaaa	900
ctaagcagcc	atatctttta	atctaggaag	actgatcata	ctcct		945

&lt;210&gt; 224

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g73 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 224

atgaaaaagt	acatggaaag	gactaattga	acaactgagt	ttgagttgat	tctcataagt	60
------------	------------	------------	------------	------------	------------	----

ctatgagtag	tcataagttg	acaaaaactc	ctttttgtca	catgcttagt	ggtgtatcta	120
gtgaccctct	tggggaacag	aatacagatc	atcccaacac	tccttggttc	ccacctatat	180
ttatgccatg	gcaatccctc	cttcctggat	atcgggctta	cgctcttttt	actccctcta	240
tcctaataaa	cttcctatca	gagggaaaaa	aactctcttt	cacagattgt	attatacaaa	300
tgtctatctt	ctattccatg	gggtccacgg	agtgtgtgct	cctagcagtg	atggcatatg	360
ataactgtgt	ggtcatcagc	aaattccctga	gataccctct	catcataaat	aagggtgaata	420
aaataaaaaa	ggtgctttgt	gttttcatgg	ctactgtctc	ttatgaatta	ggattttctca	480
acagacaaaa	tgtattaata	gttacatatg	aatgcacttt	tgtggaaaac	acatcattaa	540
tcatttttat	aaaatattac	agttaatggc	tctggcttgc	atagatattt	ccttgaatga	600
gaatataata	atattgggca	aagtaaactt	tccatttact	ttattactac	catttcagtt	660
cttttatctt	agttttttat	attttcacca	tctatgtctg	attgaaatca	attcagctga	720
aggaaggaaa	aaggtctctt	ccacctgttc	gcccacata	acagtgggtga	ttgtgtttca	780
ccggacaatc	ctcttcatgt	acataaagtc	aactctaat	ggcactactt	cagagaaact	840
ggttgacctg	ttctgctggg	tagtaatgct	catgctcaat	cttatcatct	atagcctggg	900
gaatatggag	gtgcttgggg	ttatgaagaa	attgatcagt	atgagtagac	cctggtgctg	960
gaa						963

&lt;210&gt; 225

&lt;211&gt; 974

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g74 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 225

cacacggagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtccatgtat	120
ctgggtcacg	tgctgaggaa	cctgctcagc	atcctggctg	tcagctctga	ctcccaactc	180
cacacccccca	tgtacttctt	cctctccaac	ctgtgctggg	ctgacatcgg	tttcacctcg	240
cccattggttc	ccaagatgat	catggacatg	cagtcgcata	gcagagtcat	ctctcatgcg	300
ggctgcctga	cacggatgtc	tttcttggtc	ctttttgcat	gtatagaaga	catgtcctcg	360
actgtgatgg	cctatgactg	ctttgtagcc	atctgtcgcc	ctctgcacta	cccagtcac	420
atgaatcctc	acctctgtgt	cttcttcggt	ttggtgtcct	ttttccttag	cctgttggat	480
tcccagctgc	acagttagat	tgtgttacia	ttcactttct	tcaataatgt	ggaaattgct	540
aattttgtct	atgagccatc	tcaacttctc	aaccttgact	gttctgacac	cgtcacat	600
agcgtattta	tatatcttga	tagtactgtt	tggttttctt	cccatttcag	ggatcctttg	660
tcttagtata	aaattgtccc	ctccattcta	aggatgtcat	cgtcagatgg	gaagtataaa	720
gccttcgcca	cctgtggctc	tcacctagca	gttgtttgct	gatttgatgg	aacaggcatt	780
ggcatgtacc	tgacttcagc	tgtgtcacca	ccccccagga	atggtgtggc	ggcgtcagtg	840
atgtacgctg	tggtcacccc	catgctgaac	cttttcatct	acagcctgag	aaacagggac	900
attcaaagtg	ccctgcagag	gctgagtagc	agaacagtgg	aatctcatga	tctgttccat	960
cctttttctt	gtgt					974

&lt;210&gt; 226

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g75 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 226

atgggtaact	ggactgcagc	ggtgactgag	tttgttctgc	tggggttttc	cctgagcagg	60
gaggtggagc	tgctgtcctt	ggtgtcctct	ctgcccacgt	tcctgtctgac	tcttctgggg	120
aacctgtctc	tcatctccac	tgtgtgtgct	tgctcccggc	tccacacccc	catgtacttc	180
ttcttgtgca	acctctctat	cctggacatc	ctcttcacct	cagtcacttc	tccaaaagtg	240
ttggccaact	taggatctag	ggataaaaacc	atctcctttg	ccggatgtat	cacccagtcg	300
tatttctact	ttttcttggg	cacagttgag	ttctctctgc	tgacgggtcat	gtcttatgac	360
cgttatgcc	ccatctgctg	ccccctgcgg	tacaccacca	tcagtagacc	ttctgtctgc	420
attgggaccg	ttgtattctc	ttgggtggga	ggcttctctg	ctgtgtctct	tccaaccatc	480



ctcatctccc	agctgccctt	ctgtggctcc	aatatcatta	accacttctt	ctgtgacagt	540
ggacccttgc	tggccctggc	ctgtgcagac	accactgcca	tcgagctgat	ggattttatg	600
ctttcttcca	tggtcatcct	ctgtgcata	gtcctcgtgg	cctattccta	tacgtacatc	660
atcttgacca	tagtgcgcat	tccttctgca	agtgggaagga	agaaggcctt	taatacctgt	720
gcttcccacc	tgaccatagt	catcattcct	agtggcatca	ctgtgtttat	ctatgtgact	780
ccctcccaga	aagaatatct	ggagatcaac	aagatccctt	tggttctgag	cagtgtgggtg	840
actccattcc	tcaaccctt	tatatatact	ctgaggaatg	acacagtgca	gggagtcctc	900
agggatgtgt	gggtcagggt	tcgaggagtt	tttgaaga	ggatgagggc	agtgtctg	957

&lt;210&gt; 227

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g76 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 227

atggaaactg	caaattacac	caaggtgaca	gaatttggtc	tcactggcct	atcccagact	60
cgggaggtcc	aactagtcct	atttggtata	tttctatcct	tctatttggt	catcctacca	120
ggaaatatcc	ttatcatttg	caccatcagg	ctagaccctc	atctgacttc	tcctatgtat	180
ttcctgttgg	ctaactctggc	cctccttgat	atttggtact	cttccattac	agccccataa	240
atgctcatag	acttctttgt	ggagaggaag	ataatttcct	ttggtggatg	cattgcacag	300
ctcttcttct	tacactttgt	tggggcttcg	gagatgttct	tgctcatagt	gatggcctat	360
gaccgctatg	ctgctatctg	ccgacccttc	cactatgcta	ccatcatgaa	tcgacgtctc	420
tgctgtatcc	tggtggctct	ctcctggatg	gggggcttca	ttcattctat	aatacagggtg	480
gctctcattg	ttcgacttcc	tttctgtggg	cccaatgagt	tagacagtta	cttctgtgac	540
atcacacagg	ttgtccggat	tgctctgtgc	aacaccttcc	cagaggagtt	agtgatgatc	600
tgtagtagtg	gtctgatctc	tgtgggtgtg	ttcattgtct	tgtaaatgtc	ctatgccttc	660
cttctggcct	tgctcaagaa	acattcaggc	tcagatgaga	ataccaacag	ggccatgtcc	720
acctgctatt	cccacattac	cattgtgggtg	ctaattgttg	ggccatccat	ctacatttat	780
gctcgcccat	ttgactcatt	ttccctagat	aaagtgggtg	ctgtgtttca	tactgtaata	840
ttccctttac	ttaatcccat	tatttacaca	ttgagaaaca	aggaagtaaa	ggcagccatg	900
aggaaggtgg	tcaccaata	tattttgtgt	gaagagaag			939

&lt;210&gt; 228

&lt;211&gt; 940

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g77 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 228

atggaaagtc	aaaggaacat	ataaaaattc	atactcatga	gcctttcctc	tatccagaac	60
atacaaatat	ttgtttttgt	gttcttattt	tgtaatgttg	ccatcttggg	gggaaacttt	120
ctgatcctta	tctctatttg	atgtagtcct	ctttttaacc	aaccaatgca	ctatttcttc	180
aggctatatg	aatatctact	atacctcctg	tgtcacaccc	aaaataattg	gtgatctagt	240
agtgggaaga	ataaacatct	cctatgatag	gagtccttcc	catgcacttc	tttggaatca	300
ttgaaatctt	catccttaca	gtcatggctt	ttgatcacta	tggtgccatc	tgcaaaccctc	360
cccgtacct	aattatcatg	aataggacaa	aatacaatac	tctaactctg	gttgcttggc	420
tggtggggct	ttccattctt	tgtttcagtt	ttctatgaaa	atctgggtgc	ctttctgtgg	480
ctccaacaaa	gttgatgact	aatattaaga	tatttttcct	ttactgaaag	tcgcttgtac	540
tgatacctgc	atcactggtg	tcctcgtggg	tgccaattct	ggaatgtttg	ccttggtaac	600
cttggttctgt	cgtttggctc	ttatgtcatt	atactattcc	ccttaaaaaa	tcattcagta	660
gaggggaagat	gcaaagccct	ctctacctgt	ggatctcata	tcaccatggg	aatctttttc	720
ttcgaacctt	caacttttgc	ctaccttaga	ccttctcact	tttctgagg	acaaaatac	780
tgctctgttt	tacactatta	ttgtcccaat	gttcaaccac	ctaactctata	acctgagaaa	840
tacagagatg	aaaaaggcca	tgagaaaagt	ttggtaccaa	atatcatttt	cagaagaaaa	900
acagctgatt	tgtcctactt	agtgtactaa	agaactttat			940

<210> 229  
 <211> 912  
 <212> DNA  
 <213> Unknown (H38g78 nucleotide)

<220>  
 <223> Synthetic construct

<400> 229  
 atgagaaatg gcacagtaat cacagaattc atcctgctag gctttcctgt tatccaaggc 60  
 ctacaaacac ctctctttat tgcaatcttt ctacacctaca tattaaccct tgcaggcaat 120  
 gggcttatta ttgccactgt gtgggctgag ccagggtac aaattccaat gtactttctc 180  
 ctttgtaact tgtctttctt agaaatctgg tacaccacca cagtcacccc caaactgcta 240  
 ggaacctttg tagtggcaag aacagtaatc tgcattgctt gctgcctgct gcaggccttc 300  
 ttccacttct tcgtgggcac caccgagttc ttgatcctca ctatcatgtc ttttgaccgc 360  
 tacctacca tctgcaatcc ccttcaccac ccaccatca tgaccagcaa actctgcctg 420  
 cagctggccc tgagctcctg ggtgggtggc ttcaccattg tcttttgtca gacgatgctg 480  
 ctcattccagt tgccattctg tggcaataat gttatcagtc atttctactg tgatgttggg 540  
 ccagtttga aagcgcctg catagacacc agcattttgg aactcctggg cgcatagca 600  
 accatccttg tgatcccagg gtcacttctc tttaatatga tttcttatat ctacattctg 660  
 tccgcaatcc tacgaattcc ttcagccact ggccaccaa agactttctc tacctgtgcc 720  
 tcgcacctga cagttgtctc cctgctctac ggggctgttc tgttcattga cctaagaccc 780  
 acagcacact cctcctttaa gattaataag gtggtgtctg tgctaaatac tatectcacc 840  
 ccccttctga atccctttat ttatactatt agaaacaagg aggtgaaggg agccttaaga 900  
 aaggcaatga ct 912

<210> 230  
 <211> 963  
 <212> DNA  
 <213> Unknown (H38g79 nucleotide)

<220>  
 <223> Synthetic construct

<400> 230  
 atgacaattc ttcttaatat cagcctccaa agagccactt tcttcctgac gggcttccaa 60  
 ggtctagaag gtctccatgg ctggatctct attcccttct gcttcacteta cctgacagtt 120  
 atcttgggga acctcaccat tctccacgtc atttgtactg atgccactct ccatggaccc 180  
 atgtactatt tcttgggcat gctagctgtc acagacttag gcctttgcct ttccacactg 240  
 cccactgtgc tgggcatttt ctggtttgat accagagaga ttggcaccct tgcctgtttc 300  
 actcagctct tcttcaccca cacttgtct tcaatggagt catcagttct gttatccatg 360  
 tccattgacc gctacgtggc cgtctgcaac ccactgcatg actccaccgt cctgacacct 420  
 gcatgtattg tcaagatggg gctaagctca gtgcttagaa gtgctctctc catcctcccc 480  
 ttgccattcc tcctgaagcg cttccaatac tgccactccc atgtgctggc tcatgcttat 540  
 tgtcttcacc tggagatcat gaagctggcc tgccttagca tcattgtcaa tcacatctat 600  
 gggctctttg ttgtggcctg caccgtgggt gtggactcac tgcctatctt tctctcatac 660  
 gccctcatcc ttcgcaccgt gctcagcatt gcctcccacc aggagcgact ccgagccctc 720  
 aacacctgtg tctctcatat ctgtgctgta ctgctcttct acatcccat gattggcttg 780  
 tctcttgtgc atcgcttttg tgaacatctg ccccgcttg tacacctctt catgtcctat 840  
 gtgtatctgc tgggtaccac cttatgaac ccatcatct acagcatcaa gaccaagcaa 900  
 attcgccagc gcatcattaa gaagtttcag tttataaagt cacttaggtg tttttggaag 960  
 gat 963

<210> 231  
 <211> 968  
 <212> DNA  
 <213> Unknown (H38g80 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 231

atggggaacc	acaccaccgt	caccgagttt	gtcctgctgg	ggctctcaga	gacctgtgag	60
ctgcagatgc	tcattcttct	ggggctcctc	ctgacctacc	tcctcacact	gctggggaat	120
ctggtcacgc	tggtcacac	cctcatggac	aggcgctcc	acaccaccat	gtactacttc	180
ctccgcaact	ttgtgtccc	ggagatctgg	ttcacctcgg	tcattcttcc	caagggtgctg	240
gccaacatcc	tcacaggata	caagaccatt	ccctcccagg	ctgcttctctg	caaagtttgc	300
tctatttttt	cttgggcacc	acagagttct	tcctcctggc	ggtgatgtcc	tttgacaggt	360
acgtggccgt	atgtaaccct	ttgcattatg	ccaccatcat	gagcaaaagg	gtctgtgtcc	420
agctagtcc	ctgttagtgg	atgacaggat	tccttctcat	cattattcca	agttttcttg	480
tccttcagca	gccattctgt	ggccccaaca	tcattaacca	tttcttctgt	gacaactttc	540
ccctcttgaa	actcatttgt	gcagacatga	ctctgataga	gctcctgggt	tttggtatag	600
ccaacgtcag	cttactgggc	actctgtcta	tgacggccac	ttgctatggc	cacatcctcc	660
acgccattct	gcacatcccc	tcagccaaag	agaagcagaa	agccttctcc	gcctgctcct	720
cccacatcat	tgtcgtgtct	ctcttctatg	gcagctgcat	cttcattgtac	attcagtcag	780
gcaagagtga	ccagaaggaa	gacaggaaca	aggtggcggc	attgcttaac	accgtgggtga	840
ccctgatgct	caaccccttc	atctacaccc	tgaggaacaa	acaggtgaaa	caggtgttta	900
ggcagcaggt	gagcaaacctc	ctcatataaa	gctgtgtaaa	aaaaaaactg	aagctcagca	960
tccccaga						968

&lt;210&gt; 232

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g81 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 232

gaaataaaga	tagcaaacaa	cacagtagtg	acagaattta	tcctccttgg	tctgactcag	60
tctcaagata	ttcagctctt	ggtctttgtg	ctgatcttaa	ttttctacct	tatcatectc	120
cctggaaatt	tcctcatcat	tttcaccata	aagtcagatc	ctgggctcac	agcaccctc	180
tatttctttc	tgggcaactt	ggccttctctg	gatgcaccc	actccttcat	tgtggctccc	240
cggatgttgg	tggacttctt	ctctgcgaag	aatgtaatct	cctacagagg	ctgcatcact	300
cagctctttt	tcttgcaact	ccttggagga	ggagagggat	tactccttgt	gatgtagcct	360
ttgaccgcta	catcgccatc	tgccggcctc	tgcactattc	tactctcatg	aaccccagag	420
cttgctatgc	aatgatgttg	gctctgtggc	ttgggggttt	tgtccactcc	attatccagg	480
tggtcctcat	cctccgcttg	cctttttgtg	gccccaaacca	gctggacaac	ttcttctgtg	540
atgtcccaca	ggctcatcaag	ctggcttgca	ccgacacgtt	tgtggtggag	cttctgatgg	600
tcttcaacag	tggcctgatg	acactcctgt	ctttctgggg	cttctggcct	cctatgcagt	660
catcctgtgc	catgttcgta	aggcagcttc	tgaattgaag	aacaaggcca	tgtccacgtg	720
caccactcat	gtcattatta	tacttcttat	gtttggacct	gctatcttca	tctacatgca	780
ccccttcagg	gccttaccag	ctgacaaggt	ggtttctttc	tttcacacag	tgatctttcc	840
attgatgaat	cctatgattt	atacccttcg	aaaccaggaa	gtgaaaactt	ccatgaagag	900
gttattgagt	cgacatgtag	tctgtcaagt	ggactttata	ataagaaac		949

&lt;210&gt; 233

&lt;211&gt; 857

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g82 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 233

gtcatacgaa	accagacaat	ggtaactgaa	ttcaccgggt	ctcccttctt	gctgtccagg	60
agcttcagat	ttggctatgt	gtccttctct	ggctggttca	tatgtccacc	ataacaggaa	120
acctttctgt	cattttctta	acgtggacag	ataattgtct	ccaaacccca	atggacttgt	180
tccttagaaa	aaagtcatat	cgttctcttg	ctgcatcacc	caaataatatt	tctacttctt	240
tctagggaca	gtggcgttta	tccccttggc	agtgacatcc	ttcaaact	gcatggcaac	300
ctgtgacccc	ctgtgcagca	ccatcattgc	aaaaagcagg	gcctgcctcc	tgtggctct	360
gggatgctgg	atgggaacct	tcctggctgt	gttgccctg	actattgtgg	tgtccaggtt	420

gccagactgt	actgaaaaaa	ttagtccttt	cttctgtgac	attgcctctt	tactgcagg	480
ggcctgtatt	gatattcatt	tcattgagat	gataagcttc	ctttgatcat	ctcttatgg	540
cctgacctcg	ctgggtctta	atgccacatc	ctacgcctac	atcattttct	cctcctgtgc	600
atccccctag	cccaaggatg	tcaggaggcc	ttttccacct	gtgcttcaca	catcaccatc	660
atctttattg	cctgccgaaa	ctccatctcc	acgtgtgtga	ggcctaacct	gagggtattg	720
ctggattttg	acaaagtgc	agctatcctc	actatagtag	tgacttcttt	tctgaatccc	780
cgcatttata	gcttgaggta	aaggaagtat	gaagggagtc	aatttgcaca	atactgtcac	840
cacattccaa	aggaaca					857

&lt;210&gt; 234

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g83 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 234

atggaaagcg	agaacagaa	agtgataaga	gaattcatcc	tccttgggtc	gacccagtct	60
caagatatcc	agtcctcgt	ctttgtgcta	gttttaatat	tctacttcat	catcctccct	120
ggaaattttc	tcattatatt	caccataaag	tcagaccttg	ggctcacagc	ccccctctat	180
ttctttctgg	gcaacttggc	cttcctggat	gcactcctact	ccttccactgt	ggctccccgg	240
atgttgggtg	acttcctctc	tgcaagaag	ataatctcct	acagaggctg	catcactcag	300
ctctttttct	tgcaacttct	tggaggagg	gagggattac	tccttgttgt	gatggccttt	360
gaccgtctaca	tgcccatctg	ccggcctctg	cactatccta	ctgtcatgaa	ccctagaacc	420
tgctatgcaa	tgatgttggc	tctgtggcct	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatcc	tccgcttgcc	tttttggg	ccaaaccagc	tggacaactt	cttctgtgat	540
gtccacaggg	tcatcaagct	ggcctgcacc	gacacatttg	tgggtggagct	tctgatgggc	600
ttcaacagtg	gcctgatgac	actcctgtgc	ttcttggggc	ttctggcctc	ctatgcagtc	660
attctttgtc	gcatacgagg	gtcttcttct	gaggcaaaaa	acaaggccat	gtccacgtgc	720
atcacccata	tcattgttat	attcttcatg	tttggacctg	gcacttctcat	ctacacgcgc	780
cccttcaggg	ctttccacgc	tgacaagggtg	gtttctctct	tccacacagt	gatttttctc	840
ttgttgaatc	ctgtcattta	tacccttcgc	aaccaggaag	tgaaagcttc	catgaaaaag	900
gtgtttaata	agcacatagc	c				921

&lt;210&gt; 235

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g84 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 235

atggaaaatc	aaaacaatgt	gactgaattc	attcttctgg	gtctcacaga	gaacctggag	60
ctgtggaaaa	tattttctgc	tgtgtttctt	gtcatgtatg	tagccacagt	gctggaaaa	120
ctacttattg	tggttaactat	tatcacaagt	cagagtctga	ggtcacctat	gtattttttt	180
cttaccttct	tgcccttttt	ggatgtcatg	ttctcatctg	tcgttgcccc	caagggtgatt	240
gtagacaccc	tctccaagag	cactaccatc	tctctcaaag	gctgcctcac	ccagctgttt	300
gtggagcatt	tctttgggtg	tgtggggatc	atcctcctca	ctgtgatggc	ctatgaccgc	360
tacgtggcca	tctgtaagcc	cctgcactac	acgatcatca	tgagtccacg	ggtgtgtctg	420
ctaattgtag	gaggggcttg	ggtgggggga	tttatgcacg	caatgataca	acttctcttc	480
atgtatcaaa	tacccttctg	tggctcta	atcatagatc	actttatatg	tgatttgttt	540
cagttgttga	cacttgccctg	cacggacacc	cacatcctgg	gcctcttagt	taccctcaac	600
agtgggatga	tgtgtgtggc	catctttctt	atcttaattg	cgctctacac	ggcatccta	660
tgctccctga	agtcttacag	ctctaaagg	cggcacaaag	ccctctctac	ctgcagctcc	720
cacctcacgg	tggttgtatt	gttctttgtc	ccctgtattt	tcttgtacat	gaggcctgtg	780
gtcactcacc	ccatagacaa	ggcaatggct	gtgtcagact	caatcatcac	acccatgtta	840
aatcccttga	tctatacact	gaggaatgca	gaggtgaaaa	gtgccatgaa	gaaactctgg	900
atgaaatggg	aggctttggc	tgggaaa				927

<210> 236  
 <211> 933  
 <212> DNA  
 <213> Unknown (H38g85 nucleotide)

<220>  
 <223> Synthetic construct

<400> 236

gtagaggata	tggtgccatt	ctctatgagg	atttctggca	tttttcaa	attcatttta	60
cggtatcat	caccttatct	actaatatc	tgtactgaca	tgtgtaccat	ttcagtttac	120
atattctcat	atagtaaaat	gttaactgca	agggaaatta	cctcaaacc	aaaccattaa	180
cgtaacttca	gagacaatat	ggattaagat	tatccatgat	ttccttcac	aaaccaagac	240
tatctccttt	gagggtgca	tgcccagat	attcttggtc	catgtctttg	ctggtggtga	300
gatggtgctc	ctttagacca	tgccatatga	catatatgta	gccatatgca	aacctctcca	360
ttatgcaacc	atcatgaact	tgtgcacatg	tacaggccta	gtggtaggat	cttgggtcac	420
tggaagtatg	cactccctga	gccagttagc	tttactgta	agtttgccct	tctgtggccc	480
aaacatagtg	gacagttatt	attgtgacct	tactttggtc	atcaaacttg	cctgtacaga	540
tacttatatc	cctgaagcgt	tgatgctttt	ggacagtggg	cttatggggg	tgacttcatt	600
ttgcttttgc	tgatctccta	cacggtcatt	ctgattactg	tcagcgcacc	ttcctcagca	660
ggtagggcca	aggctgcag	cactctgact	gccacgtga	ctgtggtgac	cctgttcttt	720
gggccttgta	tcttcatcta	tgccctggcct	ttcagcaact	taccagtggg	taacattttg	780
tctgtattct	ctacagtttt	cacacctata	ttaaaccctc	ttatctacac	actgagaaac	840
aaagaggtaa	aatcagcaat	tcataacctg	aagaccctgt	atgtaacttc	caggctgtct	900
tcccagctct	ctctcatagg	actagatttg	ttg			933

<210> 237  
 <211> 629  
 <212> DNA  
 <213> Unknown (H38g86 nucleotide)

<220>  
 <223> Synthetic construct

<400> 237

ttgggaaatg	tctcaacaga	gactactttt	atttttggtt	gtttcacaaa	tggaacaaca	60
ttccagcctg	tatgcttctc	ctcattttta	gtgcttgccc	actcagtgtc	tgggctaagt	120
tctctcctca	acatcctggg	gaacttggtc	tcagcttggt	ttcttttggt	tttggttttc	180
agatgtccta	ctcctttgtc	attttaatta	aaatgataat	gaactctata	tctgagaggt	240
acatcaccac	taatttgaag	tgcaagattc	tgcccttggt	tttatctgct	ttgctatcag	300
tgagcactct	aatacttttg	gcttgggggc	actgtgggat	ctgtgtgcct	caggctctgt	360
ctctgacgat	gcttggcctg	cactggggga	ggtattgatg	gtgtcatggc	ccaccagag	420
gcaatgggtc	gtctgtcttt	ctgtgaccgc	agcatcatca	accactgtgt	gtggcacact	480
tcttttctac	aaactctcct	tagagcacct	gcttcacaag	ctgggtgatt	tgtagtcatt	540
gcgtagtgtg	tgatcatctt	catctctgac	atactatcct	ttccaccatc	ctccattttc	600
tctttcctga	ggcaaaactc	aaagctttt				629

<210> 238  
 <211> 822  
 <212> DNA  
 <213> Unknown (H38g87 nucleotide)

<220>  
 <223> Synthetic construct

<400> 238

atggggaatc	tgggcatgat	catgggtcatc	aggatcaacc	ccaaactcca	caccctatg	60
tacttttttc	tcagccactt	gtcctttggt	gatttctgtt	attccaccac	aattacacca	120
aaactgctgg	agaacttggg	tgtggaagac	agaatcatct	ccttcacagg	atgcatcatg	180
caattcttct	ttgcctgtat	atttgtgggt	acagaaacat	tcatgctggc	agcgatggct	240
tatgacagat	ttgtggcagt	gtgtaaccct	ctgctttaca	cagttgcaat	gtcccagagg	300

ctttgtcct	tgtagtg	tgcatcat	tcttgag	tagttgt	ctaacat	360
acatacttt	tgtagttt	atctttt	aggactaa	tcattaata	ctttgtct	420
gagcacgtg	ccattgtt	tggtcctg	tctgacct	acatgagcc	gaaggctat	480
ttagtttctg	caacattcaa	tgaataaag	agcctggga	tcattctcac	ttcctatgt	540
ttcattttta	tcactgtcat	gaagatgc	tccactggg	ggcgcaaga	agcgttctc	600
acgtgtgc	cccacctg	cgccattac	atcttccat	ggactatcc	ttttctct	660
tgtgttct	actccaaa	ttcatggc	atgggtcaa	tggcctct	cttttacac	720
gtggtcatt	ccatgtgaa	ccccttgat	tatagcct	ggaacaaag	tgtaaaag	780
acagtcagg	agttagtc	taccaaatta	ttatgtcata	aa		822

&lt;210&gt; 239

&lt;211&gt; 1041

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g88 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 239

atgaccaaca	gcagtgtcaa	gggagacttc	atcctgggtg	gtttctctca	tcagccccac	60
ctggaaaaga	tcctctttgt	ggctgttttg	atatectatc	tccttaccct	tgtgggaaat	120
acagtaatta	ttctgatctg	ctctgtagac	cctaaactca	agacacccat	gtattttttc	180
ttactcacct	ctccttagtt	gatatctgtt	ttaccaccag	tattgtcccc	cagctgctgt	240
ggaacctaaa	aggacctgac	aaaacaatca	cattcctggg	ttgtgtcatc	cagctctaca	300
tctccctggc	attgggctcc	actgagtgtg	tctcctggc	tgtaatggct	tttgatcgct	360
atgctgcagt	ttgcaaacct	ctccactata	ccgccgtaat	gaacctcag	ctgtgccagg	420
ttctggcagg	ggttgcgtgg	ctgagtggag	tgggaaacac	tcttatccag	ggcactgtca	480
ccctctggct	tcctcgctgt	ggacaccgat	tgctccaaca	tttcttcgtg	aggtaccctc	540
catgattaag	cttgcatgtg	tggacatcca	tgataatgag	gttcagctct	ttgttgcttc	600
actggtcctg	ctcctcttgc	ccttagtgct	aatactgctg	tcctatggac	atatagccaa	660
ggtggtcata	aggatcaagt	cagtccaggc	ctggtgcaaa	ggcctgggga	catgtggatc	720
ccatttgata	gtagtgtccc	tcttctgtgg	gaccatcaca	gctgtctaca	tccagtccaa	780
cagttcttat	gcccattgct	atgggaagtt	catctccctc	ttctatacag	ttgtgacccc	840
gacctcaat	cctctcatct	acacactgag	gaataatgac	gtgaaaggag	cactgcgatt	900
atttaacaga	gacttaggca	cataaaaaat	gaagcagagt	acacagcgct	caactttttt	960
cacaaagcaa	ctttaaaggt	catcttgtat	aatttttcac	tcaagaactt	tgccagctctg	1020
taaaggaaga	gatgtaatct	t				1041

&lt;210&gt; 240

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g89 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 240

atggataagt	ccaattcttc	agtgggtgtc	gaatttgtac	tgttgggact	ctgtagtctt	60
caaaaactcc	agcttttcta	tttttgttct	ttctctgtgt	tgtatacagt	cattgtgctg	120
ggaaatcttc	tcattatcct	cacagtgact	tctgatacca	gcctgcactc	ccctatgtac	180
tttctcttgg	gaaacctttc	ctttgttgac	atttgtcagg	cttcttttgc	taccctaaa	240
atgattgcag	attttctgag	tgcacacgag	accatatctt	tcagtggctg	catagcccaa	300
attttcttta	ttcacctttt	tactggaggg	gagatgggtc	tacttgtttc	gatggcctat	360
gacaggatag	tagccatatg	caaaccctta	tactatgtgg	tcatcatgag	ccgaaggaca	420
tgcactgtct	tggtaatgat	ctcctgggct	gtgagcttgg	tgcacacatt	aagccagtta	480
tcatttactg	tgaacctgcc	tttttgtgga	cctaattgtag	tagacagctt	tttttgtgat	540
cttcctcgag	tcaccaaact	tgcctgcctg	gactcttaca	tcattgaaat	actaattgtg	600
gtcaatagt	gaattctttc	cctaagcaat	ttctctctct	tggtcagctc	ctacatcatt	660
attcttggtta	cagtttggct	caagtcttca	gctgcaatgg	caaaggcatt	ttctacgctg	720
gcttcccata	ttgcagtagt	aatattatct	tttggacctt	gcattcttcat	ctatgtgtgg	780
ccctttacca	tctctccttt	ggataaattt	cttgccatat	tttacctgt	tttcaccccc	840

gtcctaaacc	ccattatttta	tacactaagg	aatagggata	tgaaggctgc	cgtaaggaaa	900
atttgtgaacc	attacctgag	gccaaggaga	atttctgaaa	tgctactagt	agtgaga	957

&lt;210&gt; 241

&lt;211&gt; 935

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g90 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 241

atgcctgcc	agaactctc	ctccgtgaca	gcgtttatcc	tctcaggctt	aaccgaccag	60
ccgggactcc	agatccccgc	cttcttctctg	tttctaggtt	tctacgcggt	cacgggtggtg	120
gggaacctgg	gcttgataat	cctgataggg	ctcaactctc	gcctgcatat	ccccatgtac	180
tttttccccct	tcaacttgtc	cttcatagat	tttagttatt	ccactaccct	cgccccataaa	240
atgctgatga	gctttgtctc	agagaacatc	atttctctatg	cagggtgtat	gactcagctt	300
tttttcttct	gtttctttgt	cttttctgaa	tcctatatcc	tatcagcgat	ggcgtatgac	360
cgctacgtgg	gcatctgtaa	cccactgttg	tacacgggtca	ccatgtctcc	ccagatgtgt	420
ttgtctcttt	tactgggtgt	ctatgggatg	gggatttttg	ggctgtggct	catatgggaa	480
acataatgtt	tatgtccttt	tgtggagaca	accttggtcaa	tcactatatg	tgtgacatcc	540
ttctctctct	tgagctctcc	tgcaacagct	cttacataaa	tttgcgtggg	gtttttatta	600
ttgtgaccgt	tggcattggg	gtgccgattg	tcaccatttt	tctctcttat	ggtttttattc	660
tttccagcat	tctccacatt	agttccacag	agggcagggtc	taaagccttc	agtacctgca	720
gttcccatat	aattgtggta	tcgcttttct	ttgggtcagg	tgctttcatg	tacctcaaac	780
caacctctat	tctacccttg	gaccagggga	aagtgctctc	cattttttgt	actgctgtgg	840
tgcccatgtt	taaccatta	atctacagcc	tgaggaataa	agatgtcaaa	gttgccctga	900
ggagaacctt	ttgcagaaaa	ttagtctctt	aaaaa			935

&lt;210&gt; 242

&lt;211&gt; 1071

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g91 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 242

atgaattggg	taaataagag	tgtcccacag	gagttcattc	tgtagtttt	ctcagatcaa	60
ccatggctag	agattccacc	ctttgtgatg	tttctgtttt	cctatatctt	gacaatcttt	120
ggcaatctga	caataattct	tgtgtcacat	gtggatttca	aactccacac	ccctatgtac	180
ttttttctta	gcaatctctc	actcctggac	ctttgtctata	ccacaagtac	agttccacaa	240
atgctggtaa	acatatgcaa	caccaggaaa	gtaatcagtt	atggtggctg	tgtggcccag	300
cttttcattt	tcttggcctt	gggttccaca	gaatgtcttc	tcttggccgt	catgtgcttt	360
gataggtttg	tagctatttg	tcggcctctc	cattactcaa	ttatcatgca	ccagaggctc	420
tgcttccagt	tggcagctgc	atcctggatt	agtggcttta	gcaattcagt	attacagtcc	480
acctggacac	ttaagatgcc	actgtgtggt	cacaaagaag	tggatcactt	cttctgtgaa	540
gtccctgctc	tgctcaagtt	gtcctgtgtt	gacacaacag	caaatgaggc	tgaactattc	600
ttcatcagtg	tgctattcct	tctaataccc	gtgacactca	tccttatatc	gtatgctttt	660
attgtccaag	cagtgttgag	aatccagtct	gctgaaggtc	aacgaaaggc	atttgggaca	720
tgtggctccc	atctaattgt	ggtgtcactt	ttttatggta	cagctatctc	catgtacctg	780
caaccacctt	caccagctc	caaagaccgg	ggaaagatgg	tttctctctt	ctgtggaatc	840
attgcacca	tgctgaatcc	ccttatatat	acacttagga	acaaagaggt	aaaggaagcc	900
tttaaaaggt	tgggtgcaaa	gagtccttct	aatcaagaaa	taagaaatat	gcaaatgata	960
agctttgcta	aagacacagt	gcttacttac	cttactaact	tctccgcaag	ttgtcctatt	1020
tttgtcatta	ctatagaaaa	ctattgtaat	ctccctcaaa	gaaaatttcc	t	1071

&lt;210&gt; 243

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g92 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 243

cacacagagc	cacggaatct	cacaggagcc	tgagaactcc	tcctcctggg	actctcagag	60
gatccagaac	tgagcccat	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgagggaac	tcctcatcag	cctggctgtc	agctctgact	cccacctcca	cacccaatg	180
tgcttcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcacctcggc	cacggttccc	240
aagatgattg	tggacatgcg	gtcgcatagc	ggagtcattc	cttatgcgga	ctgcctgaca	300
cggatgtctt	tcttggtcct	ttttgcatgt	gtagaagaca	tgctcctgac	tgtgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcacgt	gaatcctcac	420
ctctgtgtct	tcttagtttc	ggtgtccttt	tccttagcct	gttggattcc	cagctgcgca	480
gttggattgt	gttgcaattc	accttcttca	agaatgtgga	aatctcta	tttgtctgtg	540
acctatctca	acctctcaag	cttgccctgtt	ctgacagcat	catcgatagc	atgttcatat	600
atttcgatag	tactatgttt	ggttttcttc	ccatttcagg	gacccctttg	tcttactata	660
aaattgtccc	ctccattcta	aggatttcat	ctgcagatgg	gtagtataaa	gccttctccg	720
cctgtggctc	tcacctgcca	gttgtttgct	tattttatgg	aacaggcatt	ggcgtgtacc	780
tgacttcagc	tgtggcacca	ccctcagga	atggtgtggt	ggcgtcagtg	acgtatgctg	840
tggtcacccc	catgctgaac	cctttcatct	acagcctgag	aaacagggac	attcaaagcg	900
ccctgtggag	gctggcgagc	agaacagtca	aatctcatga	tctgttccat	cctttttct	959

&lt;210&gt; 244

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g93 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 244

atggaggggt	tcaactgttc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agagattctt	ttttgtggta	ttttctgtct	tctattta	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtgcta	tcacctcac	accttactc	tcccatgtac	180
ttctgtctca	gcaacctgtc	tctcattgac	atgtgcctgt	cctcctttgc	cacaccaaag	240
atgattatgg	acttttttgc	tctgcgtaag	accatctctt	ttgaaggctg	catttctcag	300
atcttttttt	gcacctcttc	accgggactg	agattgtgct	gctgatctcc	atgtcttttg	360
acaggatata	tgccatatgt	aaacctctcc	attattcaac	aattatgagc	caaagagtgt	420
gtgttgagct	tgtggccggt	tcttgacag	tgggctttct	gcatacaatg	agccaattag	480
cttttaccct	ctatttgccc	ttctgtggtc	ccaatgttgt	agagtttttt	ctgtgatctt	540
cctttgggtca	tccagctagc	ttgtatggat	atttatgttc	ttgggatctt	catgatttca	600
actagtgggt	tgattgctct	tataagtttt	ctgcttttgc	tcacctccta	catcattgtt	660
cttattactg	tcagggaacta	ctcctccaca	ggatcctcca	aggctctttc	tacctgtaca	720
gcacatttta	ttgttgtgtt	aatgttcttt	gggcctgtga	ttttcattta	tgtgtggcct	780
tccacaaact	tcctggtaga	caaaattctc	tctgttttct	ataccatctt	cactcccttt	840
ctgaatccac	ttatctatac	tttgagaaac	caggaagtga	agacagcaat	gaagaagtaa	900
ctgaatattc	agtattttcag	tcttgggaaa	actgtctccg			939

&lt;210&gt; 245

&lt;211&gt; 1014

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g94 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 245

atgatattgc	ctgctagctt	ttcttaagga	acaatggaaa	caagcagtgt	aagttctgga	60
acagatttca	tccttctggg	gttttctgat	cgaccccaat	tagagcacat	catctcagtg	120
gttgtcttca	tcattctatat	tgtgactctg	gtaggaaata	caaccatcat	tcttgtatct	180
tatctagaca	cccagctcca	taccttcattg	tattttttct	tatccaattt	gtctttcttg	240



gacctctgtt	atacaactag	cattatcccc	cagatgctgg	caaatcaatg	gggccccaaa	300
aaatctatta	cttatggagg	gtgtgtactc	caattctttt	ttgtccttga	cttgggagcc	360
acagaatgtc	ttctgttggc	tgtgatggcc	tatgatcggt	atgctgctgt	ctgtcaacct	420
cttcactaca	ccttaaaatg	caccctcagc	tttgccactg	cctgggtgag	tggctcttgc	480
agtgccttaa	ttgtttgctc	cttgactttg	aagtgtgcaa	gatgtgggca	ccgggaagtg	540
gataattttt	tctgtgagat	gccagcattg	atcaagatgg	cttgtgtcta	ttcaaaagta	600
attgagattg	ttgtctttgc	tttcggagtg	gtatttcttt	tcgtacctct	atcactaatt	660
cttatctcat	atggagttat	cactcaagct	gtaatgagga	tcaagtcagc	aacaagggtg	720
caaaagatcc	ttaatacatg	tggctcccac	ctcacagtag	taattctggt	ttatggaaca	780
atcattttata	tatacatgaa	gccacagaat	accatatccc	aagatgaagg	gaagttcttc	840
actctttttac	acaatcatca	caccagcctc	taaccttccc	atctacactt	taagaacaa	900
agatgtaaa	agtgcactga	agagaatact	gtggatgaaa	aaatcttcag	cagaatcatg	960
aattagatgg	aaaaaagtag	aatgtagagc	actaaagaaa	tattggcatt	tatc	1014

&lt;210&gt; 246

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g95 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 246

atgcaccaag	gaaattgaac	tactgtctct	aaattctttc	tcctgggaat	cacaacaaag	60
cctaagagc	agcagtttat	cttcatgctg	tttctatgca	cgtatctggt	cactatggta	120
agaaaattac	ttatcatcct	ggcgtttg	agtgatgctc	acctccatgg	ccccatatat	180
ttcttccttg	ccaatctatc	tttactaac	gtctgcatca	caaccactac	agtccccaaa	240
atcttggcag	atattcaaag	ccagaattca	accatatcct	ttgaaggatg	ccctgcacaa	300
atgtagtttt	aaatattcct	ggtggatctg	gataatttcc	tattggtaga	catggcatat	360
aattgataca	ttgccatctg	tcacccatta	cactatatgt	ggtagtactg	agtcccaga	420
actgtgccct	gttggttgtg	actccatggg	ttatctccaa	ccttgtctca	atactgcac	480
tcagtctgct	aagccactta	actttctgtg	atttcacata	tcttctatga	cctggaaccc	540
atttttagggc	ttgcttgctc	agacacccaa	atcaacaact	tgataattac	tgccattggg	600
gaagtagtta	tcttcacccc	ctttaccttc	acattcttgt	ctcctatggc	cttattggca	660
gcactatgct	tggagtcca	tcagccaagg	ggaagtagaa	aacattctct	acatgtgggt	720
cccatctctc	agttgtgccc	caggtcttct	atgggttcat	cattggagtc	tactttctct	780
ccttttttgc	ctactcagca	gaaagggatg	aggtagctgc	tatcatgtat	acaactgtaa	840
ctcacttgat	caaatcattt	atctgtagtc	taagggaacga	ggacatgaaa	ggagcactga	900
ggagaccact	cagcagacaa	ggtttttctg	gagtggtgag	c		941

&lt;210&gt; 247

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g96 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 247

atgatgaaga	agaaccaaac	catgatctca	gagttcctgc	tcctgggcct	tccatccaac	60
ctgagcagcg	gaatctgttc	tatgccttgt	tcttggccgt	gtatcttacc	acctcctgg	120
ggaacctcct	cgtcattgtc	ctcattcgac	tggactccca	cctccacatg	cctatgtatt	180
tgtgtctcag	caacttgctc	ttctctgacc	tctgcttttc	ctcggtcaca	atgccccaat	240
tgctgcagaa	catgcagagc	caaaacccat	ccatccctt	tgcggactgc	ctggctcaga	300
tgtactttca	tctgttttat	ggagtctctg	agagcttcc	ccttgtggtc	atggcttata	360
actgctatgt	ggctatttgc	tttccctctg	actacaccac	tatcatgagc	cccaagtgtt	420
gccttggctc	gctgacactc	tcctggctgt	tgaccactgc	ccatgccacg	ttgcacacct	480
tgcttatggc	caggctgtcc	ttttgtgctg	agaatgtgat	tcctcacttt	ttctgtgata	540
catctacctt	gttgaagctg	gcctgctcca	acacgcaagt	caatgggtgg	gtgatgtttt	600
tcattggcgg	gctcatcctt	gtcatcccat	tcctactcct	catcatgtcc	tgtgcaagaa	660
tcgtctccac	catcctcagg	gtcccttcca	ctgggggcat	ccagaaggct	ttctccacct	720

```

gtggccccca cctctctgtg gtgtctctct tctatgggac aattattggt ctctacttgt    780
gcccatgtac gaatcataac actgtgaagg acactgtcat ggctgtgatg tacactgggg    840
tgaccacat gctgaacccc ttcactaca gcctgaggaa cagagacatg agggggaacc    900
ctgggcagag tcttcagcac aaagaaaatt tttttgtctt t          941

```

&lt;210&gt; 248

&lt;211&gt; 994

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g97 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 248

```

atggctgccg agaactcctc ctccgtgaca gagtttatcc tcgcaggcct aatccaccag    60
ccgggactcc aggtccccgt cttcttcctg tttctagggt tctacgcggg cacgggtggg    120
gggaacctgg gcttgataat cctgataggg ctcaactctc gcctgcatac ccccatgtac    180
ttttccccct tcaacttgtc cctcgtagat tttagtttct ctacgacat catcccaaa    240
atgtgatga gttttgtctc aaggaagaac attatttctc tcacaggggt tatgagtcag    300
ttctttctct tctgtttctt tgtcttttct gagtcttca tcctgtcggt gatgggtgtag    360
gaccgctacg tgggcatctg taaccactg ttgtacacga tcaccatgtc tcccagggtg    420
tgtttgtctc ttttactggg tgtctacggg atgggggttt ttggggctgt ggctcataca    480
ggaaatatag tgtttctcac cttttgtgca gacaaccttg tcaatcacta catgtgtgac    540
atccttcccc tcttgagct ctcctgcaac ggctcttaca taaatgtcct ggtcatcttt    600
attgttgtag ccgttggcat tggggtgccc attgttgccg tttttatctc ttatggtttt    660
attctttcca gcattctccg cgttagttct gctgagggca ggtctaaagc cttcagtagc    720
tgcagctcct acataattgc agtttctctt ttctttgggt caggagcttt tacgtacctc    780
aaacccccct ccattttacc cctggaccag gggaaagtgt cctccctgtt ctataccact    840
gtggtgcccc tgtttaaccc attaatctac agcctgagga ataaggatgt caaacttgcc    900
ctgaagagaa ccttttccag aataagcttt tcttgaaaaa aatttttagaa acagaaaaga    960
gatactagga tttttttaaa atcagattgc tttt          994

```

&lt;210&gt; 249

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g98 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 249

```

atgtcgaatg aggacatgga acaggataat acaacattgc tgacagagtt tgttctcaca    60
ggacttacat atcagccaga gtggaaaatg cccctgttct tgggtgttctt ggtgatctat    120
ctcatcacta ttgtgtggaa ccttgggtctg attgtcttta tctggaatga cccacaactt    180
cacatcccc a tgtacttttt tcttgggagt ttgaccttgg ttgatgcttg gatattcttc    240
acagtaactc ccaaaatgtt ggttaatttc ttggccaaaa acaggatgat atctctgtct    300
gaatgcatga ttcaattttt ttcttttgca tttgggtggaa ctacagaatg ttttctcttg    360
gcaacaatgg catatgatcg ctatgtagcc atatgcaaac ctttactata tccagtgatt    420
atgaacaatt cactatgcat acggctgtta gccttctcat ttttaggtgg cttcctccat    480
gccttaattc atgaagtcc t tatattcaga ttaaccttct gcaattctaa cataatacat    540
catttttact gtgatattat accactgttt atgatttctt gtactgacct ttctattaat    600
tttctaattg tttttatttt gtctggctca attcagggtat tcaccattgt gacagttctt    660
aattcttaca catttgctct tttcacaatc ctaaaaaaga agtctgttag aggcgtaagg    720
aaagcctttt ccacctgtgg agcccatctc ttatctgtct ctttatatta tggcccactt    780
atcttcatgt atttgcgccc tgcattctca caagcagatg accaagatat gatagactct    840
gtcttttata caatcataat tcctttgcta aatccatta tctacagctt gagaaataaa    900
caagtaatag attcattcac aaaaatggta aaaagaaatg tt          942

```

&lt;210&gt; 250

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g99 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 250

atggagggga	aaaatctgac	cagcatctca	gaatgtttcc	tccctgggggt	ctctgagcag	60
ctggaggagc	agaagccccct	ctttgggtcc	ttcctgttca	tgtacttggt	cacgggtggca	120
ggcaacctcc	tcatcattct	agtcattcatt	actgacactc	aactccatac	ccccatgtac	180
ttctttctag	ccaacctctc	ccttgcagat	gcctgctttg	tgtccaccac	agtccctaag	240
atgctggcaa	acatacagat	ccagagtcag	gccatctcct	actcaggggt	tctactacag	300
ttgtattttt	tcatgttatt	tgtgatgctg	gaggcattcc	tcttggcgggt	catggcctat	360
gactgctacg	tggccatatg	ccacccactt	cattacattc	tgatcatgag	ccctggggtc	420
tgcattcttc	ccgtgtctgc	atcctggatc	atgaatgccc	tccactccct	tctacacaca	480
cttctgatga	acagcctgtc	cttctgcgca	aaccatgaga	tcccacactt	cttctgtgac	540
atcaatcccc	tcctgagtct	gtcctgcaca	gaccccttca	ccaatgagct	ggtgatcttc	600
atcactgggg	gtctcacagg	actcatttgt	gtgctttgcc	tgattatctc	ttacacgaac	660
gttttctcga	ccatcctgaa	gatcccatca	gctcagggga	agcggaaaagc	cttttccacc	720
tgcagctctc	atctctccgt	ggtctctctc	ttctttggga	cttctttttg	tgttgatttc	780
agttctccct	caacccactc	ggcccagaag	gacacagttg	catcagtgat	gtacacagtg	840
gtaactccaa	tgttgaatcc	ctttatctac	agtttgagga	accaagaaat	aaagtcttcc	900
ctgagaaagt	taatctgggt	tcggaaaatt	cattccct			939

&lt;210&gt; 251

&lt;211&gt; 931

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g100 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 251

atggaagagg	aaaatgcaac	attgctgaca	gagtttgttc	tcacaggact	tttatatcaa	60
ccacagtgga	aaatacccct	gttcttgaca	ttcttggtta	tatatctcat	caccatcatg	120
gggaatcttg	gtctgattgc	gtcatctg	aaagaccctc	accttcagat	cccaatgtac	180
ttactcctcg	ggaatttagc	ttttgtagat	gcttgatgat	catctacagt	gactccaaag	240
atgctgaata	acttcttagc	taagagtaag	atgggtatctc	tgctgaaaag	caaaatacag	300
tttttttctg	ttgcaatcag	tgtaaccact	gaatgttttc	tcttggcaac	aatggcatat	360
gategctatg	tagccatatg	caaaccctta	ctttatccag	ccattatgac	caatggactg	420
tgcattccggc	tatgtagggtg	gtcttcttca	tgtcttaatac	catgaaggat	ttttattcag	480
actaaccttc	tgtaactcca	acgtagtaca	ccacatttac	tgtgacatta	tcccattgtc	540
taagatttct	tgtactgatt	cttctattaa	ttttctaatg	gtttttattt	tctcagggtc	600
aattcaagtt	ttcaccattg	ggactgggtct	tatatcttat	acatttgtcc	tctttacaat	660
cttgaaaaag	aaatctgtca	aagggtataag	aaaagccttc	tccacctgtg	gagctcatct	720
cttatctgta	tctttatacc	atgggcccct	cgacttcatg	tatatgggct	ctgcatcccc	780
acaggctgat	gacgaagaca	tgatggagtc	tctattttac	actgtcatag	ttcctttatt	840
aaatcccatg	acctacagcc	tgagaaacaa	acaagtaata	gcttcattca	caaaaatggt	900
caaaagaaat	aatatttaga	tctcttactc	a			931

&lt;210&gt; 252

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g101 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 252

ttctgtttgt	tcccagccac	agtctccaag	gcagtgggtga	aatttttggc	agagacaatt	60
tccttctcct	attatgtgat	acaaatgctg	gtatttttgt	tctttgtgac	tactgaatgc	120
aatcttttag	cctccctggg	caaggacatt	tatatgccaa	tcagacaacc	catgctctat	180

cctgtcacta	tgtcccaagt	ttgttgatc	caattagtg	cttcatgtta	cgggcatgga	240
gttatccata	ctatgttttt	aggaggttca	atctctatat	ttgccttttg	taagttcaaa	300
ccatcatcag	cttttttgg	gacagtttcc	cactcttggt	cctctcctgc	tcagacacct	360
acataatgaa	ttctttgttc	tttttcactg	ggtgcttcat	ttggatgagc	tcttgaccag	420
tcactccttg	ctcccacatg	ttcatcattg	tcactttctt	gaggatcttc	tcagttgttag	480
ttgaatctaa	agggttttctt	gctttttctt	cacatctaac	tgctatcatt	ctcttctatg	540
gggacattat	atttatatat	gtgacattct	tccaactatt	ttctgaacca	agaccagact	600
gtatccattt	tctacatggt	aagaattctt	ttgttaagcc	ccattatcta	ttgtttaata	660
aaaatgcaag	tgatttggtt	tcttgaaaat				690

&lt;210&gt; 253

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g102 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 253

cttttttttt	ttgtctgaca	cagcatcctg	acctgatagg	aaggagtaaa	agaaatttgg	60
tactttcagg	aatttctgac	atatccaaga	catagaaact	cctgtttgtc	tcttctcgca	120
tgtattattc	ctcaagaatt	ttcctaagga	ggacagtaaa	cattctattt	ctgcttaagg	180
ttatctcatt	gctttgttat	gggtcaaaac	tcagttgtgt	catttttgtt	gttactgcag	240
aatttttagct	tttggcctcc	aggatctgcc	attgctatat	tattatttgt	aaccttctct	300
ctacccaatt	ctcacattaa	aagcttttaa	tttcaattct	gacggctcat	tacaataaga	360
gagtatgtat	ttcaataaca	acatcaaaca	ctatgtctta	gctcttcttt	ggcagatcca	420
atgtggtgaa	caacttctct	gatcttctct	tgctcttaga	tttatcctgc	acatttgtga	480
gtttctgac	tccatctcag	cttctctgac	atagtcctgg	tcccataat	tttatcattg	540
tggtcaatat	aaagatttag	ttagctgaag	ggaagcaca	agacttctct	atctgtccat	600
tataatttgc	tactgtcagc	aattttttaa	tggcacacat	acatatt		647

&lt;210&gt; 254

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g103 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 254

ttcatggaaa	ataggaatat	tgctactgtc	tttattctcc	tgggactttc	tcaaaacaag	60
aacattgaag	ttttttggtt	tgtattattt	gtattttgct	acattgctat	ttggatggaa	120
aacttcatca	taatgatttc	tatcatgtac	atthagctaa	ttgaccaacc	catgtatttc	180
ttccttaatt	acctcgact	ctcagatctt	tgctacatat	ccactgtggc	ccccaagcta	240
atgattgacc	tactaacaga	aaggaagatc	gtttctata	ataactgcat	gatacagcta	300
tttatcactc	acttccttgg	agacattgag	atcttcatac	tcaaagcaat	ggcctatgac	360
cactacatag	ccatctgcaa	gcacctgcac	tacaccatca	tcacgaccaa	gcaaagctgt	420
aacaccatca	tcatagcttg	ttgtactggg	ggatttatac	actctgccag	tcagtttctt	480
cttaccatct	tcttaccggt	ctgtggtctt	aatgagatag	atcagtactt	ctgctatgtg	540
tatcctctgc	tgaagttggc	tcgcattgat	atatacagaa	ttggtttctt	ggtaattgtt	600
aattcaggcc	tgatttcttt	gttggctttt	gtgattttga	tgggtgtctta	ttatttgata	660
ttatccacca	tcagggttta	ctctgctgag	agtcatacca	aagctctttc	aacctgtagc	720
tctcacataa	tagttgtggt	cctattcttt	gtgctgccc	tcttcattta	catcagacca	780
gccataaact	ttccagaaga	taaagtgttt	gttctcttct	gtgccatcat	tgctcccatg	840
ttcagtcctc	ttatctacat	gctgagaaag	gtggagatga	agaacgctgt	aaggaaaatg	900
tggtgtcatc	aattgcttct	ggcaaggaag	taactt			936

&lt;210&gt; 255

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g104 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 255

atggccatgg	acaatgtcac	agcagtgttt	cagttttctcc	ttattggcat	ttctaactat	60
cctcaatgga	gagacacggt	tttcacatta	gtgctgataa	tttacctcag	cacattgttg	120
gggaatggat	ttatgatctt	tcttattcac	tttgacccca	acctccacac	tccaatctac	180
ttcttcctta	gtaacctgtc	tttcttagac	ctttgttatg	gaacagcttc	catgccccag	240
gctttgggtgc	attgtttctc	tacccatccc	tacctctctt	atccccgatg	tttgggtcaa	300
acgagtgtct	ccttggcctt	ggccacagca	gagtgcctcc	tactggctgc	catggcctat	360
gaccgtgtgg	ttgctatcag	caatcccctg	cgttattcag	tggttatgaa	tggcccagtg	420
tgtgtctgct	tggttgctac	ctcatggggg	acatcacttg	tgctcactgc	catgctcatc	480
ctatccctga	ggcttcactt	ctgtggggct	aatgtcatca	accattttgc	ctgtgagatt	540
ctctccctca	ttaagctgac	ctgttctgat	accagcctca	atgaatttat	gatcctcatc	600
accagtatct	tcaccctgct	gctaccattt	gggtttgttc	tcctctccta	catacgaatt	660
gctatggcta	tcataaggat	tcgtcactc	cagggcaggc	tcaaggcctt	taccacatgt	720
ggctctcacc	tgaccgtggg	gacaatcttc	tatgggtcag	ccatctccat	gtatatgaaa	780
actcagtcga	agtccctacc	tgaccaggac	aagtttatct	cagtgtttta	tggagctttg	840
acaccatgt	tgaaccccct	gatatatagc	ctgagaaaaa	aagatgttaa	acggggcaata	900
aggaaagtta	tgttgaaaag	gaca				924

&lt;210&gt; 256

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g105 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 256

atggaagcag	aaaaccttac	agaattatca	gaattcctcc	tcttaggact	ctcagatgat	60
cctgaaactgc	agcccgtcct	ctttgggctg	ttcctgtcca	tgtacctggg	catgggtgctg	120
gggaacctac	tcatactcct	ggccgtcagc	tctgactccc	acctccacag	ccccatgtaa	180
ttcttcctct	ccaacttgte	ctttgtggac	acctgtttca	tctgcaccac	agtccccaag	240
atgctagtga	acatccaggc	acggagcaaa	gacatctcct	acatgggggtg	cctcactcag	300
gtgtattttt	aaatgatgtt	tgctggaatg	gatactttcc	tactggctgt	gatagcctat	360
gaccggtttg	tggccatctg	ccaccactg	cagtacatgg	tcatacataa	cccccatctc	420
tgtggcctcc	tggttctggc	atcttggttc	atcattttct	ggttctccct	ggttcatatt	480
ctactgatga	agaggctgac	cttctccaca	ggcactgaga	ttccgcattt	cttctgtgaa	540
ctggctcagg	tcctcaaggt	ggcccgtctc	gatgctctcc	tcattaacat	tgtcttgtat	600
gtggccacgg	cactgctggg	tgtgtttcct	gtagctggga	tcctcttctc	ctactctcag	660
attgtctcct	ccttaatgag	aatgtcctcc	accgagggca	agtacaaagc	cttttccacc	720
tgtggatctc	acctctgtgt	ggtctccttg	ttctatggaa	caggacttgg	ggtctatctg	780
agttctgctg	tgacccattc	ttcccagagc	agctccatgg	cctcagtgat	gtacgccatg	840
gtcaccacca	tgtgaacct	cttcatctac	agcctgagga	acaaggatgt	gaagggggcc	900
ctggggagac	tccttagcag	ggcagcctct	tgtctcttac	ggtacacaac	ctcagaacta	960
agaggatgct	a					971

&lt;210&gt; 257

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g106 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 257

atggaggggt	tcaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaaactcc	agatattctt	ttctgtggtg	ttttctgtct	tctatttaat	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtccta	ttcacctcac	accttcactc	tcgcatgtac	180

ttcctgctca	gcaacatgct	tcattgacat	gtgcctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgctc	tgcgtaacac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgctg	ttgatctcca	tgtcttttga	360
caggatatatt	gccatatgta	aacctctcca	ctattcaaca	attatgagcc	aaagagtgtg	420
tgttgagctt	gtggcagttt	cttggtggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttccttttg	tcattccagtt	agcttgatata	gataatttatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgattgc	tcttataagt	tttctgcttt	tgctcacctc	ctacatcatt	660
gttcttaata	ttgtcaggga	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcgcat	ttattgttgt	gttaatgttc	tttgggccc	gtattttcat	ttatgtgtgg	780
ccttcacaaa	acttctcgtg	agacaaaatt	ctctccggtt	tctataccat	cttcactccc	840
tttctgaatc	cacttatcta	tactttgaga	aac			873

&lt;210&gt; 258

&lt;211&gt; 985

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g107 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 258

tacacagagc	cacagaatct	cacaggtgtc	tcagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctggg	ctgttcctgt	ccatgtacct	ggtcacggtg	120
ctggggaacc	tgctcatcat	cctggctgtc	agctctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttggct	gacatcggtt	tcacctccac	cacggtcccc	240
aagatgattg	tggacatgca	aactcacagc	agagtcatct	cctatgaagg	ctgcctgact	300
cagatgtctt	tttttgcctt	ttttgcatgt	atggatgaca	tgctcctgag	tgtgatggcc	360
tatgaccggt	ttgtggccat	ctgtcaccac	ctgcactacc	gaatcatcat	gaaccacgc	420
ctctgtggct	tcttaatctt	gttgtctttt	tttattagtc	ttttggactc	ccagttgcac	480
aatttgatta	tgttacagct	cacctgcttc	aaggatgtgg	acatttctaa	tttcttctgt	540
gacccttctc	aactcctcca	ccttaggtgt	tccgacacct	tcataaatga	aatggtcata	600
tatttcatgg	tggtcatatt	tggtgtcttc	cctatctcag	ggatcctttt	ctcttactat	660
aaaattgttt	ccccattctt	gagagtcca	acatcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacagggct	tgtagggtac	780
ctcagttcag	ctgtgttacc	atcccccagg	aagagtatgg	tggcttcagt	gatgtacact	840
gtggtcaccc	ccatgctgaa	ccccttcac	tacagcctga	ggaacaagga	cattcaaagt	900
gccctgtgca	ggctgcatgg	cagaatcatc	aaatctcatc	atctccatcc	ttttgttat	960
atgggataga	aatggcagca	aaatt				985

&lt;210&gt; 259

&lt;211&gt; 976

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g108 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 259

ctcaccatgc	cacacctcag	caacaccaca	tctgagttcc	caatcttctt	cctaacaggc	60
ttccctgggc	tggaggcctt	ccacatctgg	atctcaattc	ccttcttctt	tctgagcaca	120
gttgctctct	tagggaacag	catgactcta	ttggttggtta	ttctggagcc	aaacctccat	180
gaaccatagt	actgttttct	cttcatgctg	tctgccgctg	acctggggct	gacctctctc	240
acaatgcccc	cgacctcag	tgctctctgg	ttcagtgcac	gtgaaatcat	cctcaatgca	300
tgtatcatcc	agctcttttt	cctccacagc	tctggcttta	tggaatcctc	agtactgatg	360
gccatggctt	ttgaccgctt	tggtgccatt	tgcagacccc	tcagatatgc	taccatcctg	420
acagactcca	gaattctaaa	gattggtgta	gcaatagtc	taagaacatt	gatcagcctc	480
tctccatccc	tctttctcat	taagagactg	tcattttgca	aagtcaatgt	cctttcccat	540
tcttactgct	tccaccctga	tgcgcttaaa	gttgcatggt	ctgattcaag	gatgaacagc	600
tatggaggct	tagctgttct	cattctgggt	accgggggtg	gtacaccatg	tgttgcgctt	660
tctacatcc	tgataatcca	ctctgtacta	aacatcatct	cttcagaggg	acggaggaag	720

gccttcgaca	cttgtggatc	tcacattggg	gcagttgcag	tcttctacat	tccctggggt	780
gttctttcag	ttgtccacag	atttttccac	aaggcttcac	caatatgtcc	accactatt	840
gtccaacatc	tatttccttg	gcccctctcg	gtgaacccc	atcatatata	gtgtgaagac	900
taaacaaatc	cgcagggcta	tcttcaaact	ctttcaaaca	aaatcaaaag	aaatgtaatg	960
ggggcttttc	ttcctg					976

&lt;210&gt; 260

&lt;211&gt; 884

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g109 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 260

atccaatgca	agggctaata	gaagtgaatt	aagacattct	ctgtaactcc	aatattaaat	60
ggaaaccggg	aaatagccag	attcctctcc	aacctgtcct	tggctggcat	cggtttcccc	120
tccaccatag	tctccaagat	gattgtggac	atccagtctc	acagcagagt	catctcctat	180
gcgggctgcc	tgactcaggt	atctcttttt	gccgtttttg	gatgcatgga	agacatgctt	240
ctgagtgatg	tggcttatga	ccggtttggt	gacatctgtc	accctctgga	ttatccagtc	300
atcatgaacc	catgtttctg	tggcttccct	gttttgttgt	ctttttttct	cagtctttta	360
gactcccagc	tgcacaattg	gattgcctta	caaattacct	gcttcaagga	tgtggaaatt	420
cccaatttct	tctgtgaccc	ttctcaacac	cccacccttg	cctgttgatg	caccttcacc	480
aatgacatag	tcatgtattt	ccttgctgcc	atatttggtt	ttcttcccat	ttcggggacc	540
ttttcatctt	actataaaat	tgtttccctc	attctgaggg	tttcatcatc	aagtgggaag	600
tataaagcct	tctccacctg	tggctctcac	ctgtcagttg	tttgcttatt	ttatggaaac	660
ggctttggag	gggacctcag	ttcagacatg	tcctcttata	ccagaaaagg	tgcagtggcc	720
tcagtgatgt	acacggtggt	tactcccata	ctgaaccctt	tcattctacg	cctaacaggg	780
aaattaaaag	tgccctgcgg	cagctgcact	gcagaatagt	ctaattctcat	tttcttatta	840
tctgttccat	tccttccgta	gtgtgagtta	gaaaaggcag	caag		884

&lt;210&gt; 261

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g110 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 261

tacacagact	cgcagaatct	cacaggtgtc	ttagaatttc	tcttctctgg	actctcagag	60
gatccagaac	tgcagcccg	cctcgctggg	ctgttcctgt	ccatgtacct	gatcacgggtg	120
ctggggaacc	tgctcatcat	cctggccggt	agctgtgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaactt	gtccttggtt	gacatcggac	tcacctctgc	caccatccct	240
aagatgattg	ttgatatgca	atctcacagc	agaatcatct	cctatgaggg	ctgcctgatg	300
cagatgtctt	tatctatttt	gtgtgtatga	atgacatggt	cctgactgtg	atggcctatg	360
accagtttgt	ggccatttgt	cacccccctac	gctaccaggt	catcatgaat	ccccatctct	420
gtgtcttctt	agttttgggt	tcttttattc	ttagcctgtt	gaactcccag	ctgcacaatc	480
agattgtgtt	acaattcacc	tgcttcaaga	atgtggaaat	ctttaatttt	ttctgtgagc	540
catctcaact	tctcaacctt	gcctgttctg	acagtgtcat	caataacata	ttcatgtatt	600
tagatagagt	tatatttggt	tttcttccca	tctcagggat	ccttttgtct	tactataaaa	660
ttgtctcttc	cattctaaga	attccatcat	cagatgggaa	gtataaagcc	ttctccacat	720
gtggctctca	cctggcagtt	gtttgcttat	tttatggaa	aggacttgga	gcctacctca	780
gttcagctgc	gtcctctttc	cccaggaagg	gtgcggtcac	ctcagtgtatg	tacactgtgg	840
tcattccctat	gctgaacccc	ttcatctaca	gcctgagaaa	cagggacatt	aaaagtggcc	900
tgtggagggt	gcacagcaga	acagtcta	ctcattatct	gttccatcct	ttctgtagt	959

&lt;210&gt; 262

&lt;211&gt; 955

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g111 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 262

cacacagagc	cacagaatct	cacagggtgc	tcagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccact	ccttgctggg	ctgttcctat	ccatgtgcct	ggtcacgatg	120
ctggggaacc	tgetcatcat	cctggccgtc	agccctgact	cccacctcca	catccccatg	180
tactttcttc	tctccaacct	gtccttgctc	gacattgggt	tcaccttggc	cacgggtcccc	240
aagatgattg	tagacatgca	atcacatagc	agagtcactc	cccatgcagg	ctgtctgaca	300
cagatacctt	tctttgtcct	ttttgtatgt	atagatgaca	tgtccttgac	tgtgatggcc	360
tatgactgat	ttgtggccat	ctgtcaccct	ctgcactacc	cagtcacatc	gaatcctcac	420
ctctgtgtct	tcttagtggt	gatgtctttt	tccttagcct	gttggattcc	tagctgcaca	480
actggattgt	tacaattcac	ctgcttcaag	aatgtggaaa	tctctaattt	tttctgtgac	540
tgatctcaac	ttctcaacct	tgcctgttct	gactgtcatc	agtaacatat	tcatacattt	600
agatagtact	atatttgggt	ttcttcccat	ttcagggatc	cttttgtctt	actataaaat	660
tgtgccctcc	attctaagaa	ttccattgtc	agatgggaag	tataaagcct	tctccacctg	720
tggtctctac	ctggcaattg	tttgettatt	ttatggaaac	ggcattggca	tgtacctgac	780
ttcagctgtg	tcaccagccc	ccaggaatgg	tgtggtggca	tcagtgttgt	acgctatggt	840
cacccccatg	ctgaaccctt	tcattctgcg	cctgagaaac	aggggcattc	aaagtgcctt	900
gtggaggctg	tgcaggagga	aagtctaadc	tcattgatctg	tttcatcctt	tttct	955

&lt;210&gt; 263

&lt;211&gt; 1049

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g112 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 263

atgtcccaac	tggaagggga	caacataacc	tgggtgagtg	agttcatcct	aatgggtctc	60
tccagtgaac	ggcagaccga	ggctggactc	tttatcttat	ttggggctgc	ctacctgctg	120
accctgctgg	gcaatgggct	catcctgtct	ctgatctggc	tggacgtgag	actccacctg	180
cccatgtatt	tcttctcttg	caacctctca	cttgtgaaca	tctgctacac	ctccagcagg	240
gtccctcaga	tgtgtgtgca	ctgcaccagc	aaagaaagac	catctccttt	gcccgatgtg	300
ggacccagct	ctttttctcc	ctggccctcg	gggggaccga	gtttttgttg	ctggccgcaa	360
tggcctatga	ccgctacgtg	gctgttttgc	acccctgtg	ttacatagca	gtgatgagcc	420
caaggctctg	catggcactg	gcagctgtct	cttggctagt	gggcctggct	aattctgcta	480
tggagacggc	actgaccatg	cacctgccca	cctgtgggca	caacgtgctg	aacctgtgg	540
cctgtgagac	actggcactg	gtcaggtcgg	cctgcgtgga	catcaccttc	aatcaggtgg	600
tcatagtggc	ctccagtgtg	gtggtgctgc	tgggtgccctg	ctgcctggtc	tcgctgtcct	660
acaccctcat	tgtagtgtcc	gtcctgcaga	tccactccac	ccaggggcac	cgcaaggcct	720
ttgggacctg	tgcctcccac	ctcactgtgg	tctccatata	ctatgggatg	gccctcttta	780
cctacatgca	gcctcgctcc	atggcctcag	ctgagcagga	aaaggtgatg	gtactctctt	840
atgtgtgtgt	gacccccatg	ttgaatcctt	tcattctacg	tctgcggaac	aaggatgtga	900
aggcagctct	gagtcgagct	ctgatgagga	gctctgaatt	aaaacattag	agagtggttt	960
gagtaacaag	aaggcctcac	tctgaaaaca	gtgggcattg	gactgtgctc	tccagtataa	1020
cgtgtgtacg	catgtgtgtg	tatgtgtgtg				1049

&lt;210&gt; 264

&lt;211&gt; 955

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g113 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 264

atggacagtc	ccagcaatgc	caccgtgccc	tgtggctttc	tccttcaagg	cttctccgaa	60
ttccccgacc	tgagaccctg	gctcttctct	ttgctgctgg	gggtgcacct	ggccaccctg	120



ggcggaacc	tgctcaccct	ggtggccgtg	gcctcgatgc	caagccggca	gcccattgctg	180
ctcttcctgt	gccagctgtc	agccatcgag	ctgtgctaca	cgctgggtggt	ggtgccccgc	240
tccctggctg	acctgagcac	gccggggcca	ccgcaggggc	agccctatct	ccttcctgag	300
ctgcgccctt	cagatgcaga	tgtttgtggc	tctgggcggg	gccgagtgtc	tcctgctggc	360
cgccatggct	aatgaccgct	acgtggccat	ctgccaccgc	ttgcgctacg	cgccgtgggtg	420
acccccgggc	tgtgcgcgcg	actggctctg	gctgctgcct	caggggactg	gcggtgtcgt	480
ggggctcacg	gtgccatctt	ccacctgcct	ttctgcggtc	cccgcctgct	gctgcacttc	540
ttctgcgaca	tcacggcgct	gctgcacctg	gcctgcacgc	ggactacgcc	gacgagctgc	600
ctctgctggg	cgccctgcctg	gtgctgctgc	tgctgccctc	ggtgctcctc	ctggcctcct	660
atggcgccat	cgccgcgcgc	ctggccgcct	gcgtgcccc	aaaggccggg	gcaaggccgc	720
ctccacctgc	gccttgccac	tggcagtcac	cttctgtcac	tacggctgcg	ccaccttcct	780
gtacgtgcgg	cccaggggcca	gctactcccc	gcgcctggac	cgcacctcgg	cgctggtcta	840
caccaacgtc	acgcgcgtgc	tgtgcccact	catctacagc	ctgcgcaacc	gcgagatcac	900
cgccgcctcg	agcagggtgc	tggggcgccg	gcggccaggc	caagctccag	gcggg	955

&lt;210&gt; 265

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g114 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 265

atgggagact	ggaataacag	tgatgctgtg	gagcccatat	ttatcctgag	gggttttctc	60
ggactggagt	atgttcattc	ttggctctcc	atcctcttct	gtcttgcata	tttggttagca	120
tttatgggta	atgttaccat	cctgtctgtc	atgttgtag	aatcctctct	ccatcagccc	180
atgtattact	ttatttccat	cttagcagt	aatgacctgg	ggatgtccct	gtctacactt	240
cccaccatgc	ttgctgtgtt	atggttggat	gtccagaga	tccaggcaag	tgcttgctat	300
gctcagctgt	tcttcattcca	cacattcaca	ttcctggagt	cctcagtgtt	gctggccatg	360
gcctttgacc	gttttgttgc	tatctgccat	ccactgcact	acccaccat	cctcaccaac	420
agtgttaattg	gcaaaattgg	tttggcctgt	ttgctacgaa	gcttgggagt	tgtacttccc	480
acacctttgc	tactgagaca	ctatcactac	tgccatggca	atgccctctc	tcacgccttc	540
tgtttgcacc	aggatgttct	aagattatcc	tgtacagatg	ccaggaccaa	cagtatttat	600
gggctttgtg	tagtcattgc	cacactaggt	gtggattcaa	tcttcatact	tctttcttat	660
gttctgattc	ttaatactgt	gctggatatt	gcattctcgt	aagagcagct	aaaggcactc	720
aacacatgtg	tatcccatat	ctgtgtgggt	cttatcttct	ttgtgccagt	tattgggggtg	780
tcatgggtcc	atcgcttttg	gaagcatctg	tctcccatag	tccacatcct	catggcagac	840
atctaccttc	ttcttcccc	agtccttaac	cctattgtct	atagtgtcag	aacaaagcag	900
attcgtctag	gaattctcca	caagtttgtc	ctaaggagga	ggttt		945

&lt;210&gt; 266

&lt;211&gt; 869

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g115 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 266

tttcatggct	ggatttccat	gcccttttgc	tgtatttact	tgatgcctct	gctgagcaat	60
gctacaattc	tactgacaat	ctggctctgat	cgtactcttc	gggaccttat	gttctacttt	120
ctagccatct	tatcagccat	agacctagcc	ctctcaacat	cctcagtggc	tcgtatgttg	180
ggatctctct	ggtttgatgc	acataaaatt	ggctttggag	cctgggtagc	ccagatgttt	240
ctgatacaca	ctttcacagg	aatggagtcc	actgtgctgc	tggcaatggc	ctttgaccgc	300
tatgtggcca	tctgtacatc	actccactat	acctctactc	tgacaccccg	agtattggca	360
ggcattgggtg	tgagcattat	aatgcgcccc	gtcctgctca	tgttgcccat	tctctacctc	420
accatcgctc	tgcccttctg	tgaggctcgg	attattgccc	actcctactg	tgagcacatg	480
ggtattgcta	agttggcctg	tgctagcatt	cacatcaatg	ctatttatgg	gctttttgtg	540
gcttcttatt	ttggatgtcg	cacttgttgg	aatctcctat	acctacattc	tccgagctgt	600
tttccacctc	ccatctcaag	acgctcgtca	caaagcactg	agaacgtgtg	gctcacatgt	660

tggggtcatg tgtgttttct atacaccctc cctcttctcc ttctcacct accgatttcg	720
caaaaaaaaaat tccccgttat gtccacattc ttgttgccaa cctctatgtg gtcattccac	780
ctgccctcaa tcctattatc tatggtgtga gaaccaaaca gattcatgag catgtgggtcc	840
atactttcac ctcaaagtaa ggtctctta	869

&lt;210&gt; 267

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g116 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 267

acatgctggg ttttgatggt gaacgtgggt aatgcctaca cctgaggact atcaggagcc	60
actttcaaca ccatctgcac atttgccgc ttcttctgtg atgacaatta gatcaaatc	120
tgacacatcc tgccctgct gaagctcatt tgaataactt caggaaacag caagataatt	180
attgtgatct ttgacagctt ttatgattat agctggcact aggtcatcc tgatctctta	240
cctgctaate atcagggctt tgaggatgaa atcatcgagt ggcaaagcca ataattttat	300
ccatccactt gtgcctccca cctaactgct atgaccttcc tttgggatcc ccatcttcag	360
acatgtgaag tacctcagat aaatcactga cagaagacaa gttggcatca tgacttgac	420
catctttatt cctatgctag aacttttgat ccaaagtcta aagaaggata tacaagttgc	480
cttcaaaaag gccataggta acttctgggt ttttgagagg	520

&lt;210&gt; 268

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g117 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(952)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 268

attagcacia tgtctgtctt caaaagttct gcataaaacc ctgcttcct ccaaacgggc	60
ctctcaggcc ttgaaagcag atatgacttg atttcctgc ccatcttctt ggtttatgcc	120
acctcaattg ccgggaacat tagcatcctc ttcatatca gaactgagtc ttccctccac	180
caaccgatgt attactttct gtcaatgctg gcattcactg acctgggcct atctaact	240
accttaccta ccatgttcag tgtcttcttg ttccatgcc gggagatctc cttcaatgct	300
tgtctgggtcc aaatgtactt cattcatgtt ttctcgatta ttgagtcagc tgtactcctg	360
gctatggcct ttgactgctt tatagcaatc tgagaacctt tgcgctatgc agccatccta	420
accaatgatg taatcattgg gattgggttg gcaattgctg gaaggccctt ggctctggtc	480
tttccagctt ctttctctt gaagaggctt caatatcatg atgtcaatat tctgtcctac	540
ctcttctgcc tgcaccagga cctcataaag acgactgtat ccaactgtcg agtcagcagc	600
atctatggcc tcatgggtgg catctgttcc atgggacttg attcagtgtc tctcctctc	660
tcctatgtcc tcatcctggg cacagcgttg agtatagcct ccaaggcaga gagagtgaga	720
gccctcaata cttgcatctc ccacatctgt gctgtactca ccttctatac accaatgatt	780
gggtatctta tgatccatcg ctatggacag aatgtcctc aattgtccat gtgctgatgg	840
ccaatgtcta cttgntgggt ccacctctca tgaaccccg gttctacagt gttagaccag	900
ncagattcgt gacagaatct ttcaataaaa attcagaaac atgaagtgtga ga	952

&lt;210&gt; 269

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g118 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 269

atggaagagg	aaaatgcaac	attactgaca	gaatttggtc	tcacaggatt	tttatgtcaa	60
caaggatttt	tatgggaaat	accctgttc	ctggcattct	tggtaataga	tctcatcacc	120
atcatgggga	atcttggctc	gatttttctc	atctggaaag	accctcacct	tcatatttca	180
atgtacttat	tccttgggag	tttagctttt	gtggatactt	ggttatcatc	cacagtgact	240
ccgaagatgc	tgatcaactt	cttagctaag	agtaagatga	tatctctctc	tgaatgcatg	300
gtacaatttt	ttttcccttg	caatcagtg	aaccacagaa	tgttttatct	cggcatcaat	360
ggcatatgat	cgctatgcag	acatatgcaa	acctttactt	tatccagtca	ttatgaccaa	420
tgaactatgc	atctggctat	ttgtcttgtc	atttctaggt	ggcctttttc	atgctttaat	480
ccatgaaggt	tttttattca	gactaacctt	ctgtaactcc	aacatgatac	aacattttta	540
ctgtgacatt	atcccatgtg	taaagatttc	atgtactgat	tcttgattta	attttctaata	600
gtttttttat	ttctcagggt	caattcaagt	tttaaccatt	gggattggtt	ttgtatctta	660
tatgtttgtt	ctctttacaa	tcttaaaaaa	gaagtctaac	aaaggcataa	gggaagcctt	720
ttccacctgt	ggagcccatt	acatacctct	ctctttatgt	tatggcctcc	ttctcttcat	780
gtatgtgggc	cctgcagctc	cacaagcaga	taatcaagat	atgatggagt	atctatttta	840
ccctatcatt	gtgcgtttgt	taaacatat	tactacagcc	tgagaaataa	gcaataatag	900
gttcactcac	aaaaatgtta	aaataaaaata	tttgcattgc	atac		944

&lt;210&gt; 270

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g119 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 270

atgtccatta	tcaacacatc	atatgttgaa	atcaccacct	tcttcttggt	tgggatgcca	60
gggctagaat	atgcacacat	ctggatctct	atccccatct	gcagcatgta	tcttattgct	120
attctaggaa	atggcaccat	tctttttatc	atcaagacag	agccctcctt	gcattggccc	180
atgtactatt	ttctttccat	gttggctatg	tcagacttgg	gtttgtcttt	atcatctctg	240
cccactgtgt	taagcatctt	cctgttcaat	gcccctgaaa	cttcttctag	tgcttgcttt	300
gcccaggaat	tcttcattca	tggattctca	gtactggagt	cctcagtcct	cctgatcatg	360
tcatttgata	gattcctagc	catccacaat	cctctgagat	acacctcaat	cctgacaact	420
gtcagagtgt	cccaaataag	gatagtattc	tcctttaaga	gcattgctct	ggttcttccc	480
ttccctttca	ctttaagaag	cttgagatat	tgcaagaaaa	accaattatc	ccattcctac	540
tgtctccacc	aggatgtcat	gaagttggcc	tgttctgaca	acagaattga	tgttatctat	600
ggcttttttg	gagcactctg	ccttatggta	gactttatc	tcattgctgt	gtcttacacc	660
ctgatcctca	agactgtacc	gggaattgca	tccaaaaagg	aggagcttaa	ggctctcaat	720
acttgtgttt	cacacatctg	tgcatgtatc	atcttctacc	tgcccatcat	caacctggcc	780
gttgtccacc	gctttgcegg	gcattgtctc	cccctcatta	atgttctcat	ggcaaatggt	840
ctcctacttg	tacctccgct	gatgaaacca	attgtttatt	gtgtaaaaac	taaacagatt	900
agagtgcagag	ttgtagcaaa	attgtgtcaa	tggaagatt			939

&lt;210&gt; 271

&lt;211&gt; 940

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g120 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 271

atggaagaga	aaaatgcaac	attgctgaca	gagtttggtc	tcacattatt	tttatatcaa	60
cctcactgga	aaatacccct	gttcctggca	ttcttggtaa	tatatctcat	caccatcttt	120
gggaatcttg	gtctgattgc	tgctgtatgg	aaagaccctc	accttcatat	cccaatatac	180
ttattccttg	agaatttagc	ttttgtggat	gatttggtat	catccacatg	actctgaaga	240
tgctgatcaa	cttcttcact	aagagtaagt	tgatttctct	ctgaatgctg	gatacatttt	300
ttttcccttg	caattgggtg	aaccacagaa	tgttttatct	tggcaacaat	ggcatatgat	360
cgctatgtag	ccatatgcaa	acctttactt	tatccagtca	ttatgaccaa	tggactgtgc	420

atctggctat	taatcttgtc	atttctaggt	ggccttcttc	atgctttaat	tcataaggt	480
tttttataga	ttaaccttct	gtaattccaa	cacaatacat	cacttttaat	gtgacattat	540
cccattgtta	aaaattttct	gtactgattc	ttctattaac	tttccaatgg	tttttatttt	600
ctcatgttca	attcaagttt	tcaccattgg	gactgttctt	gtatcttata	catttgcctt	660
ctctacaatc	ttgaaaaaga	agtctgtcaa	aggcataaga	aaagacttct	ccacctgtgg	720
agctcatatc	ttacctgtat	ctttatacta	tgggcccttc	gccttcatgt	atgtgggctc	780
tgcaccccaa	cgggctgatg	accaagatat	gatggagtct	ctattttaca	ctgtcatagt	840
tcctttatta	aatcccatga	tctacagcct	gagaaataag	caagtaatag	attcattcac	900
aaaaatgttc	aaaggaaata	atgttttagat	ctcttactca			940

&lt;210&gt; 272

&lt;211&gt; 512

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g121 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 272

tgtctagctc	aagtttctctg	agtagcagaa	aagtattgat	aaattttatt	tgttgcactt	60
tttaacaaaa	caaaaagcat	ctgccaaaca	cagaacattg	caacacctag	gccctgggct	120
ttccccagc	attcattcac	tagcacctca	tgttttgggg	gcacaagcac	agggctttct	180
taggctgtaa	aatcacctat	atcatctgtc	tgtccactgc	ttcaactcct	tctgcagtat	240
ccctgcaaca	atattacatg	cttatgaaat	gctgcagaca	gggaattcct	gtccttctag	300
gacctctctc	tggctgtggg	cagctttacc	ataagttctt	gtcttcttat	gctgaaattg	360
atttcatttt	catcttcacg	tattattgct	tctttgctct	ctcgggtgtc	aactgagctt	420
catcgtcttc	ccttctaata	ctccttctgt	catctatttt	gtcttttctt	cttcagactg	480
aaaatccctg	gtagtacctg	tagtttctt	cc			512

&lt;210&gt; 273

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g122 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 273

atgaatacca	ctctatttca	tccttactct	ttccttcttc	tgggaattcc	tgggctggaa	60
agtagcctc	tctgggttgg	ttttcctttc	tttgctgtgt	tcctgacagc	tgtccttggg	120
aatatcacca	tcctttttgt	gattcagact	gacagtagtc	tccatcatcc	catgttctac	180
ttcttgcca	ttctgtcatc	tattgacctg	ggcctgtcta	catccaccat	ccctaaaatg	240
cttggcacct	tctggtttac	cctgagagaa	atctcctttg	aaggatgcct	taccagatg	300
ttcttcatcc	acctgtgcac	tggcatggaa	tcagctgtgc	ttgtggccat	ggcctatgat	360
tgtatgtgg	ccatctgtga	ccctctttgc	tacacgttgg	tgctgacaaa	caagggtggg	420
tcagttatgg	cactggccat	ctttctgaga	cccttagtct	ttgtcatacc	ctttgttcta	480
tttatcctaa	ggcttccatt	ttgtggacac	caaattattc	ctcatactta	tgggtgagcac	540
atgggcattg	ccgcctgtc	ttgtgccagc	atcagggtta	acatcatcta	tggcttatgt	600
gccatctcta	tcctggtctt	tgacatcata	gcaattgtca	tttcttatgt	acagatcctt	660
tgtgctgtat	ttctactctc	ttcacatgat	gcacgactca	aggcattcag	cacctgtggc	720
tctcatgtgt	gtgtcatgtt	gactttctat	atgcctgcac	ttttctcatt	catgacccat	780
aggtttgggc	ggaatatacc	tcactttatc	cacattcttc	tggctaattt	ctatgtagtc	840
attccacctg	ctctcaactc	tgtaatattt	ggtgtcagaa	ccaaacagat	tagagcacaa	900
gtgctgaaaa	tgtttttcaa	taaa				924

&lt;210&gt; 274

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g123 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 274

atggaagagg	aaaatgcaac	attgctgaca	gagtttgttc	tcacaggatt	ttacatcaa	60
cctgactgta	aaataccgct	cttcctggca	ttcttggtaa	tatatctcat	caccatcatg	120
gggaatcttg	gtctaattgt	tctcatctgg	aaagaccctc	accttcatat	cccaatgtac	180
ttattccttg	ggagtttagc	ctttgtggat	gcttcgttat	catccacagt	gactccgaag	240
atgctgatca	acttccttagc	taagagtaag	atgatatctc	tctctgaatg	catggtacaa	300
tttttttccc	ttgtaaccac	tgtaaccaca	gaatgttttc	tcttggcaac	aatggcatat	360
gatcgctatg	tagccatttg	caaagcttta	ctttatccag	tcattatgac	caatgaacta	420
tgcatcagc	tattagtctt	gtcatttata	ggtggccttc	ttcatgcttt	aatccatgaa	480
gctttttcat	tcagattaac	cttctgtaat	tccaacataa	tacaacactt	ttactgtgac	540
attatcccat	tgtaaagat	ttcctgtact	gattcctcta	ttaactttct	aatgggtttt	600
attttcgcag	gttctgttca	agtttttacc	attggaacta	ttcttatatc	ttatacaatt	660
atcctcttta	caatcttaga	aaagaagtct	atcaaaggga	tacgaaaagc	tgtctccacc	720
tgtggggctc	atctcttata	tgtatcttta	tactatggcc	ccctcacctt	caaatatctg	780
ggctctgcct	ctccgcaagc	agatgaccaa	gatatgatgg	agtctctatt	ttacactgtc	840
atagtccctt	tattaaatcc	catgatctac	agcctgagaa	acaagcaagt	aatagcttca	900
ttcacaaaaa	tggtcaaaag	caatggtt				927

&lt;210&gt; 275

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g124 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 275

atggcgaaata	gaaacaacgt	gacagagttt	attctatttg	ggcttacaga	gaatccaaaa	60
atgcagaaaa	tcataattgt	tgtgttttgt	catctacatc	accaccatga	taggaaatgt	120
gctcattgtg	gtcaccatca	ctgccagccc	atcattgagg	tcccccattg	aatttttcct	180
ggcctatctg	tcctttattg	atgcctgcta	ttcctctgtc	aatgtctcta	agctgatcac	240
agattcactc	tatgaaaaca	agactatctt	actcaatgga	tgtatgactc	aagtcttttg	300
agaacatttt	ttcagagggt	ttgagggtcat	cctacttact	gtaatggcct	atgactgcta	360
tgtgggtcatc	tgcaagccct	tgcgctatac	caccatcatg	aagcagcatg	tttgtagcct	420
gctagtggga	gtgtcacggg	tgggaggcct	tcttcattgca	accatacaga	tcctcttcat	480
cttccaatta	cctttctgta	gttctaattg	catagatcac	tttactgtga	tctcaaccct	540
ttgtctaatc	ttgcctgcac	taatacccac	actcaggac	tcttcgttgc	tgccaacagt	600
gggttcatat	gcctgttaaa	ctttctcttg	ctcctggtct	cctatgtggt	catactgtac	660
tccttaagga	cccacagctt	agaggcaagg	cacaaaggcc	tctccacctg	tgtctccacc	720
aacacagttg	tcattcttatt	ctttataccc	tgcataattg	tgtacatgag	acctccagct	780
actttaccca	ttgataaagc	agttgctgta	ttctacacta	tgataactcc	tatgttaaac	840
cccttaatct	acaccttgag	gaatgctcag	atgaaaaatg	ccattaggaa	attgtgtagt	900
aggaaagcta	tttcaagtgt	caaa				924

&lt;210&gt; 276

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g125 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 276

atgttccttc	ccaatgacac	ccagtttcac	ccctcctcct	tcctgttgct	ggggatccca	60
ggactagaaa	cacttcacat	ctggatcggc	tttccttctt	gtgctgtgta	catgatcgca	120
ctcatagga	acttcactat	tctacttggt	atcaagactg	acagcagcct	acaccagccc	180
atgttctact	tcctggccat	gttggccacc	actgatgtgg	gtctctcaac	agctaccatc	240
cctaagatgc	ttggaatctt	ctggatcaac	ctcagagggg	tcactcttga	agcctgcctc	300
accagatgt	tttttatcca	caacttcaca	cttatggagt	cagcagtcct	tgtggcaatg	360

gcttatgaca	gctatgtggc	catctgcaat	ccactccaat	atagcgccat	cctcaccaac	420
aagggtgttt	ctgtgattgg	tcttggtgtg	tttgtgaggg	ctttaatttt	cgtcattccc	480
tctatacttc	ttatattgcg	gttgcccttc	tgtgggaatc	atgtaattcc	ccacacctac	540
tgtgagcaca	tgggtcttgc	tcatctatct	tgtgccagca	tcaaaatcaa	tattatttat	600
ggtttatgtg	ccatttgtaa	tctgggtgtt	gacatcacag	tcattgccct	ctcttatgtg	660
catattcttt	gtgctgtttt	ccgtcttcct	actcatgagc	cccgaactca	gtccctcagc	720
acatgtggtt	cacatgtgtg	tgtaatcctt	gccttctata	caccagccct	cttttctttt	780
atgactcatt	gctttggccg	aaatgtgcc	cgctatatcc	atatactcct	agccaatctc	840
tatgttgtgg	tgccaccaat	gctcaatcct	gtcatatatg	gagtcagaac	caagcagatc	900
tataaatgtg	taaagaaaat	attattgcag	gaacaaggaa	tggaaaagga	agagtaccta	960
ata						963

&lt;210&gt; 277

&lt;211&gt; 894

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g126 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 277

atgagaaatc	acacaatggt	gactgaattc	atcctttctg	gaatccctga	gacagagggc	60
ctagagacag	cccttttatt	cctgtttctc	tcattttatt	tatgcaccct	cttgggaaac	120
gtgcttatcc	ttacagctat	catctcctcc	actcgacttc	acactcctat	gtattttttc	180
ttgggaaacc	tctccatctt	tgacctgggt	ttctcttcaa	cgactgttcc	caagatgttg	240
ttctaccttt	cggggaacag	ccatgctatc	tcgtatgcag	gctgcgtgtc	ccagcttttc	300
ttctaccatt	tcctaggctg	tactgagtgt	ttcctctaca	cagtgatggc	ctgtgaccgc	360
tttgttgcca	tatgttttcc	tttgagatac	acggtcatca	tgaaccacag	ggtgtgcttt	420
atgttggcca	cggggacctg	gatgattggc	tgtgtccatg	ccatgatcct	aactccccctc	480
accttccagt	taccttactg	tggccctaac	aagggtgggt	attactttctg	tgatattcct	540
gcagtgttac	ctctagcctg	taaggacaca	tccttagccc	agagggtagg	ttttacaaat	600
gttgggtctt	tgtctctcat	ttgctttttt	ctcatccttg	tttctataac	ttgcattggg	660
atttccatat	caaaaatccg	ctcagcagag	ggcagcgagc	gggcctttctc	cacctgcagc	720
gctcacctca	ctgcaatcct	ttgtgcttat	gggccagtca	tcgttatcta	tctacaaccc	780
aatcccagtg	ccttgcttgg	ttccataatt	cagatattga	ataatctggt	aaccccaatg	840
ttgaatccac	taatctatag	ccttaggaat	aaggatgtaa	aatcagatca	gccc	894

&lt;210&gt; 278

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g127 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 278

atggaggagg	aaaatacaac	attgctgaca	gagtttggtc	tcacaggatt	tttatatcaa	60
ccacagtggg	aaatacccct	gttccctggc	ttcttggtta	tatagctcat	caccatcatg	120
gggaatcttg	gtctaattgt	tctcatctgg	aaagaccctc	accttcatat	cccaatgtat	180
ttattccgtg	ggagtttggt	ctttgtggat	gcttggttat	catccacagt	gactccaaag	240
atgctgatca	acttcttagc	taagagtaag	atgatatctc	tctctgaatg	catgggtacaa	300
tttttttctt	ttgtaatcag	tgtaaccaca	gaatgtttta	tctcggcatac	aatggcatat	360
gatcgctatg	tagccatttg	caaagcttta	ctttatccag	tcattatgac	caacggacta	420
tgcattccagc	tattagtctt	gtcattttata	ggtggccttc	ttcatgcttt	aatccatgaa	480
atttttttat	tcagattaac	cttctgtaat	tccaacataa	tacaacactt	ttactgtgac	540
attatcccat	tgtaaagat	ttcctgtact	gattctttta	ttacttttct	aatgggtttt	600
atttttcgag	attcaattca	agttttttacc	attggaacta	ttcttatatc	ttatacactt	660
gtctctctta	taactcttaa	aaataagtct	gtcaaaagga	tacaaaaagc	tgtctccacc	720
tgtggagctc	atctcttatc	tgtatcttta	tactatgggc	cccttgtctt	catgtatgtg	780
ggctctgcat	ccccgcaagc	agatgaccaa	gatatgatgg	agtctctatt	ttacactgtc	840
atcgttcctt	tattaaattc	catgatctac	agcctgagaa	acaagcaagt	aatagcttca	900

ttcacaaaaa tgttcaaaag aaatgttttag atctcataca atctctgttc tctgtttact 960  
 aaaattttcc ca 972

<210> 279

<211> 924

<212> DNA

<213> Unknown (H38g128 nucleotide)

<220>

<223> Synthetic construct

<400> 279

atgatgagta	accagacgtt	ggtaaccgag	ttcatcctgc	agggcttttc	ggagcaccca	60
gaataccggg	tgttcttatt	cagctgtttc	ctcttctct	actctggggc	cctcacaggt	120
aatgtcctca	tcaccttggc	catcacgttc	aacctggggc	tccacgtcc	tatgtacttt	180
ttcttactca	acttggttac	tatggacatt	atctgcacct	cttccatcat	gccaagggcg	240
ctggccagtc	tgggtgcgga	agagagctcc	atctcctacg	ggggctgcat	ggcccagctc	300
tatttctctca	cgtgggctgc	atcctcagag	ctgctgctcc	tcacgggtcat	ggcctatgac	360
cggtagcgag	ccatctgcca	cccgtgcat	tacagcagca	tgatgagcaa	ggtgttctgc	420
agcgggctgg	ccacagccgt	gtggctgctc	tgcgcgctca	acacggccat	ccacacgggg	480
ctgatgctgc	gcttggattt	ctgtggcccc	aatgtcatta	tccatttctt	ctgcgaggtc	540
cctccccctgc	tgcttctctc	ctgcagctcc	acctacgtca	acgggtgcat	gattgtcctg	600
gcggatgctt	tctacggcat	agtgaacttc	ctgatgacca	tcgcgtccta	tggcttcctc	660
gtctccagca	tcctgaaggt	gaagactgcc	tgggggaggg	agaaagcctt	ctccacctgc	720
tcttcccacc	tcaccgtggg	gtgcatgtat	tacaccgctg	tcttctacgc	ctacataagc	780
ccggtctctg	gtcacagcgc	aggggaagagc	aagttggctg	gcctgctgta	caactgtgctg	840
agtcttacct	tcaacccccct	catctatact	ttgagaaaca	aggaggtcaa	agcagccctc	900
aggaagcttt	tccttttctt	caga				924

<210> 280

<211> 958

<212> DNA

<213> Unknown (H38g129 nucleotide)

<220>

<223> Synthetic construct

<400> 280

atggatgacg	aaaatgcaac	attgctgaca	gagtttgctc	tcacaggact	tacatatcaa	60
tcagagtggg	aaataccctt	gttcttgcca	ttcttggtta	tatatctcat	caccatcatg	120
gcaaatcttg	gtctgattgc	tgtcatctgg	aaagactcac	accttcacat	tccaatgtac	180
ttattccttg	ggagtttagc	ctttgtggat	gcttggttat	catcctcagt	gacccctaag	240
atgctgatca	gcttttttagc	taagagtatg	attatttctg	tctctgaatg	caagatacaa	300
tttttttctt	ttggaatcag	tgggaaccaca	gaatgttttc	tcttggaac	aatggcatat	360
gatcgctatg	tagccatatg	caaaccctta	ctttatccag	tcattatgac	caatggactg	420
tgtatctggc	tattagtctt	gtcatttata	ggtggctttc	ttcatgcctt	aattcatgaa	480
ggtattttat	tcagattaac	cttctgtaat	tccaacataa	tacatcactt	ttactgtgac	540
attatcccat	tgttaaagat	ttcctgtact	gaccttcta	ttaatttttt	aatgcttttt	600
atthttgtctg	gttcaatata	ggtattcact	atthttgactg	ttcttgcttc	ttatacattht	660
gtcctcttta	caatcttaaa	aaaaaaagtc	tgccaaagac	ataaggaaag	ccttttccac	720
ctgtggagcc	catctcttat	ctgtttcttt	atactatggc	cccttctctt	tcagtatgt	780
gcacctgca	tctccacaag	cagatgatca	agatatgggtg	gagtccttat	tttacctgt	840
cataattcct	ttcttaaatc	ccattatcta	cagcctgaga	aataagcaag	tcatagattc	900
actgacaaaa	acattaaaag	gaaatgttta	gatctcatat	tggaatgtat	tctctatt	958

<210> 281

<211> 933

<212> DNA

<213> Unknown (H38g130 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 281

atggttgaag	aaaatcatatc	catgaaaaat	gagtttatcc	tcacaggatt	tacagatcac	60
cctgagctga	agactctgct	gtttgtggtg	ttctttgcca	tctatctgat	caccgtgggtg	120
gggaatatata	gtttgggtggc	actgatattt	acacaccgtc	ggcttcacac	accaatgtac	180
atctttctgg	gaaatctggc	tcttgtggat	tcttgtgtg	cctgtgctat	tacccccaaa	240
atgttagaga	acttcttttc	tgagggcaaa	aggatttccc	tctatgaatg	tgagtagacag	300
ttttattttc	tttgactgtg	ggaaactgca	gactgctttc	ttctggcagc	agtggcctat	360
gaccgctatg	tggccatctg	caaccactg	cagtaccaca	tcatgatgtc	caagaaactc	420
tgcatcaga	tgaccacagg	cgcttcata	gctggaaatc	tgcatccat	gattcatgta	480
gggcttgat	ttaggttagt	ttctgtgga	ttgaatcaca	tcaaccactt	ttactgtgat	540
actcttccct	tgtatagact	ctcctgtgtt	gaccctttca	tcaatgaact	ggttctattc	600
atcttctcag	gttcagttca	agtctttacc	ataggtagt	tcttaatatc	ttatctctat	660
attcttctta	ctattttcag	aatgaaatcc	aaggaggga	gggcaaagc	cttttctact	720
tgtgcatccc	acttttcac	agtttcatta	ttctatggat	ctattttttt	cctatacatt	780
agaccaaatt	tgcttgaaga	aggaggtaat	gatataccag	ctgctatttt	atttacaata	840
gtagttccct	tactaaatcc	tttcatttat	agtctgagaa	acaaggaagt	aataagtgtc	900
ttaagaaaaa	ttctgctgaa	aataaaatct	caa			933

&lt;210&gt; 282

&lt;211&gt; 979

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g131 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 282

tatacagacc	cacagaatct	aacagatgtc	tttatattcc	tcctcctaga	actctcagag	60
gatccagcac	tgcagctggg	cgtcactggg	ctgtgcctgt	gtgcctgggc	acgggtgctgt	120
ggaacctgct	cagcatcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
tcttccctctg	caacctgtcc	ttgcctgaca	tcgggtttcac	ctccaccacg	gtccccaaga	240
tgatcgtgga	catccaatct	cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	300
tgtctctctc	tgccattttt	ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	360
tatgaccagt	ttgtagccat	ctgtcaccct	ctgtatcatt	cagccatcat	gaacctcgtgt	420
ttctgtggct	tcctgggttt	gttgtctttt	ttttctcagt	cttttagact	cccagctgca	480
aaactgatcg	ccttacaaat	caactgctca	aaggatgtgg	aaattcctaa	ttttttctgt	540
gaccttcttc	aactccccc	tcttgcatgt	tgtgacacct	tcaccaataa	cattatcatg	600
tatttccctg	ctgccaatatt	tgggttttct	cccatctcgg	ggacctttt	ctcttactat	660
aaaattgttt	cctccattct	gagggtttca	tcattcaggt	ggagctataa	agccttcgcc	720
acctgtggat	ctcactgtc	agttgtttgc	tgattttatg	gaacaggcgt	tggagggtac	780
ctcagttcag	atgtgtcgtc	ttccctgaga	aagcgtgcag	tggcctcagt	gatgtacacg	840
gtggtcaccc	ccatgctgaa	tcccttgatc	tacagcctga	gaaacaggga	tattaaaggt	900
gtcctgtggc	agccgtgcag	ccgcacggca	gcacagtctc	atctcaatat	cttatctgtt	960
ccatttcttt	tgcaggatg					979

&lt;210&gt; 283

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g132 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 283

atggaaccac	agttcaccac	ccagggatca	atgtttgtcc	tgtagggta	gtcacagacc	60
caagagctcc	agagagtcac	gttcattctg	ttcctgttag	tctatgttac	caccattgtg	120
ggaaacctcc	ttatcatggg	cacagtgaat	tttgactgcc	ggctccacac	ccatgtattt	180
tctgtcccg	aatctagctc	tcatagacgt	ctgctattcc	acagtcacct	ctccaaagat	240
gctgggtggac	ttcctccatg	agaccaagac	gatctcctac	cagggtgca	tggcccagat	300



```

cttcttcttc caccttttgg gaggtgggac tgtctttttt ctctcagtca tggcctatga 360
ccgctacata gccatctccc agcccctccg gtatgtcacc atcatgaaca ctcaattgtg 420
tgtgggcctg gtagtagccg cctggcgtgg ggggctttgt ccactccatt gtccaactgg 480
ctgtgatacg tccacagcct ctatgtggcc ccaatacct agataacttc tactgtgatg 540
ttccccaagt actgagactt gctgcaactg atacctccct cctggagtgc ctcatgatct 600
ccaacagtgg gctgctagtt atcatctggt tcctcctcag tctgatgtct tatactgtca 660
tcctggtgat gctgaggtcc cactcgggaa aggcaaggag taaggcagct tccacttgca 720
ccaccacat catcgtggtg tccatgatct tcattccatg tatctatata tatacctggc 780
cctttcaccc cattcatcat ggacaaggct gtgtccatca gctacacagt catgaccccc 840
atgctcaacc ccatgatcta caccctgaga aaccaggaca tgaaagcagc catgaggaga 900
ttaggcaagt gcctagtaat ttgcaggag ttaaacttta agtaagttga ctttaaata 960
caaattgctc tggattttta ttttccc 987

```

&lt;210&gt; 284

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g133 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 284

```

atgcaaggag aaaacttcac catttggagc atttttttct tggagggatt ttcccagtac 60
ccagggttag aagtggttct ctctgtcttc agccttgtaa tgtatctgac aacgctcttg 120
ggcaacagca ctcttatttt gatcactatc cttagttcac gccttaaac ccccatgtac 180
ttattccttg gaaatctctc tttcatggat atttggtaca catctgcctc tgttcctact 240
ttgctggtga acttgtgtgc atcccagaaa accattatct tttctgggtg tgctgtacag 300
atgtatctgt cccttgccat gggctccaca gagtgtgtgc tcctggccgt gatggcatat 360
gaccgttatg tggccatttg taacccg 387

```

&lt;210&gt; 285

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g134 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 285

```

tctacagacc cacagaatct aacagatgtc tctatatctc tcctcctaga acctcagagg 60
atccagaacg gcagctgggc ctgtctgggc tgttctctgc catgtgcctg gtcacggtgc 120
tggggaacct gatcatcatc ctggacgtca gccctgactc ccacctcccc acccccatgt 180
acttcttctc ctccaacctg tccttgccctg acatcggttt cacctccacc acgggtccca 240
agatgattgt ggacatccaa tctcacagca gagtcatctt ctatgcaggc tgccctgactc 300
agatgtctct ctgtgccatt tttggaggca tggaagagag acacgctcct gagtgtgatg 360
gcctatgacc gggttgtagc catctgtcac cctcatgtgc attcagccag catgaacccg 420
tgtttctgtg gctttctagt tttgttgtct ttttttttct tcagtctttt agacacccag 480
ctgcacaact tgattgcctt acaaatgacc tgcttcaagg atgtggacat tcctaatttc 540
ttctgtgacc ctctcgaact ccccatctt gcattgtgtg acaccttcac caataacata 600
atcatgtatt tccctgctgc catatttggg tttcttcaga tctcggggac ctttttctct 660
tactataaaa ttgtttctct cattctgagg gtttcttcat cagggtggga ctataaagcc 720
ttctccacct gtgggtctca cctgtcagtt gtttctgtat tttatggaac aggcgttgga 780
gggtacctca gttcagatgt gtcattctcc ccgagaaagg gtgcagtggc ctcatgtgat 840
tacacgggtg tcacccccat gctgaacccc ttcatctaca gcctgagaaa cggggatatt 900
aaaagtgtcc tgcggcggcc gcaaggcagc aaggctaat atcaatatct tcttatctgt 960
tccattcctt ttgtagggtg ggttaaaaaa ggcagcaagg tcaaa 1005

```

&lt;210&gt; 286

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g135 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 286

atgaagaata aaaggaatgt gactgaattc gttttaacag gtcttacaca gaaccctaaa	60
atggagaaag tcatgtttgc agtatttttg gttctttaca tgataacact ttcaggcaac	120
ctgctccttg tggttacaat taccaccagc caggctctta gctcccccat gtacttcttc	180
ctgagccacc tttctttgat agacacagtt tattcttctt cttcagctcc taagttgatt	240
gtcgattccc ttcatgagaa gaaaatcatc tcctttaatg ggtgtatggc tcaagcctat	300
gaagaacaca tttttggtgc tactgagatc atcctgctga cagtgatggc ctgtgacaac	360
tatgtggcca tctgcaaacc tctgcactac acaaccatca tgagccacag cctgtgcatt	420
ctcctagtgg tagtggcctg gataggagga tttctccatg caaatattca gattctattt	480
acagtatggc tgccctcttg tggccccaat gtcataagacc acttcatgtg tgacttgtgc	540
cctttgttaa aactgtttg cctggacact catacccttg gtctctttgt tgctgccaac	600
agtgggttca tctgcttatt aaacttcctt ctctaggtgg tatcctatgt gatcatcttg	660
agatgtttaa agaactatat cttggagggg aggggtaaag ccctctccac ctgtatttct	720
cacatcataa tagtgtctt attctttgtg ccttgtatat ttgtgtatct gcaccagtg	780
acaaactctg cccattgata aagctgctgc tgtattttat actatgggtg tcccaatggt	840
aaatcctttg atctacacac tcagaaatgc tgaggtaaaa agtgcaataa ggaagctttg	900
gagaaaaaaa gttatttcag ataatgacta aataagacca ttgagcactc atcataga	958

&lt;210&gt; 287

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g136 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 287

atggagattg gaaaccatac cacagtgaca gagtttatta ttttggggtt aactgaggat	60
cctacacttt gtgacatctt ctttgtgata tttctaggaa tctacattgt caccttaata	120
ggcaatatca gcataataaa gaagctgttc ccaacttcac actcccatgt acctgttctt	180
cagccacttg gcttttgttg acatagggct tgccacagta gtcacaccta taatgcttat	240
gggattccta agacgtggaa cagccctccc tgtcactagc tgtgaagccc agctctgttc	300
tgtagtcatg tttgggacgt ctgaatgctt cctactggcg accatggcct atgatcgcta	360
tgtggccatc tgctcaccct tgggtgaact caccacttg tccccataa tctgcatact	420
cttagtgggg gtttgctacc tgggtggatg tgtgaatgcc tcaacattta ctagtgttt	480
attgagtctg tctttctgtg gaccaaatac gatagatcat tttttctgtg atttctctcc	540
tttgttgaac ctttctgtc caaatatctc cattcctgaa attatccctt ccatctcttc	600
tggatctatc atttgtgtca cagtatttgc catagccatc tcctacatct acatcctcat	660
caccatcctg aagatgcgct ccgccgaggg gcgccacaag gccttctcca cctgtacctc	720
ccacctcgct gcggttactc tctactatgg aacgattacc ttcatttatg tgatgccccaa	780
atccagttac tcaactagcc agaacagatt gatacgctg tcctacacag tggtaatccc	840
catactgaac ccctttatct atagtctgag gaacagagat gtaaaggagg cactaagaaa	900
ggcaactgtc agaatatatt cttaggatca atttga	937

&lt;210&gt; 288

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g137 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 288

cacacagagc cacggaatct cacagggtgc tgagaattcc tcctcctggg actctcagag	60
gatccagaac tgcagccggc cctcgctttg ctgtccctgt cctgtccat gtatctggtc	120
acgggtgctga ggaacctgct gagcatcccc gctgtcagct ctgactcccc gctccacacc	180
cccacgtact tcttctctc catcctgtgc tgggctgaca tcggtttcac ctgggccacg	240

```

gtttccaaga cgattgtgga catgcagtc catagcagag tcatctctca tgcgggctgc 300
ctgacacaga tgtcttttctt ggtccttttt gcatgtatag aaggcatgct cctgactgtg 360
atggcctatg actgctttgt aggcattctgt cgccctctgc actaccagct catcgtgaat 420
cctcatctct gtgtcttctt tgttttggtg tectttttcc ttagcctgtt ggattcccag 480
ctgcacagtt ggattgtggt acaattcacc atcatcaaga atgtggaaat ctctaatttt 540
gtctgtgacc cctctcaact tctcaaaact gctgttctg acagcgtcat caatagcatc 600
ttcatatatt ttggtagtac tatgtttggt tttcttccca tttcagggat ccttttgtct 660
tactataaaa tcgtccctc cattctaagg atttcatcgt cagatgggaa gtataaagcc 720
ttctccacct atggctctca cctagcagtt ttttgctgat ttgatggaa aggcatggc 780
gtgtacctga cttcagctgt ggcaccacc ctcaggaatg gtgtggtggt gtcagtgatg 840
taagctgtgg tcaccccat gctgaacctt tcatctaca gcctgagaaa cagggacata 900
caaagtgcc tgcggaggct gcgcagcaga acagtcgaat ctcatgatct gttccatcct 960
ttttctggtg t 971

```

&lt;210&gt; 289

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g138 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 289

```

atgattcagc ctatggcgtc acccagcaac agctccactg tcccagtctc tgaattcctc 60
ctcacctgct tcccactt ccagagttgg cagcactggc tctccctgcc cctcagcctt 120
ctcttctctc tggccatggg agctaacc accctctga tcaccatcca gctggaggcc 180
tctctgcacc agccctgta ctacctgctc agcctctct cctgctgga catcgtgctc 240
tgcctcaccg tcatcccaa ggtcctggc atcttctggt atgatcttag gtcgatcagc 300
ttccctgctt gtttctcca gatgttcac atgaacagtt tctcccccatt ggagtcctgc 360
acgtttatgg tcatggccta tgaccgttat gtggccatct gccaccact gcggtacca 420
tccatcatca ctaatcaatt tgtggccaaa gctagtgtct tcattgtggt gcggaatgcg 480
cttcttactg caccattcc tatcctcact tccctgctcc attactgtgg ggaaaatgct 540
attgagaact gcatctgtgc caacttgtct gtgtccaggc tctcctgtga taatttcacc 600
cttaacagaa tctaccaatt tgtggctggt tggacctgct tgggctcaga tttattcctc 660
atcttctctt cttacacctt cattctaaga gctgtgctta gattcaaagc agagggggcg 720
gcagtgaagg ccctgagcac atgtggctcc cacttcatcc tcattctttt cttcagcacc 780
atactgctgg ttgtggtggt gacaaacgtg gccagaaaga aggtcccat ggacatcctg 840
atcctgctga acgtccttca tcaccttatt cctcctgcgt tgaaccctat tgtgtatggg 900
gttcggacca aagagataaa acaggggaatt cagaagttac tgcagagagg gagg 954

```

&lt;210&gt; 290

&lt;211&gt; 713

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g139 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(713)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 290

```

cccaaggctc cggacttttt tgtgtttggc ctaagggcc ttagttttcc ggccggtttt 60
ctccaaaagt acattaagaa ttgtttccaa gccaggagtt ttggccattc aaggtcaggg 120
ccataggatc gttaaggaac cttctgccca ccccttgaa atatccctcc attcatcacg 180
gatccctttg gagtcaaggc tgccaggttt attttgccca gnaatggtgt taatgactct 240
gcccatcccc catcctttca gcacaactcc gttattgtgg aagaaatgct attgagaact 300
gcatctgtgc caatatgtct gtttcagac tctcctgcga tgatgtcacc atcaatcacc 360
tttaccatt tgctggaggc tggactctgc taggatctga cctcatcctt atcttctct 420
cctacacctt cattctgcga gctgtgctga gactcaaggc agagggtgcc gtggcaaagg 480

```

ccctaagcac	atgtggctcc	cacttcatgc	tcatectctt	cttcagcacc	atccttctgg	540
tttttgcct	cacacatgtg	gctaagaaga	aagtctcccc	tgatgtgcca	gtcttgctca	600
atgttctcca	ccatgtcatt	cctgcagccc	ttaaccccat	catttacggg	gtgagaaccc	660
aagaaattaa	gcaggggaatg	cagaggttgt	tgaagaaagg	gtgctaacaa	gga	713

&lt;210&gt; 291

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g140 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 291

atgaattccc	tgaaggacgg	gaatcacacc	gctctgacgg	ggttcatcct	attgggctta	60
acagatgatc	caatccttcg	agtcacctc	ttcatgatca	tcctatctgg	taatctcagc	120
ataattattc	ttatcagaat	ttcttctcag	ctccatcatc	ctatgtatct	ctttctgagc	180
cacttggtct	ttgctgacat	ggcctattca	tcttctgtca	caccaacat	gcttgtaaac	240
ttcctgggtg	agagaaatac	agtctcctac	cttggatgtg	ccatccagct	tggttcagcg	300
gctttctttg	caacagtcga	atgcgtcctt	ctggctgcca	tggcctatga	ccgctttgtg	360
gcaatttgca	gtccactgct	ttattcaacc	aaaatgtcca	cacaagtcag	tgtccagcta	420
ctcttagtag	ttacatagc	tggttttctc	attgctgtct	cctatactac	ttccttctat	480
tttttactct	tctgtggacc	aaatcaagtc	aatcattttt	tctgtgattt	cgctccctta	540
cttgaactct	cctgttctga	tatcagtgct	tccacagttg	ttctctcatt	ttcttctgga	600
tccatcattg	tggtcactgt	gtgtgtcata	gccgtctgct	acatctatat	cctcatcacc	660
atcctgaaga	tgcgctccac	tgaggggcac	cacaaggcct	tctccacctg	cacttccacc	720
ctcactgtgg	ttaccctggt	ctatgggacc	attaccttca	tttatgtgat	gcccaatttt	780
agctactcaa	ctgaccagaa	caaggtgggtg	tctgtgttgt	acacagtggg	gattcccatg	840
ttgaaccccc	tgatctacag	cctcaggaac	aaggagatta	agggggctct	gaagagagag	900
cttgttagaa	aaatactttc	tcat				924

&lt;210&gt; 292

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g141 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 292

gatacagacc	cacagagtct	aacagatgtc	tctatattcc	tcctcctcga	actctcagag	60
gatccagaac	tgcaaccggg	cgctcgctggg	ctgttcctgt	ccatgtgcct	cgtcagtggg	120
ctggagaacc	tgctcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgctt	gacatcggtt	tcacctccac	cacgggtcccc	240
aagatgattg	tggaatcca	gtctcacagc	agagtcactt	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tgaggcatg	gaagagagac	atgctcctga	gtgtgatggc	360
ctatgaccgg	tttgtagcca	tctgtcaccc	tctatatcgc	tcagccatct	tgaaccctgt	420
tttctgtggc	ttcctagatt	tggtgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctggga	accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	600
tcagcatgta	tttccctgct	gccgtatttg	gttttctttc	catctcgggg	acccttttct	660
cttactgtaa	aatgggtttc	tccattctga	gggtttctac	atcagggtggg	aagtataaac	720
cttctccacc	tgagggtccc	acctgtcagt	tgtttctcga	ttttatggaa	caggcggttg	780
agagtacctc	gggttcagatg	tgcatctctc	cccgagaaag	gggtcagtgg	cctcagtgat	840
gtacacgggtg	gtcaccccca	tgctgaaccc	cttcatctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcgggcggc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	tttgtagggt	gggttaacaa	agacagcaag	gtcaaaa		1006

&lt;210&gt; 293

&lt;211&gt; 933

&lt;212&gt; DNA

<213> Unknown (H38g142 nucleotide)

<220>

<223> Synthetic construct

<400> 293

atgggggactg	gaaatgacac	cactgtggta	gagtttactc	ttttgggggtt	atctgaggat	60
actacagttt	gtgctatttt	atttcttgtg	tttctaggaa	tttatgttgt	caccttaatg	120
ggtaatatca	gcataattgt	attgatcaga	agaagtcac	atcttcatac	acccatgtac	180
attttcctct	gccatttggc	ctttgtagac	attgggtact	cctcatcagt	cacacctgtc	240
atgctcatga	gcttcctaag	gaaagaaacc	tctctccctg	ttgctgggtg	tgtggcccag	300
ctcgtttctg	tagtgacgtt	tggtacggcc	gagtgccttc	tgctggctgc	catggcctat	360
gatcgctatg	tggccatctg	ctcaccctg	ctctactcta	cctgcatgtc	ccctggagtc	420
tgcacatctt	tagtgggcat	gtcctacctg	gggtgatgtg	tgaatgcttg	gacattcatt	480
ggctgcttat	taagactgtc	cttctgtggg	ccaaataaag	tcaatcactt	tttctgtgac	540
tattcaccac	ttttgaagct	tgcttggtcc	catgatttta	cttttgaaat	aattccagct	600
atctcttctg	gatctatcat	tgtggccact	gtgtgtgtca	tagccataac	ctacatctat	660
atcctcatca	ccatcctgaa	gatgcactcc	accaagggcc	gccacaaggc	cttctccacc	720
tgcacctccc	acctcactgc	agtcactctg	ttctatggga	ccattacctt	catttatgtg	780
atgcccaagt	ccagctactc	aactgaccag	aacaagggtg	tgtctgtgtt	ctacaccgtg	840
gtgattccca	tgttgaaccc	cctgatctac	agcctcagga	acaaggagat	taagggggct	900
ctgaagagag	agcttagaat	aaaaatattt	tct			933

<210> 294

<211> 942

<212> DNA

<213> Unknown (H38g143 nucleotide)

<220>

<223> Synthetic construct

<400> 294

atgctcctta	gcaattcaag	ctggaggcta	tcccagcctt	cttttctcct	ggtagggatt	60
ccagggttag	aggaaagcca	gcaactggatt	gcaactgccc	tgggcaccc	ttacctcctt	120
gcttttagtg	gcaatgttac	cattctcttc	atcatctgga	tggaccacac	cttgaccacaa	180
tctatgtacc	tcttccctgc	catgctagct	gccatcgacc	tgggtctggc	ctcctccact	240
gcacccaaag	cccttgacgt	gtccttggtt	catgcccacg	agattgggta	catcgtctgc	300
ctgatccaga	tggtcttcat	ccatgcattc	tcctccatgg	agtcaggggt	acttggtggc	360
atggctctgg	atcgctatgt	agccatttgt	cacccttggc	accattccac	aatcctgcac	420
ccaggggtca	tagggcgcat	cggaatgggtg	gtgctgggtg	ggggattact	actccttacc	480
cccttcccca	ttttgttggg	aacacttacc	ttctgccaag	ccaccatcat	aggccatgcc	540
tattgtgaac	atatggctgt	tgtgaaactt	gcctgctcag	aaaccacagt	caatcgagct	600
tatgggctga	ctatggcctt	gcttgtgatt	gggctggatg	ttctggccat	tgggtgttcc	660
tatgccaca	tcctccaggc	agtgtgaag	gtaccaggga	gtgaggcccg	acttaaggcg	720
tttagcacat	gtggctctca	tatttgtgtc	atcctggctc	tctatgtccc	tggaaatttc	780
tccttctca	ctcaccgctt	tggtcatcat	gtacccatc	atgtccatgt	tcttctggcc	840
acacggatc	tcctcatgcc	acctgcgtc	aatcctcttg	tctatggagt	gaagactcag	900
cagatccgcc	agcgagtgtc	cagagtgttt	acacaaaagg	at		942

<210> 295

<211> 945

<212> DNA

<213> Unknown (H38g144 nucleotide)

<220>

<223> Synthetic construct

<400> 295

atgacaaaag	gcaatcgtag	cacagtgaac	gaatttgtcc	tcattgggatt	cacagaccgt	60
cctgagctgc	agctccccct	ctttgtgggtg	ttccttgtca	tttatctcat	caccctgggtg	120
ggaaaccttg	gcatgatcct	gctgatcaga	gcagactcgc	ggctccacac	ccccatgtac	180

tacttctca	gtcacctggc	attcattgat	ctgtgttact	catcttctat	tgggccaag	240
atgctgcaaa	atgtattggg	gaagaaaaaa	accatctcct	tttcaggctg	ttttgctcag	300
ctgtacttct	cgggtgcttt	tgccactaca	gaatgattcc	tcttggccac	aatgccctac	360
gaccgctacg	tggccatctg	caacccccctg	atttacacag	ctattatgac	gcagcgggtc	420
tgcagggagt	tagtgatagg	ggtctatacc	tatggcttcc	gaaactctgt	gatacagaca	480
gctctgacgt	ttcagctgtc	tttctgcaac	tccgacgtca	tccaccactt	ctactgtgct	540
gacccccctc	tcttggccct	ctcctgctct	gacaccacac	acaaagaaaa	gcagctcatg	600
atcttctctg	cagtaaactc	cactgggtcc	ctccttacca	tcttcatctc	ctacatttgc	660
atcctctttt	ccattataaa	aatccagtct	tccgagggca	agtgcagagc	attttccacc	720
cgtgcctccc	acctcactgt	cgtcaccatc	ttttatggca	cactattttt	catgtacctg	780
cagcaaccaa	aagcggggaa	ttcatggaag	caaacaag	tagtctctgt	gttttatagt	840
cttgtaattc	ccatgcttaa	ccctcttatc	tatgcctga	gaaacacaga	agtaaaggat	900
gccctgaaaa	aaatgctaga	gggcaaagag	ttatagttag	tgagt		945

&lt;210&gt; 296

&lt;211&gt; 605

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g145 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 296

atgacaacac	accgaaatga	caccctctcc	actgaagctt	cagacttcct	cttgaattgt	60
tttgtcagat	ccccagctg	gcagcactgg	ctgtccctgc	ccctcagcct	ccttttctc	120
ttggccgtag	gggccaacac	caccctcctg	atgaccatct	ggctggaggc	ctctctgcac	180
cagccctgt	actacctgct	cagcctctc	tccaaactgg	acatcgtgct	ctgcctcact	240
gtcatcccca	aggctctgac	catcttctgg	tttgacctca	ggcccatcag	cttccctgcc	300
tgcttctctc	agatgtacat	catgaattgt	ttcctagcca	tggagtcttg	cacattcatg	360
gtcatggcct	atgatcgta	tgtagccatc	tgccaccac	tgagatatcc	atcaatcatc	420
actgatcact	ttgtagtaa	ggctgccatg	tttattttga	ccagaaatgt	gcttatgact	480
ctggccatcc	ccatccttcc	agcacaactc	ttattgggaa	caatgttttt	aaaaccatc	540
ttggcaaatg	ttttgttcac	aatttctgcg	gagatgcacc	ttaataacct	tacacatttc	600
tgaag						605

&lt;210&gt; 297

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g146 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 297

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagtcca	60
agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	tacccctaaa	240
atgattgcag	actttctggg	tgagcacaag	actatttctt	ttgatgccca	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtgc	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgtgtgac	tcgtcctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcacgt	taatctgcca	ttttgtgggc	ctaataaggt	agatagtttt	tttctgtgac	540
cttctcttag	cgtcgaagtt	agcctgcata	gacacttatg	ttgtcagcct	actaatagtt	600
gcagatagt						609

&lt;210&gt; 298

&lt;211&gt; 912

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g147 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 298

atggcactta	gcaattccag	ctggaggcta	ccccagcctt	cttttttcct	ggtaggaatt	60
ccgggttttag	aggaaagcca	gcactggatc	gcactgcccc	tgggcatcct	ttacctcctt	120
gctctagtg	gcaatgttac	cattctcttc	atcatctgga	tggacccatc	cttgacacaa	180
tctatgtacc	tcttctgtc	catgctagct	gccatcgacc	tgggtgtggc	ctctccact	240
gcacccaaag	cccttgca	gctcctggt	cgtgcccaag	agattgggta	caactgtctgc	300
ctgatccaga	tggtcttcac	ccatgcattc	tcctccatgg	agtcaggggt	acttgtggcc	360
atggctctgg	atcgctatgt	agccatttgt	cacccttgc	accattccac	aatcctgcat	420
ccaggggtca	tagggcacat	cggaaatggg	gtgctggg	ggggattact	actcctcatc	480
cccttcctca	ttctgttgcg	aaaacttatc	ttctgccaag	ccaccatcat	aggccatgcc	540
tattgtgaac	atatggctgt	tgtgaaactt	gcctgctcag	aaaccacagt	caatcgagct	600
tatgggctga	ctgtggcctt	gcttgtgggt	gggctggatg	tcctggccat	tggtgtttcc	660
tatgccacaca	ttctccaggc	agtgtggaag	gtaccaggaa	atgaggcccg	acttaaggcc	720
tttagcacat	gtggctctca	tggttgtgtc	atcctgggtc	tctatatccc	gggaatgttc	780
tccttcctca	ctcaccgctt	tggtcatcat	gtaccccatc	acgtccatgt	tcttctggcc	840
atactgtatc	gccttgtgcc	acctgcactc	aatcctcttg	tctatagggt	gaagaccag	900
aagatccacc	ag					912

&lt;210&gt; 299

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g148 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 299

agtcacacag	aaccacagaa	tctcacaggt	gtctcagaat	tcctttctct	gggactctca	60
gaggatccag	aactgcagcc	tgctctcgct	tggtgtgctc	tgctccattta	cctgggcaca	120
gtgctgggga	acctgctcat	catcctggct	gtcagctctg	actcccacct	ccacaccccc	180
atatactttct	tcctcttcaa	cctgtccttg	gctgacattg	gtttcacctc	ggccatgggt	240
cccaagatga	ttgtggacat	gcaatcgcat	agcagagtca	tctcttatgc	gggctgcctg	300
acatagatgt	ctttctttgt	cctttttttt				330

&lt;210&gt; 300

&lt;211&gt; 980

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g149 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 300

tttttttcca	ataattctgt	tctcttccca	catactttct	tcctggctgg	catcccagga	60
ttgactgcca	cccacatttg	gattttactt	cccttttgct	ttatgttttt	cctgtcattg	120
actgggaatg	gtgtcctgct	ttttctcatc	cggacagaat	gcagccttcg	ccagcccatg	180
tttctttttc	ttgccatgct	ctcctttgtc	gacttgggtc	tctctctctc	caactgcct	240
aagatgctgg	ccattttctg	gtttgggtgt	acagccatca	gctcgcatc	ctgtctttcc	300
cagatgttct	tcatccatgc	attctctgcc	atggagtcag	gggtgctagt	ggccatggcc	360
ctggaccgct	ctgtggccat	ctgcaaccca	ctgcgttatg	caaccatcct	tccacctgtt	420
gttgttgcca	agattggagg	cctgggtggg	ttgtgagggg	tgggattgac	catctccttt	480
ccaagcttgg	cccataggct	gcactaccat	ggctcacaca	tgattgccta	taccttctgt	540
gagcatatgg	cagtggtgaa	gcttgccctg	gaggccacca	ctgtggacaa	cctctatgcc	600
tttgtgggtg	caatctttct	tggtgggggg	gatgtgggtc	tattgcctat	tcttatgggc	660
tgattgtgag	gactgtaatg	cattttcctt	cacctgagga	acgtgcgaaa	gcaggcagca	720
catgtacagc	ccatgtctgt	gtcatcctct	tcttctatgg	actgggcttt	ctttctgtgg	780
tcatgcagcg	ctttggagca	cccacagctt	ctatgcccaa	ggtcatcctt	gccaatctct	840
acttgcctct	tccccagca	ctggatccca	ttgtctatgg	catggagacc	aagcagatct	900

aggagcggct attgatgatt ctaagcccca agcagattga gcttacctga gtatagttat 960  
caccagctgg acttcagggt 980

<210> 301  
<211> 721  
<212> DNA  
<213> Unknown (H38g150 nucleotide)

<220>  
<223> Synthetic construct

<400> 301  
cttagacaac ttcacaacct ttttcttcct gttggatttt ttctttcttt tactcctttt 60  
aagttatatg cataatctaa attctgtgac taaattttcc agtaaaacag atgaatcaaa 120  
gctcaaaagc taatgtaaag tcaaatctct tttctttacc tatgctggat gctgtgagaa 180  
actactgctt gctgtagaaa agagagatct tcctttttgt tcattcattt cctccttcac 240  
tagtcaactg ctgtttctga ccatgccaaag gtggaacctg gagtaggaag gagagagaga 300  
gggtaaggga agtctcattg actgacgcta aaataagatg gcttcacatt ttctggtcct 360  
ggccaatggt tactatttct tactcatatt aaacctctct gaatgcattt aaccatggga 420  
gcaagtcttc tccccgaggt gcgtcccca gatttcttcc agttcccagt ggtcccat 480  
aatctctcac agctggacgt tcaactcagta tgtaagacta ccatcttggg tacaatccct 540  
ttcaaagcaa ctaaccact ttagtttcca tggccagtc ttcaaactg catatatctg 600  
actagctata agtggagctg taactcccat tttgctgcaa agaccacggg gccagagttc 660  
ggttgacgtc tgacatatcc ctgatgacag gatacacaca ttaaaacctc tgagtggccc 720  
c 721

<210> 302  
<211> 939  
<212> DNA  
<213> Unknown (H38g151 nucleotide)

<220>  
<223> Synthetic construct

<400> 302  
atggcatctc ccaacaatga ctccactgcc ccagtctctg aattcctcct catctgcttc 60  
cccaacttcc agagctggca gcaactggtg tctctgcccc tcagccttct ctctcctctg 120  
gccatgggag ctaacaccac cctcctgac accatccagc tggaggcctc tctgcaccag 180  
ccccgtact acctgctcag cctcctctcc ctgctggaca tcgtgctctg cctcacctgc 240  
atccccaagg tcttgccat cttctggttt gacctcaggt cgatcagctt cccagcctgc 300  
ttcctccaga tgttcacat gaacagtttt ttgaccatgg agtcctgcac gttcatggtc 360  
atggcctatg accgttatgt ggccatctgc catccattga gatacccgtc tatcatcact 420  
gaccagtttg tggctagggc cgtggtcttt gttatagccc ggaatgcctt tgtttctctt 480  
cctgttccca tgctttctgc caggctcaga tactgtgcag gaaacataat caagaactgc 540  
atctgcagta acctgtctgt gtccaaactc tctgtgatg acatcacttt caatcagctc 600  
taccagtttg tggcaggctg gactctgttg ggctctgac ttatccttat tgttatctcc 660  
tattctttta tattgaaagt tgtgcttagg atcaaggccg aggggtgctg ggccaaggcc 720  
ttgagcacgt gtggttccca cttcatctc atcctcttct tcagcacagt cctgctggtt 780  
ctggtcatca ctaacctggc caggaagaga attcctccag atgtcccat cctgctcaac 840  
atcctgcacc acctcattcc cccagctctg aacccattg tttatggtgt gagaaccaag 900  
gagatcaagc agggaaatcca aaacctgctg aagaggttg 939

<210> 303  
<211> 405  
<212> DNA  
<213> Unknown (H38g152 nucleotide)

<220>  
<223> Synthetic construct

<221> misc\_feature



&lt;222&gt; (1)...(405)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 303

aaagatttgt gaaggagaag taatattaac tttagaatag aaagtattat atttttttat	60
ataggggtgg gagagangat gggtttatga aattaattgt taatgttttg tgaaagtttt	120
taatgataaa aaactgtgtt aaggattaag ggtgagggag atatggccaa agctctaggt	180
acttgtggtt cccacttcat cctcatcctc ttcttcacca cagtctgtgt ggttctgggtc	240
atcactaacc tggccaggaa gagaattcct ccagatgtcc ccatcctgtc caacatcctg	300
caccacetta ttccccagc tctgaacccc attgtttatg gtgtgagaac caaggagatc	360
aagcagggaa tccagaacct gctgaggagg ttgtaaaaaa taaaa	405

&lt;210&gt; 304

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g153 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 304

atggctccga ccaacctcac atctgcccc gtgttcctcc tcctcgccct ggtggacgga	60
acagacagac gccacccgc tgctgttcc gctctgcctt ggcattctatc tgctcaacgc	120
cctgagcaac ctgagcatgg tggcgctggg gagatctgac ggggccctcc gctcccccatt	180
gtattacttc ttgggtcacc tgagcctcgt ggacgtctgc ttaccaccg tcacgggtccc	240
caggctgctg gccggcctgc tccacccggg ccaggccata tccttccagg cgtgctttgc	300
cgagatgtac ttcttcgtgg ctctgggcat caccgagagc tacctccgg cgccatgtc	360
ctacgaccgc gcgacggcgg cgtgccggcc cctgcgtac ggcgcgtgg tgacgccatg	420
ggcgctgcgc ctgcgtggg cgtgcgtcgt gggccgtgac gcacctgcac tcgtgctgc	480
acacgctgct cctctccgcg ctctcctacc cctacccccc ccccgctgcgc cccttctttt	540
gcgacatgac ggtgatgctg agcttggcga cctcggacac gtccgcgcgg gagacggcca	600
ttttctccga gggcctggcc gtggtgttgg ccccgctgct cctcgtgttc cttttcctac	660
gcgcgcatec tggctcgctg gctcggcttg ccgcggccgg cgccgcgcct tctccacctg	720
cggggcccac ctagtggcgg tggcggtggc ggtggcgctt ttctttggct ctgtcctctc	780
cgtgtatttc ccgcgctcgt ctgcctactc agcccgctac gaccgcctgg ccagcgtggg	840
ctacgctgtc atcacgccga ccttgaaccc ttcatcaac agccttcgca acaaagaggt	900
caagggcgcc ctgaaaaggg ggctcagatg gagggctgca cccaagagg cgtgagggca	960

&lt;210&gt; 305

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g154 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 305

atgttccttc ccaataacac ccagtttcac cctcctcct tcctgttgct ggggatccca	60
gggctagaaa cacttcacat ctggatcggc ttccctttt gtgctgtgta cataattgca	120
ctcatagggc gcttcactat tctacttggt atcaagactg acagcagcct ataccagccc	180
atgttctact tcctggccat gttggccacc attgacttgg gcctttcaac agctaccatc	240
cctaagatgc ttgggatctt ctggtttagc ctcagggaga ttatctgtga tgccgtcctc	300
atccagatgt ttttcatcca caactttact ggcattggagt cagcagccct cgtgggaatg	360
gcttatgacc actttgtggc catctgcaac ccgctacgat atagcatcat cctcaccaaa	420
aaggctgttt ctgtgattgg tcttgggtgtg ttagtgaggt catttatgtc tgttattcca	480
tttgtttttc tcatttttgc gttgcccttc tgtggggatc atgtcattcc ccacaccaac	540
tgtgagcaca tgggtcttgc tcactgtctt tgttccagta tcaagatcaa tataatctat	600
ggcttgggtg ctatttcaat cctagtattc gacatcatag ccattgccct ttcttatgtg	660
caaatacttc acgctgtttt ccactcttct tcctgtaaag cctgactcaa gtcctcagc	720
acatgtggtt cacatgtgtg tgtaatcctt gccttctata caccagccct cttttccttt	780
gtgactcatc gctttggcca aaatgtgccc cgctatatcc atatactcct agccaatctc	840

tatgttgtgg	tgccaccaat	gctcaatcct	gtcatatatg	gagtcagaac	caagcagatc	900
tatgtctgtg	tgaagaatat	attctttacaa	aaataagaaa	ttgaaaagaa	atcgcatcta	960
atacatataa	gaagg					975

&lt;210&gt; 306

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g155 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 306

atgtctcttc	ttaatgacac	aaaaatggaa	gtccttagat	tcttccttat	cgggatcact	60
ggactggaga	aaagtcgcac	ctggatatcc	attcctttct	tatctgtgta	ccttctttct	120
tggatgggta	attttaccgt	cctctttttt	atcaagacag	agcaaagcct	ccatgaacct	180
atgtattatt	tgctttccat	gctctccatc	tctgacctag	ggctgtctct	gtcttcttta	240
ccctcacttt	tgggactatt	cctatttgat	gtccatgaaa	ttcatgcagc	tccatgcttt	300
gcctaggaaat	tttttatcca	tctgtttaca	gtcagtgaag	cctctgtact	gtctgtaattg	360
gcatttgact	ggatatgtgc	aatccacagt	cctttgagat	acagcactat	cttaactagt	420
cccagagcca	tcaaaacagg	ggttcttctg	acttccaaga	atgttctttt	gaccttcca	480
ctgccctttc	tcttgcaaag	gctgagatat	tgtcatcaaa	acctgctctc	ccactcctat	540
tgtctccacc	aggatgtcat	gaagctgatg	tgttctgaca	acacagtcaa	tgttgtctac	600
ggactctgtg	caggactttc	tactatgctg	gacttgggtg	tgattacctt	ctcctaaatt	660
atgattttaa	gggctgtact	gggaattgct	accccagac	agcagttcaa	ggccctcaac	720
acgtgcatct	ctcacatctg	tgtgtgtctt	atcttctatg	tgcccacgct	gagtgtgtcc	780
atgtccacc	agtttgccag	ggatgtgtct	cctatgatcc	acgtcctcat	ggctgatatt	840
tttctgtctg	tgccaccctt	gttgaatccc	atcgtgtact	gtgtgaagac	ccaccaaact	900
cgagaaaagg	ttgtggggaa	actttgtcca	aaagtaagtt	gatcaaagga	atgagaa	957

&lt;210&gt; 307

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g156 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 307

atgtccatta	tcaacacatc	atatgttgaa	atcaccacct	tcttcttggg	tgggatgcca	60
gggctagaat	atgcacacat	ctggatctct	atccccatct	gcagcatgta	tcttattgct	120
attctaggaa	atggcaccat	tctttttatc	atcaagacag	agccctcctt	gcatgagccc	180
atgtactatt	ttctttccat	gttggctatg	tcagacttgg	gtttgtcttt	atcatctctg	240
cccactgtgt	taagcatctt	cctgttcaat	gtcctgaaa	tttcatccaa	tgctgtcttt	300
gcccaggaat	tcttcattca	tggattctca	gtactggagt	cctcagtcct	cctgatcatg	360
tcatttgata	gattcctagc	catccacaac	cctctgagat	acacctcaat	cctgacaact	420
gtcagagtgg	cccaaataag	gatagtattc	tctttaaaga	gcatgctcct	ggttcttccc	480
ttccctttca	ctttaagaaa	cttgagatat	tgcaagaaaa	accaattatc	ccattcctac	540
tgtctccacc	aggatgtcat	gaagttggcc	tgttctgaca	acagaattga	tgttatctat	600
ggcttttttg	gagcactctg	ccttatggta	gactttatct	tcattgctgt	gtcttacacc	660
ctgatcctca	agactgtacc	gggaattgca	tccaaaaagg	agcagcttaa	ggctctcaat	720
acttgtgttt	cacacatctg	tgcagtgate	atcttctacc	tgcccatcat	caacctggcc	780
gttgtccacc	gctttgcccg	gcatgtctct	ccccctatta	atgttctcat	ggcaaatgtt	840
ctcctacttg	tacctccact	gacgaaccca	attgtttatt	gtgtaaaaac	taaacagatt	900
agagttagag	ttgtagcaaa	attgtgtcaa	cggaagatt			939

&lt;210&gt; 308

&lt;211&gt; 925

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g157 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 308

atgggtgaata gaaacaatgt gacagagttt attctactgg ggcttataga gaatccaaaa	60
atgcagaaaa tcatatttgt tgtgttttgt catctacatc accaccatga taggaaatgt	120
gctcattgtg gtcaccgtca ctgccagccc atcattgagg tccccatgt acttttacct	180
ggcctatctg tcctttattg atgcctgcta ttccctccgtc aatgcccta agctgatcac	240
agattcactc tatgaaaaa agactatctt actcaatgga tgtatgactc aagtctttgg	300
agaacatttt ttcgagggtg ttgagggtcat cctacttact gtaatggcct atgaccgcta	360
cgtggtcacg tgcaagccct tgcactatac caccatcatg aagcagcatg tttgtagcct	420
gctagtggga gtgtcatggg taggaggctt tcttcatgca accgtacaga tcctcttcat	480
cttccaatta cttttctgtg gtccaatgt catagatcac tttatgtggg atctcaaccc	540
tttgcctaat cttgtctgca ctaataccca cactctagga ctcttcgttg ctgccaacag	600
tgggttcata tgcctgttaa actttctctt gctcctgggc tcctatatgg tcatactgta	660
ctccttaagg acccacagct tagaggcaag gtgcaagcc ctctccacct gtgtctccca	720
catcacagtt gtcactttat tctttatacc ctgcatattt gtgtacatga gacctccagc	780
tactttaccc attgataaag cagttgctgt attctacact atgatagctc ctatgttaaa	840
ccccttaac tacaccttga ggaatgctca gatgaaaaat gccattagga aattgtgtag	900
taggaaagct atttcaagtg tcaaa	925

&lt;210&gt; 309

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g158 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 309

atggcatacc atggcaacag gggcactttt caccagcca cattttttct cattggaatc	60
ccaggctctgg aagacgtcca tatgtgaatc tccctgcact tctgctctgt ttaccttttg	120
gctttgctgg gaaatgctac cattctgcta gtcacaaagg cagaacagac cctccgggag	180
cccattgtct actttctggc catcctttcc acaattgatt tggccctttc tacaacctct	240
gtgcctcgta cgctgggtat cttctggttt gatgctcatg agattaactt tggagcatgt	300
gtggcccaga tgtttctgat ccatgccttc actggcatgg aggctgaggt ctgggtggcca	360
tggcctttga ccgttacgtg gccatctgca atccacttca ctacacaaac atcttgacat	420
ccgggtgtct ggtgggcacg actatgtgca ttgtaattcg tccagttctg tttacactcc	480
cgataatcta tctcatctac cgtttaccat tttggtcagg gtcataataa tagcccattc	540
ctactatgag cacatgggca ttgcaaaatt gtctctgtga aacatccgtg tcaatgctat	600
ctatgggctc tttgtggctc cctctatctc ctgaacctgg tccttattgt tatctcatat	660
gtgtacattc tctgtgctgt cttctgcctc gcatcacatg atgctcggct aaaagcccta	720
agcaacatgt ggctctcatg ttgggtcat ctgtgttttc tatatcccggt cggacttctc	780
tttcctactc attgatttgg acacaacatt ccacattaca tgcaattct tgttgctact	840
ctctatttgg ttatcccacc ctctctcaac cccatcattt gtgggtgag gaccaaattg	900
aaacgagagc gagtgtctta tgtacttact aaaaaataag attctgacca tgttctttta	960
cta	963

&lt;210&gt; 310

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g159 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 310

ggcacagttt agatcctctc ccaggtctga cttcctttct atgatcccaa tgtcatagct	60
cattcatgtg tgactttaa acctttgttga aactcctctg catgggtact actaatacac	120
ttggtttctt tgttgctgcc aatgggtgggt tcaactacct attaaacatc attttcttga	180
tggtttctta agtggccatc ctatgtactt tgaaaactca cagcttgagg gaaagatgct	240

aaagccctct	ctacctgcat	ctctcacacc	accgtgggtca	tcttatcttt	gggttctgta	300
tatctgtgta	tctgtgcccc	gtgacccttc	cccaatcaat	aaagcagtg	ctgtgtttta	360
taccatgata	aatcctatgt	taaaaccttt	agtctaacc	tcagaaatgc	agaggtgaaa	420
agtgtcttga	gaaagctctg	ggtcaaaaga	tgaactgaag	agagaaataa	tccaaacata	480
aga						483

&lt;210&gt; 311

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g160 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 311

atgtttttatc	acaacaagag	catattttcac	ccagtcacat	ttttcctcat	tggaatccca	60
gggtctggaag	acttccacat	gtggatctcc	gggcctttct	gctctgttta	ccttgtggct	120
ttgctgggca	atgccacat	tctgctagtc	atcaaggtag	aacagactct	ccgggagccc	180
atgttctact	tcctggccat	tctttccact	attgatttg	ccctttctgc	aacctctgtg	240
cctcgcatgc	tgggtatctt	ctggtttgat	gctcacgaga	ttaactatgg	agcttgtgtg	300
gcccagatgt	ttctgatcca	tgccttccat	ggcatggagg	ctgaggtctt	actggctatg	360
gcttttgacc	gttatgtggc	catctgtgct	ccactacatt	acgcaaccat	cttgacatcc	420
ctagtgttgg	tgggcattag	catgtgcatt	gtaattcgtc	ccgttttact	tacacttccc	480
atggtctatc	ttatctaccg	cctacccttt	tgtcaggctc	acataatagc	ccattcctac	540
tgtgagcaca	tgggcattgc	aaaattgtcc	tgtggaaaca	ttcgtatcaa	tggtatctat	600
gggctttttg	tagtttcttt	ctttgttctg	aacctggtgc	tcattggcat	ctcgtatggt	660
tacattctcc	gtgctgtctt	ccgcctccca	tcacatgatg	ctcagctaaa	agccctaagc	720
acgtgtggcg	ctcatgttgg	agtcattctgt	gttttctata	tccttccagt	cttctctttc	780
cttactcatc	gatttggaca	ccaaatacca	ggttacattc	acattcttgt	tgccaatctc	840
tatttgatta	tcccaccctc	tctcaacccc	atcatttatg	gggtgaggac	caaacagatt	900
cgagagcgag	tgctctatgt	ttttactaaa	aaa			933

&lt;210&gt; 312

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g161 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 312

atggagaata	ggaataacgt	gacagagttt	gttttactag	ggcttacaga	gaatccaaag	60
atgcagaaaa	tcatatttgt	tgtgtttttt	tgctatctat	atcatcactg	tggtgggaaa	120
tgcgtcatt	gtggtcacca	tcactgccag	cccatcactg	gggtccccc	tgtacctttt	180
cctggcctat	ctctccttta	tagatgcctg	ctattcttct	gtcaataccc	ctaagctgat	240
cacagattca	ctctatggaa	agaacaccat	cctattcaat	ggatgcatga	ctcaagtctt	300
tggagaacat	ttcttcggag	gtgcagaggg	tatcctactt	actgtgatgg	cctatgaccg	360
ctatgtggcc	atctgcaagc	ccttgcaacta	tatgactatc	atgaaccagt	gtgtgtatgc	420
cctgctaata	ggagtgggtg	ggatgggagg	ctttcttcat	gcaaccatac	agatcctctt	480
catcttccaa	ttacctttct	gtggctcctaa	tgctatagat	cactttatgt	gtgatctgaa	540
ccctttgtct	aacctgcct	gcaactgacac	ccatagtctg	ggactcttca	ttgctgccaa	600
cagtggatc	atctgcttgt	ttaaactttgt	cctcctgctg	gtctcctatg	tggtcatctt	660
gcgctcccta	aggactcaca	gcttggaggc	aaggcacaaa	gccctctcca	cctgtgtctc	720
ccacatcaca	gttgtcatct	tattctttgt	gccctgcata	tttgtgtaca	tgagacctgc	780
agctacttta	cctattgata	aagcagttgc	tatattctac	actatgataa	ctcctatggt	840
aaacccttta	atctatacct	tgagggaatgc	ccagatgaaa	aatgccatca	ggaaattgtg	900
tagtagaaag	gacatttcag	gtaacaaata	aatgtaacta	gagctc		946

&lt;210&gt; 313

&lt;211&gt; 966

&lt;212&gt; DNA

<213> Unknown (H38g162 nucleotide)

<220>

<223> Synthetic construct

<400> 313

tcaaatactg	ggatgtccat	tctcaatacc	tctgaaatgg	aaatctctat	tttctacttg	60
ggtgggatcc	caggtttga	gcatgccaat	atttggatct	ctatcccat	atgtctcatg	120
tacactgttg	ctatcctagg	gaattgtacc	attctgtttt	tcataaaaac	agagccttct	180
ttgcctgagc	ccatgtacta	ttttctctcc	atgttggttc	tctctgacct	gggactatcc	240
ctctcctctc	tccctaccat	gttaaggatt	tccctgttca	atgctccagg	aatttccct	300
gatgcctgta	ttgctcaaga	gtttttcatc	catggattct	cagctatgga	gtcatctgta	360
cttcttataa	tgtcctttga	tcgctttatt	gccatctgca	acccctgag	atacacttcc	420
atcctcacca	gtgccagagt	cattcaaatt	gggcttgctt	tttctctcaa	aaatgttttg	480
ttgatcctcc	catttccttt	cactctaaaa	catctaaaat	attgtaagaa	gaacctcctg	540
tcccaatcct	actgcctcca	tcaagatgtc	atgaaactgg	cctgcactga	caacaaggtc	600
aacatcatct	atggcttatt	tgtggctctc	acaggcatcc	tagacttgac	atttatttct	660
atgtcctaca	tggtgatact	gaaagcagtg	ttgagcatag	catcatgaaa	gaaaaggctc	720
aaggctctca	atacatgtgt	ttcccacatc	tgtgctgtgc	tcattctcta	tgtgcccatt	780
atctccctag	ctgtcatcta	cgggtttgcc	aaacacagtt	tcccaatcac	taggatcctc	840
atagctgatg	ctttcttgct	ggtgcctcca	ttgatgaacc	ccattgtata	ctgtgtgaag	900
agccagcaga	taagaaatct	tgtcttagaa	aaactgtgcc	agaagcaaag	ctgaagcgga	960
tgctta						966

<210> 314

<211> 961

<212> DNA

<213> Unknown (H38g163 nucleotide)

<220>

<223> Synthetic construct

<400> 314

agtcacacag	agccacagaa	tctcacaggt	gtctcagaat	tcctcctcct	gggactctca	60
gaggatccag	aactgcagcc	actccttgct	gggctgttcc	tatccatgtg	cctgggtcacg	120
atgtctggga	actgctcatc	atcctggccg	tcacctgac	tcccacctcc	acatcccat	180
gtactttctc	ctctccaacc	tggtccttgg	ccatgacatt	gcgtttcacc	ttaggccacg	240
gtccccaaga	tgattgtaga	catgcaatca	catagcagag	tcattctcca	tgcaggctgt	300
ctgacacaga	tacctttctt	tgtccttttt	gtatgtatag	atgacatgct	cctgactgtg	360
atggcctatg	actgatttgt	ggccatctgt	cacccctgc	actaccagt	catcatgaat	420
cctcacctct	gctgtcttct	tagtgttgat	gtcttttct	tagcctgttg	gattcctagc	480
tgcacaactg	gattgttaca	attcacctgc	ttcaagaatg	tggaaatctc	taattttttc	540
tgtgactgat	ctcaacttct	caaccttgcc	tgttctgact	gtcatcagta	acatattcat	600
acatttagat	agtactatat	ttggttttct	tcccatttca	gggatccttt	tgtcttacta	660
taaaattgtg	ccctccattc	taagaattcc	attgtcagat	gggaagtata	aagccttctc	720
cacctgtggc	tctcacctgg	caattgtttg	cttattttat	ggaacaggca	ttggcatgta	780
cctgacttca	gctgtgtcac	cagccccag	gaatggtgtg	gtggcatcag	tgttgtacgc	840
tatgtcaccc	ccatgctgaa	ccccttcac	tgcagcctga	gaaacagggg	gcattcaaag	900
tgccctgtgg	aggctgtgca	ggaggaaagt	ctaattctcat	gatctgtttc	atcctttttc	960
t						961

<210> 315

<211> 960

<212> DNA

<213> Unknown (H38g164 nucleotide)

<220>

<223> Synthetic construct

<400> 315

atgcgtctca	tatgagatga	agaaatgtcc	agaagaaact	atactgaact	gacagaattt	60
------------	------------	------------	------------	------------	------------	----

```

gttctcttgg gtctaacaag ccgccagag ctgaggttg cttctctggc actgttcctt 120
tttgtctaca tagccactgt ggtaggaaac ttggggatga ttattttaat caaagttgat 180
tctcgacttc acactcccat gtaatttttt ctctccagtt tgtccattct agatctgtgt 240
ttctccacaa atttcaactcc caaaatgcta gaaaatttct tatcagagaa gaagaccatt 300
tccatgacag gttgtttgat gcagtgtatg gttgtcattg ctgtggtcct tgcagagcac 360
tgcattgttg cagtcattgc atatgaccgc tatatggcca tctgtaatcc attgctctac 420
agtagcaaaa tgtcccaagg tgtttgtgtc cacctgggtc ttgtccctta tgtctatggc 480
tttctttctc gtgtgatgga aaccttaagg acctacaacc tctccttctg tggacaaaat 540
gaaatcaacc atttctactg tgctgatcct cctcttatca aactggcatg ctctgacacg 600
tacagcaagg agctgtccat gtacatagta gccgggtaca gcaacgtcca gtctcttctg 660
atcattctca catcctacat gttcatcctt gtcgctatcc tcagaagcca ttctgcagag 720
ggaaggaaaa aagctttttc cacatgtggt tcccacctga cagttgtcac aatcttctat 780
ggaacctctt tctgcatgca tttgagacgt cccacagacg agtccgtgga gcaggggaaa 840
atggtggctg tgttttacac cacagtgtga ctcatgtctg actccatgat ctatggcctc 900
aggaacaagg atgtgaaaga ggcgttgaaa aaagcaatag gaaaacaaac attgggaaaa 960

```

&lt;210&gt; 316

&lt;211&gt; 947

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g165 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 316

```

aggaggatgg gcaatcacac tgcagtgtgc ctattccttc tgtggggatt ttccagtttt 60
tcagacctgc agagtctact ttttgtgtg attctcttct acatgtgacc atcctagctg 120
caaacgtgtc cataatgggg gccatcaagc tcagccacaa ccttcacact cctatgtact 180
ttttcctctg tggcctgtcc ttttcagaaa cttgtaccac tgtggttagta atccctcgca 240
tgttgggtgga ctttctatca gagagcaaga ccatttctct tctgagtgt gccacacaga 300
tgtttttctt tctgggcttt gcattcaaca actgtttcat catggccgct atgtcctacg 360
accgctacac ggccatccac aacctactgc agtaccacac ccttatgaca agaaagatct 420
gcttgacagat gatgatggct tcttggatgg ttgggttctt gttttctctg tgcattcatg 480
tcaactgtatt caacttgtct ctttgcgact tgaacactat ccagcactat ttctgtgata 540
tctcaccagt ggtctccctt gcttgtaatt acactttcta tcatgaaatg gctatttttg 600
tgctctctgc ctttgtgttg gtgggcagct gtattttaat tatgatttcc tatgtcttca 660
ttgtgttcat agtcataaag atgccctctg caaaggggag gtctaaggcc ttctcaactt 720
gtcctcccca cctcactgtt gtgtccatac actatggatt tgcttgcttt gtctatttga 780
ggcccaagaa cagcaactcc ttcgatgaag acatgctgac ggccatgata tatacaatac 840
tgatgcctct gcttaacccc atcgtgtaca gtctgagaaa caaagaaatg cagatagccc 900
taagaaaaac actaggcagt gtatttgggg ttttccttca gaagaca 947

```

&lt;210&gt; 317

&lt;211&gt; 955

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g166 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 317

```

atgtcagcat acaataacac caatgcccg ccatcaacct ttattcttat tggcattcct 60
gggttggaag ctgtcacat ctggatctcc atcccccttt gtgtggtcta cctgttggcc 120
ctactgggaa acggctctct tctgtttatc atcaagacag agcccagcct ccatgagcca 180
atgtacctct tctatgcat gctggctgta gttgatcttg ttgtgtgttc tacagctgtg 240
cccaaaactc tcagtctctt ctggttccat gatggagaga ttcgctttga aacctgcctc 300
actcgtgttc ctgattcaact cttgtccac catggaatct ggcttcttcc tggccatggc 360
ttttgacoga tatgtggcca tttgcaatcc attaaagacat tcagctattc tgacacgcgc 420
tgtaattggg agagtgggcc tagctattgt tctcaggggc atagcacttc tcagtcttca 480
ctctttccta ctacgtggc ttcctactg cagaacctat atcatttctc acacctactg 540
tgagttcatg gccctcatca ggattgcctg tgctgagaca aaattccgca gagcctacag 600

```

cctcattggt	gccttcctta	ctgggggtgt	agactttata	ttgatcattt	attcttatgt	660
cctcactctc	cacactgtct	tccagctccc	atccaaagat	gcccggctca	aatctttggg	720
cacctgtggc	tcccatgtct	gtgtcatctt	agtatcctat	actccagcct	tcttctcggt	780
tctcaccac	agggttgggc	accatgtggc	tccccatttt	cacatatttg	tggccaacat	840
ctatcttctt	gtcccacca	tgggtgaacc	cattatctat	ggggtaagaa	ccaaaaggat	900
ttgggacagg	ttccttaaag	ttttcagttt	ttcaaagcct	ctaagtaa	cattt	955

&lt;210&gt; 318

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g167 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 318

atgctcaatt	tcaccgatgt	gacagagttc	attcttttgg	ggctaacgag	ccgtcgagaa	60
tggcaagttc	tcttcttcat	catctttctt	gtggtctaca	tcataccat	ggtgggcaat	120
atcggcatga	tgggtgta	caaggtcagt	cctcagctta	acaaccccat	gtacttttct	180
ctcagtcact	tgctatttgt	tgatgtgtgg	ttttcttcca	atgtcacccc	taaaatgttg	240
gaaaacctgt	tatcagataa	aaaaacaatt	acttatgctg	gttggttagt	acagtgtttc	300
ttcttcattg	ctcttgtcca	tgtggaaatt	tttattcttg	ctgcgatggc	ctttgataga	360
tacatggcaa	ttgggaatcc	tctgctttat	ggcagtaaaa	tgtcaagggt	tgtctgtatt	420
cgactgatta	ctttccctta	catttatggg	tttctgacga	gtctggcagc	aacattatgg	480
acttacggct	tgtacttctg	tggaaaaatt	gagatcaacc	atttctactg	tgcagatcca	540
cctctcatca	aaatggcctg	tgccgggacc	tttgtaaaag	aatatacaat	gatcatactt	600
gcccgcatta	acttcacata	ttccctgact	gtaattatca	tctcttactt	attcatcctc	660
attgccattc	tgccaatgag	ctcagcagaa	ggaaggcaga	aggccttttc	cacatgtggg	720
tcccatctga	cagctgtcat	tatattctat	ggtactctga	tcttcatgta	tctcagacgt	780
cccacagagg	agtctgtgga	gcaggggaag	atgggtggctg	tggtctatac	cacagtgatc	840
cccattgtga	atcccatgat	ctacagtctg	aggaacaagg	atgtgaaaaa	ggccatgatg	900
aaagtgatca	gcagatcatg	t				921

&lt;210&gt; 319

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g168 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 319

atgaccatga	caacggagaa	ccccaaccag	actgtggtga	gccacttctt	cctggagggt	60
ttgaggtaca	ccgctaaaca	ttctagcctc	ttcttctctc	tcttctcctc	catctacagc	120
atcactgtgg	ctgggaatct	cctcatcctc	ctaactgtgg	gctctgactc	tcacctcagc	180
ttacctatgt	accacttcct	ggggcacctc	tccttctctg	atgectgttt	gtctacagtg	240
acagtgccca	aggatcatgg	aggcctgctg	actctggatg	ggaaggatgat	ctcctttgag	300
ggctgtgccc	tacagcttta	ttgcttccac	tttctggcca	gcaactgagt	cttctgttac	360
acagtcatgg	cctatgaccg	ctatctggct	atctgtcaac	ccctgcacta	cccagtggcc	420
atgaacagaa	ggatgtgtgc	agaaatggct	ggaatcacct	gggccatagg	tgccacgcac	480
gctgcaatcc	acacctccct	caccttccgc	ctgctctact	gtgggccttg	ccacattggc	540
tacttcttct	gcgacatacc	ccctgtccta	aagctcgctc	gtacagacac	caccattaat	600
gagctagtca	tgcttgccag	cattggcatc	gtggctgcag	gctgcctcat	cctcatcggt	660
atttcttaca	tcttcatcgt	ggcagctgtg	ttgctgcatc	gcacagccca	gggcccgcag	720
cgggccttct	ccccctgcac	tgcccagctc	actgggggtg	tcctgtacta	cgtgccacct	780
gtctgtatct	acctgcagcc	tcgctccagt	gaggcaggag	ctggggcccc	tgctgtcttc	840
tacacaatcg	taactccaat	gctcaaccca	ttcatttaca	ctttgcggaa	caaggagggtg	900
aagcatgctc	tgcaaaggct	tttgtgcagc	agcttccgag	agtctacagc	aggcagccca	960
ccccca						966

&lt;210&gt; 320

<211> 967  
 <212> DNA  
 <213> Unknown (H38g169 nucleotide)

<220>  
 <223> Synthetic construct

<400> 320  
 aaaatgctca atttcaccga tgtgacagag ttcattcttt tggggctaac gagccgctcg 60  
 gaatggcaag ttctcttctt catcggtttt cttgtgggtc acattatcac cgtgggtgggc 120  
 aatatcgga tgatgttggt aatcaagggtc agtcctcagc ttaacagccc catgtacttt 180  
 ttctctcagtc acttgtcatt tgttgatgtg tggttttctt ccaatgtcac ccctaaaatg 240  
 ttggaaaatc tgttatcaga taaaaaaaaa aacaatttct tatgctggct gtttagcaca 300  
 gtgtttcttc ttcattgttc ttgtccatgt ggaaattttt attcttgctg cgattgcctt 360  
 tgatagatac acagtgattg gaaatccttt gctttatggc agcaaatgt caagggatgt 420  
 ctgtattcga ctgattactt tcccttacat ttatggtttt ctgacgagtc tgacagcaac 480  
 attatggact tatggcttgt acttctgtgg aaaaattgag atcaaccatt tctactgtgc 540  
 agatccacct ctcatcaaaa tggcctgtgc cgggaccttt gtaaaagaat atacaatgct 600  
 catacttgcc ggcatacaact tcacatattc cctgactgta attatcatct cttacttatt 660  
 catectcatt gccattctgc gaatgcgtc agcagaaggga aggcagaagg ccttttccac 720  
 atgtgggtcc catctgacag ctgtcatcat attctatggg actctgatct tcatgtatct 780  
 cagacgtccc acagaggagt ctgtggagca ggggaagatg gtggctgtgt tctataccac 840  
 agtgatcccc atgttgatc ccatgatcta cagtctgagg aacaaggatg tgaaaaaggc 900  
 catgatgaaa gtgatcagca gatcatgtta aacaaaataa aatcaagttt gaattaattt 960  
 tgtcttc

<210> 321  
 <211> 933  
 <212> DNA  
 <213> Unknown (H38g170 nucleotide)

<220>  
 <223> Synthetic construct

<400> 321  
 atgtccaacg ccagcctcgt gacagcattc atcctcacag gccttcccca tgccccaggg 60  
 ctggacgccc tcctcttttg aatcttcttg gtggtttacg tgctcactgt gctggggaac 120  
 ctctcatcc tgctgggtgat cagggtggat tctcacctcc acaccccat gtactacttc 180  
 ctcaccaacc tgtccttcat tgacatgtgg ttctccactg tcacgggtgcc caaaatgctg 240  
 atgaccttgg tgtccccaag cggcagggtc atctccttcc acagctgcgt ggctcagctc 300  
 tattttttcc acttctctgg gagcaccgag tgtttcctct acacagtcac gtcctatgat 360  
 cgctacttgg ccatcagtta cccgctcagg tacaccagca tgatgagtgg gagcaggtgt 420  
 gccctcctgg ccaccggcac ttggctcagt ggctctctgc actctgctgt ccagaccata 480  
 ttgactttcc atttgccta ctgtggaccc aaccagatcc agcactactt ctgtgacgca 540  
 ccgcccaccc tgaaactggc ctgtgcagac acctcagcca acgtgatggg catctttgtg 600  
 gacattggga tagtggcctc aggtcgtctt gtcttgatag tgctgtccta tgtgtccatc 660  
 gtctgttcca tcctgcggat ccgcacctca gatgggaggg gcagagcctt tcagacctgt 720  
 gcctcccact gtattgtggg cctttgcttc tttgttccct gtgttgatcat ttatctgagg 780  
 ccagggtcca tggatgccat ggatggagtt gtggccattt tctacactgt gctgacgccc 840  
 cttctcaacc ctgttggtga caccctgaga aacaaggagg tgaagaaagc tgtgttgaag 900  
 cttagagaca aagtagcaca tcctcagagg aaa 933

<210> 322  
 <211> 953  
 <212> DNA  
 <213> Unknown (H38g171 nucleotide)

<220>  
 <223> Synthetic construct

<400> 322



ggagttggat	tgtaaaaact	ttgatggcaa	atttatattct	ccggagactc	tttctcaaca	60
tgggaaatgt	tttctctctc	aattttacaa	cttccttaga	tgtacactgt	ggccctctca	120
gggacatcta	ttctgatttt	cttgatttag	acagatttct	gagttcacac	atcattgtac	180
tctttctgag	ttctcattga	tatagccatt	tctgttggtt	aaattgggtat	tgagggttttc	240
tctggaaaga	taaactttct	acatactggg	tgtggaactc	agattttctt	ctttctgact	300
gctggcattt	tcaaatatgt	ccttctcact	tatatggctt	atgaccataa	cgtggctatc	360
tgtgcctgag	tgaccaacct	tcatgagtga	tcagggtctt	tagcaatggg	cagtagagtc	420
ttggattgga	ggaaaacttt	cttctttggc	tcataccatt	tatatatttc	atttattcag	480
ctataaagca	aaggagatta	gccacttatg	gccaagctc	ttttaagct	cctctgtggg	540
gatccccat	atacaaatg	atgttttttt	cacaataatt	acattcttgt	tcaccctgct	600
tcctcttact	ctgaccttat	cctccaagct	tattgtgttc	actatcctac	acatgaactc	660
ctcaaattgg	ggagcaaagt	cttggccaca	tactgcttct	atctgagtgt	gctgattccc	720
tgctgtggcc	aggccacttc	gtctacatga	cttccagctc	cttctgaact	gtaaacaaat	780
accagaccat	gtctgcttga	cagcataatt	atatccacgt	tgaaaccctt	gatagacatt	840
ctgaagaatg	cagaagtggc	aggagcttgg	agcaagttct	tgtaaaagaa	agcgctaaaa	900
agtcaacacc	ttattatcgt	agctgtgaaa	ataaataaac	aacagagcag	agt	953

&lt;210&gt; 323

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g172 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 323

atgctggtac	ctaagaaaat	ggttagagga	aattctactt	tggtgacgga	atttattctc	60
ttgggattaa	aggatcttcc	agagcttcag	cccacctctt	ttgtactgtt	cctgctaata	120
tacctgatca	ctgtcggggg	gaaccttggg	atgttggtgt	tgatcaggat	agattcacgc	180
ctccacaccc	ccatgtattt	ctttcttgct	agtttgtcct	gcttggattt	gtattactcc	240
actaatgtga	ctcccaagat	gttgggtgaac	ttcttctcag	acaagaaagc	catttcctat	300
gctgcttggt	tagtccagtg	ctattttttc	attgctgtgg	tgattactga	atattatatg	360
ctagctgtaa	tggcctatga	taggtatgtg	gccatctgta	accctttgct	ttacagcagc	420
aagatgtcca	aagggtctctg	tattgccttg	attgctgttc	catatgtcta	tggttttctt	480
agtggactga	tggaaacat	gtggacatac	cacttgacct	tctgtggctc	caatatcatt	540
aatcacttct	actgtgctga	cccacccctc	atccgacttt	cctgctctga	cactttcatt	600
aaggaaacat	ccatgtttgt	ggtagcatga	tttaacctct	ccagctccct	catcataatc	660
ctcatctcct	acatcttcat	tctcattgcc	atcctgagga	tgcttcttgc	tgaaagtagg	720
cgcaaagcgt	tctccacctg	cgggtcccac	ctggtggcag	tgactgtgtt	ttatggaacc	780
ctgttctgca	tgtacgttag	acctccacg	gacagctcag	tggaacagtc	caaagtcatt	840
gctgttttct	acacttttgt	aagccctatg	ttgaacccca	tcatctatag	tttgagggaac	900
aaggatgtga	aacaagcttt	ttggaaactg	atcagaagaa	acgtgctttt	gaagtaaaat	960

&lt;210&gt; 324

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g173 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 324

atgctcttta	tatcccagtg	gggagagaga	tgaagggtga	gaagaaatgt	ccaactcatg	60
acagcattca	tcctcatgga	ccttccccat	gtcccagctc	tggaagcccc	actctttgga	120
gtcttctctg	tggtttatgt	gcttactgtg	ctggggaacc	tcctcatcct	gctgggtgatc	180
aggggtgtact	ctcacctcca	caccccccaag	tactacttcc	tcaccaatct	gtccttcatt	240
gacttgtggt	tcttctactgt	catggtgccc	aaaatgccga	ggaccttgtt	gtccctgtgt	300
ggcaaggctg	tgctcttcca	cagttgtatg	acccaactct	atttcttcta	cttctctggg	360
agcaccgagt	gtttgtctcta	cacgggtcatg	tcctatgatc	gctatagagg	aaataactcag	420
cacttcccag	gtagtgaata	cactccccac	gaagtgcagc	aaatgctagt	ggcccgggg	480
gcacacgggc	tcccactcat	catcctggca	gatctgagtg	ggtaactaag	agttgatagt	540

tcttagtggg	caattcaaaa	ttagtaatat	aatttagtta	tccaagtga	atttattaca	600
tgtataggtc	tcagcattaa	acattattcc	aaacaacttg	cacagttata	attccttcac	660
agattatcta	agacattttt	aaattcacag	ctagattttt	attta		705

&lt;210&gt; 325

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g174 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 325

atgatcacgg	agttcatcct	tataggttc	tcaaacctgg	gggatctgca	gaccccttc	60
ttctttatct	tctattagt	ctacctgacc	actctgatgg	ccaacaccac	catcatgaca	120
gtcattcacc	tggacagggc	tttgacacct	cctatgtact	tcttcctctt	tgccctttca	180
tgttctgaaa	cctgctacac	cttggtcatt	gtacccaaaa	tgcttaccac	cctgctatcc	240
gcaattccaa	ctatttcttt	ctctggatgt	gtgggtccagc	tctatttatt	tggtggcttg	300
gcttgtacca	actgttttct	cattgctgtg	atgggtacg	atcgctatgt	tgccatctgc	360
aacccctta	actacacact	cattgtcagc	tgagccacct	gcatgcagct	ggttctagcc	420
tccagctttt	gtggcttctt	gacttctgtg	attgtcaata	tcttggtgtt	cagtgtgctc	480
ctctgtgcct	ccaatcggat	caaccacttt	ttctgtgaca	tttcccctgt	cataaaactg	540
ggctgcacag	acaccaacct	gaaggagatg	gtcatctttt	tcctcagcat	tctgggtattg	600
ctgggtcccc	ttgtgttgat	attcatctcc	tacatcttca	tagtttccac	catcctcaag	660
atctcctcag	tggaaggaca	gtgcaaagcc	ttcgccacct	gtgcttccca	cctcacagt	720
gtcgctgctc	actatggctg	tgcttctttt	atctacttga	ggcccacatc	cctgtactct	780
tcagataagg	accggctcgt	ggcagtga	tatactgtga	ttactccact	actcaacccc	840
cttgtctata	cactgagaaa	taaagaagta	aagatggctc	tgagaaaggt	tctgggtaga	900
tgcttaaatt	ccaaaactgt	a				921

&lt;210&gt; 326

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g175 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 326

atttgccaca	atagaaaagt	catccctgca	tctatgtgaa	atatgtttta	tttctcttga	60
aagttgccta	agacaatttt	ctgcatgtac	tgttcatact	agctaaaact	gctccccact	120
cttattcctc	taggaaattc	ctagttattt	ttcaagcccc	agtttagatta	ttgtcctttg	180
atgcttacc	tgattcctga	aacaattagt	tattttgttt	gtatttttat	tattgaacta	240
atcatattta	actttaattt	tcatgtcctt	taccatgaaa	atcaaccagc	tctttcaagg	300
caagcactgt	gatcagttgt	cttcaattcc	ccagaaaagc	aacttgcatg	catggagtgt	360
tcagtgtgtg	ttgtgcacaa	atgtaaccat	attacaatgg	ttaaatcatt	tagcatcctg	420
aaagcatcac	agagtcaaag	tagctaactt	gtgtgaaccc	ttaattcaat		470

&lt;210&gt; 327

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g176 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 327

gggaccaagt	caatcaagct	aacttctctg	tcagagttcc	tgcttcttga	gttctccagc	60
cttgaagaaa	tccagcagat	cctttttctg	tctgcttggtg	gctatatctg	attgttctga	120
gtggaaatat	caccactgtc	actgtcatcc	gcctggatca	aagcctccac	atacctgtat	180
acttattcct	agggatcctc	tccatttctg	ggacatgcta	tacctttgtc	attctgcccc	240

agatgctcat	agatctgttg	tctttgctca	gaacaatctc	atattattaac	tgccactcca	300
gtgttcttct	ttctgggttt	tgtgtcact	aatttcatgt	tcctgggcat	gacagtttat	360
gattcctatg	ttgccatctg	ccatccactt	cactaccctg	tccttacgag	ctggcagata	420
tgtaaacaac	tggcagcaac	gtgtgctgtg	attgtttttt	ttgtttgtt	tgttttcact	480
gataggctcc	ttcttagatt	ttcagctgct	tttctgtggc	ccaaacaaga	tcaaccacta	540
cttctgtgac	atctcactgc	ttattcagct	tgctgtact	gatacctaca	tcaggagact	600
agtcactctt	attggtggaa	ttctagcact	tacggttcct	ctgattttat	ttgcatctcc	660
tatggcttca	ttgttcacac	catcctgagg	atcccatatg	tgaaagcaag	caaaaagcca	720
tctctacttg	tgccctcccat	cttattatgg	tcgttgtcca	ttatggctgt	gcctcctttg	780
tcaacctgtg	accatcagcc	aaataatcat	ccagcaaata	accatctagc	aagaacaggc	840
tggtgacagt	gaccttacac	agttgtgact	ccgttgttga	atccatggta	tatagcttca	900
agaataagaa	cgttcagatg	gccatttggg	aagtgatttg	ccaaggagga	tttcctcct	959

&lt;210&gt; 328

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g177 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 328

atgagaagaa	actgtacatt	ggtgactgag	ttcattctcc	tgggactggc	caatcaccgg	60
gaattacaga	ttttcctctt	cacgctgttt	ctcaccattt	acatggtcac	ggtggcagga	120
aatcttggca	tgattgcctt	catccaggcc	aacgccccgg	ctccacacgc	ccatgtactt	180
tttcttgagc	aacttatcct	ttgtggatct	gtgcttctct	tccaatgtga	ctccaaggat	240
gctggagatt	ttcctttcag	agaagaaaag	catttcttat	cctgcccgtc	ttgtgcagtg	300
ttaccttttt	atcaccttgg	tcacggttga	gctctacatc	ctggctgtga	tggcctttga	360
ccggtacatg	gccatctgca	accctctgct	ttatggcagc	agaatgtcca	agagcgtgtg	420
ctctttcctc	atcacagtgc	tttatgtgta	tggagcactc	actggcctga	tgagacttat	480
gtggacctac	aacctagcct	tctgtggccc	cagtgaatt	aatcacttct	actgtgtgga	540
cccaccactg	attaagctgg	cttgttctga	cacctacaac	aaggagggtg	caatgtttgt	600
tgtggtgggt	ttcaacttca	cttatcctct	ccttatcatc	ctcatttctt	atctctacat	660
atttctctgc	accctaagga	tctgctctac	agaaggcagg	cacaaagctt	tttctacctg	720
tggtctccat	ctgacagccg	ttactatttt	ctattcagct	cttttcttca	tgtatctcag	780
acgtccatca	gaagagtcca	tggagcaggg	gaaaatggta	gctgtatttt	ataccactgt	840
aatccccatg	ttgaatccca	tgatctacag	tctgaggaac	aaagatgtga	aagaggcatt	900
atgcaaagaa	ctgttcaaaa	gaaaattgtt	ttctaaataa	acattactac	tg	952

&lt;210&gt; 329

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g178 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 329

acagatgtct	gagaattcct	cctcctggga	ctctcagagg	atccagaact	gcagccggtc	60
ctcgttttgc	tgctccctgtc	cctgtccatg	tatctgttca	cgggtgctgag	gaacctgtct	120
agcatectgg	ctgtcagctc	tgactcccc	ctccacaccc	ccatgtactt	cttctctctc	180
aacctgtgct	ggcctgacat	cggtttcacc	tcggccatgg	ttcccaagat	gattgtggac	240
acgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	tgacacagat	gtctttcttg	300
ctccttgttg	catgtataga	aggcatgtct	ctgactgtga	tgccctatga	ctgctttgta	360
gccatctgtc	gccctctgca	ctacccaatc	atcgtgaatc	ctcacctctg	tgtcttcttc	420
gttttgggtg	cctttttcct	tagcctgttg	gattccccagc	tgacacagtg	gattgtgtta	480
caattaacca	tcatcaagaa	tgtggaaatc	tctaatttgg	tctgtgaccc	ctctcaactt	540
ctcaaacttg	cctgttctga	cagcgtcatc	aataacatat	tcatatattt	cgatagtact	600
atgtttgggt	ttcttcccat	ttcagggatc	ttttgtctt	actataaaat	tgccccctcc	660
attctaagga	tttcatcgtc	agatgggaag	tataaagcct	tctccacctg	tggtgtgtcat	720
ctagcagttg	tttctgtggt	ttatgggaaca	ggcatttggt	tgtacctgac	ttcagctggg	780

tcaccacctc	ccaggaatgg	tgtgggtggct	tcagtgatgt	acgctgtggt	caccccatgc	840
tgaacctttt	catctgcagc	ctgagaaaca	gggacataca	aagtgccctg	cggaggctgc	900
gcagcagagc	agtcgaatat	catgatctgt	tccatccttt	ttcttgtgt		949

&lt;210&gt; 330

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g179 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 330

atgcgaggtt	tcaacaaaac	cactgtggtt	acacagttca	tcctgggtggg	tttctccagc	60
ctgggggagc	tccagctgct	gctttttgtc	atctttcttc	tcctatactt	gacaatcctg	120
gtggccaatg	tgaccatcat	ggccgttatt	cgcttcagct	ggactctcca	cactcccatg	180
tatggcttct	tattcatcct	ttcattttct	gagtcctgct	acacttttgt	catcatccct	240
cagctgctgg	tccactgct	ctcagacacc	aagaccatct	ccttcattggc	ctgtgccacc	300
cagctgttct	ttttccttgg	ctttgcttgc	accaactgcc	tcctcattgc	tgtgatggga	360
tatgatcgct	atgtagcaat	ttgtcaccct	ctgaggtaca	cactcatcat	aaacaaaagg	420
ctgggggttg	agttgatttc	tctctcagga	gccacaggtt	tctttattgc	tttgggtggc	480
accaacctca	tttgtgacat	gcgtttttgt	ggccccaaca	gggttaacca	ctatttctgt	540
gacatggcac	ctgttatcaa	gttagcctgc	actgacaccc	atgtgaaaga	gctggcctta	600
tttagcctca	gcacctcgtt	aattatgggt	ccttttctgt	taattctcat	atcctatggc	660
ttcatagtta	acaccatcct	gaagatcccc	tcagctgagg	gcaagaaggc	ccttctcacc	720
tgtgcctcac	atctcactgt	ggcttttctc	cactatggct	gtgcctctat	catctatctg	780
cggcccaagt	ccaagtctgc	ctcagacaag	gatcagttgg	tggcagtgac	ctacacagtg	840
gttactccct	tacttaatcc	tcttgtctac	agtctgagga	acaaagaggt	aaaaactgca	900
ttgaaaagag	ttcttggaaat	gcctgtggca	accaagatga	gc		942

&lt;210&gt; 331

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g180 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 331

atgatgggac	aaaatcaaac	cagcatctca	gacttcctgc	tcctgggcct	gcccattcaa	60
ccagagcagc	aaaacctgtg	ctatgccctg	ttcttggcca	tgtatcttac	caccctcctg	120
gggaacctcc	tcatcattgt	cctcattcga	ctggactccc	atctccacac	gcctatgtat	180
ttgtttctca	gcaacttgct	cttctctgac	ctctgcttct	cttccgtgac	cattcccaag	240
ttgttacaga	acatgcagaa	ccaggaccca	tccatcccc	atgcggactg	cctgacccaa	300
atgtacttct	tcctgttatt	tggagacctg	gagagcttcc	tccttgtggc	catggcctat	360
gaccgctatg	tggccatctg	cttccccctg	cactacaccg	ccatcatgag	ccccatgctc	420
tgtctcgccc	tgggtggcgt	gtcctgggtg	ctgaccacct	tccatgccat	gttacacact	480
ttactcatgg	ccaggttgtg	tttttgtgca	gacaatgtga	tccccactt	tttctgtgat	540
atgtctgctc	tgctgaagct	ggccttctct	gacactcgag	ttaatgaatg	ggtgatattt	600
atcatgggag	ggctcattct	tgtcatccca	ttcctactca	tccttgggtc	ctatgcaaga	660
attgtctcct	ccatcctcaa	ggcccttctt	tctaagggtg	tctgcaaggc	cttctctact	720
tgtggctccc	acctgtctgt	gggtgtcactg	ttctatggaa	ccgttattgg	tctctactta	780
tgctcatcag	ctaatagttc	tactctaaag	gacactgtca	tggctatgat	gtacactgtg	840
gtgaccccca	tgctgaaccc	cttcatctac	agcctgagga	acagagacat	gaaggagacc	900
ctgagcagag	tcattcatca	gaagaaaact	ttcttctctc	tc		942

&lt;210&gt; 332

&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g181 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 332

accataataa	atgtcaatat	tagtcctgag	tttgtccttg	tgggattttc	cagtgatgca	60
gagatccaga	tcatgctctt	tgtgctaata	ctgggtgattc	atctcctgac	tttgacgggg	120
aagctgggtga	tgatcctgga	gatcagggct	gattctcacc	ttcaaagacc	catgtacttc	180
ttcctttgac	atctgtcctt	tctggatctc	agctactcct	agttactgtg	cccaggatgc	240
tacaaaattt	cctctcagaa	gaaaagcatc	tcaatgtggg	gctgcctcac	caagtttctt	300
tttcactctc	tctgggggaa	cggaagcctg	tctgttctct	gccatggcct	atgatcacta	360
tgctaccatc	cgccaccctg	tggtctatac	catgggtcatg	aacagatctc	tctgtatggt	420
gattttgaga	attgcttggg	cagcgggatt	tctgatttcc	ttgatggaca	gtcttttcac	480
ccacaagtta	catttctgtg	ggcctgacat	catccttatt	tcaggtgtaa	gctgectcca	540
ttcttccctc	tgctctacat	tgatcccaat	gtcaatgaga	ttcttctagc	tgtgtcacag	600
gcattctggg	ggctactgac	actttcccta	atcttctctc	cttactctag	aatcacatct	660
gtcatactga	gcactctgctc	ctctgagggc	caaggcaaag	ccttctccgc	atgcccttct	720
catctcgtg	tggttctctc	attctatggg	acagcttttt	tcagataccc	aggctctact	780
tcaggttcgg	tggtggggca	agtggctctc	gttcagtata	gt		822

&lt;210&gt; 333

&lt;211&gt; 935

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g182 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 333

atgagaagga	acttcacggt	ggtgactgag	ttcattctcc	tgggactgac	gaatcaccag	60
gaattacaga	ttctcctctt	catgctgttt	ctggccattt	acatggtcac	agtggcaggg	120
aatcttagca	tgattgccct	catccaggcc	aatgcccggc	tccacacgcc	catgtacttt	180
ttcctgagcc	acttatcctt	cctggatctg	tgcttctctt	ccaatgtgac	cccaaagatg	240
ctggagattt	tcctttcaga	gaagaaaagc	atttcctatc	ctgcctgtct	tgttcagtgt	300
tacctttata	tcactcttgg	acacgttgag	atctacatcc	tggtctgtat	ggcctttgac	360
tagtacatgg	ccatctgaaa	ccctctgctt	tatggcagca	aaatgtccaa	aagtgtgtgt	420
tccttctca	tcacggtgcc	ttatgtgtat	ggagcgtca	ctggcctgat	ggagaccatg	480
tggacctaca	acctagcctt	ctgtggcccc	aacgaaatta	atcacttcta	ctgtgcagac	540
ccaccactga	ttaagctggc	ttgttctgac	acctacaaca	aggagtgtgc	aatgtttgtt	600
gtggctggct	ggaatcttct	gttttctctc	ttcatcatat	ttatttccta	cttttacatt	660
tttctgcta	tcttaaggat	tcgctctaca	gagggcaggc	aaaaagcttt	ttctacctgt	720
ggctcccatc	tgacagctgt	tactatttct	tatgcaactc	tggtcttcat	gtgtctcaga	780
cctccatcag	aagagtccat	ggagcaagga	caaatggtag	ctgtacttta	taccactgtg	840
atccccatgt	taatcccatg	atctacagtc	tgaggaacaa	ggatgtgaaa	aaggctttat	900
ccaaagaact	gttcaaaaga	aaattgttct	ctaaa			935

&lt;210&gt; 334

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g183 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 334

atggagccag	aagctggggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgtccc	tcctctttgc	ctatctggtc	120
acaattgggg	gcaacctcag	catcctggca	gccgtcttgg	tggagcccaa	actccacgcc	180
cccatgtact	tcttcttggg	gaacctatca	gtgctggatg	tcggatgtat	cactgtcact	240
gttctctgaa	tgttgggtcg	tctcttgtcc	cacaagtcca	caatttccta	tgacgcctgc	300
ctctccagc	tcttcttctt	ccacctcttg	ctggggatgg	actgcttctc	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagccctcca	cctacagcac	ccgcatgagt	420

cagacagtcc	agaggatggt	ggtggctgcg	tcctgggctt	gtgccttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgctcaac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	ccccacagct	cttccagctc	tcctgtctca	gcacccaact	caatgagctg	600
ctgctctttg	tagcagcagc	cttcatggct	gtggcaccct	tggtcttcat	cagtgtgtcc	660
tatgccccatg	tggtagctgc	tgtgctgcaa	atccgctctg	ctgagggcag	aaagaaggcc	720
ttctccacat	gtggctccca	cctcactgtg	gtgggcatct	tctatgggac	agggtgtcttc	780
agctacatga	ggctgggttc	agtggaatct	tcagacaagg	ataagggggt	tgggggttttc	840
atgactgtga	tcaaccccat	gctgaaccca	cttatctaca	gcctcagaaa	tactgatgtt	900
cagggcgctc	tgtgtcagct	acttgtgggg	gagcgatcac	tgacc		945

&lt;210&gt; 335

&lt;211&gt; 950

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g184 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 335

atgctaagga	atggcagcat	agtgcaggaa	tttatcctcg	tgggctttca	gcagagctcc	60
acttccacac	gagcattgct	ctttgccctc	ttcttggccc	tctacagcct	caccatggcc	120
atgaatggcc	tcatcatctt	tatcacctcc	tggacagacc	ccaagctcaa	cagcccatg	180
tactttcttc	tggcctctg	tctctcctgg	atgtctgctt	catcaccact	accatcccac	240
agatgttgat	ccacctcgtg	gtcagggacc	acattgtctc	ctttgtatgt	tgcatgacct	300
agacgtactt	tgtcttctgt	gttgggtgtg	ccgagtgcac	cctcttggct	ttcatggcct	360
atgaccgtta	tgttgcctac	tgctaccac	ttaactatgt	cccgatcata	agccagaagg	420
tctgtgtcag	gcttgtggga	actgcctggt	tctttgggct	gatcaatggc	atctttctcg	480
agtatatattc	attccgagag	cccttccgca	gagacaacca	catagaaagc	ttcttctgtg	540
aggcccccac	agtgattggc	ctctcttgtg	gggaccctca	gtttagtctg	tgggcaatct	600
ttgccgatgc	catcggtgta	attctcagcc	ccatggtgct	cactgtcact	tcctatgtgc	660
acatcctggc	caccatcctc	agcaaagcct	cctcctcagg	tcgggggaag	actttctcta	720
cttgtgcctc	tcacctgact	gtggtcatct	ttctctacac	ttcagctatg	ttctcttaca	780
tgaaccccca	cagcacacat	gggcctgaca	aagacaaacc	tttctccctc	ctgtacacca	840
tcattacccc	catgtgcaac	cccatcattt	atagtttccg	caacaaggaa	attaaggagg	900
ccatggtgag	ggcacttgga	agaaccaggc	tggcccagcc	acagtctgtc		950

&lt;210&gt; 336

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g185 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 336

atgttttact	tctttccccc	tttgcagatc	ttggcagaaa	acctcaccat	ggtcaccgaa	60
ttcctgttgc	tgggtttttc	cagccttggg	gaaattcagc	tggccctctt	tgtagttttt	120
ctttttctgt	atctagtcat	tcttagtggc	aatgtcacca	ttatcagtgt	catccacctg	180
gataaaaagcc	tccacacacc	aatgtacttc	ttccttggca	ttctctcaac	atctgagacc	240
ttctacacct	ttgtcattct	acccaagatg	ctcatcaatc	tactttctgt	ggccaggaca	300
atctccttca	actgttgtgc	tcttcaaatg	ttcttcttcc	ttggttttgc	cattaccaac	360
tgccctgctat	tgggtgtgat	gggttatgat	cgctatgctg	ccatttgtca	ccctctgcat	420
taccccactc	ttatgagctg	gcaggtgtgt	ggaaaactgg	cagctgcctg	tgcaattggg	480
ggcttcttgg	cctctcttac	agtagtaaat	ttagttttca	gcctcccttt	ttgtagcgcc	540
aacaaagtca	atcattactt	ctgtgacatc	tcagcagtea	ttcttctggc	ttgtaccaac	600
acagatgtta	acgaatttgt	gatattcatt	tgtggagtgc	ttgtacttgt	ggttcccttt	660
ctgtttatct	gtgtttctta	tctctgcatt	ctgaggacta	tcctgaagat	tcctcagct	720
gagggcagac	ggaaagcggt	ttccacctgc	gcctctcacc	tcagtgttgt	tattgttcat	780
tatggctgtg	cttccctcat	ctacctgagg	cctacagcaa	actatgtgtc	caacaaagac	840
aggctgggtga	cgggtgcata	cacgattgtc	actccattac	taaaccctat	ggtttatagc	900
ctcagaaaca	aggatgtcca	acttgcctac	agaaaagtgt	tgggcaagaa	aggttctcta	960

aaactatata at

972

&lt;210&gt; 337

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g186 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 337

aagcttcaat	taaacaattt	tactgaagtc	accatgttta	tattaataag	cttcacagaa	60
gaatttgatg	tgcaagtctt	cctattttta	ttatttttag	caatctatct	attcactcta	120
ataggcaatt	tagggctggt	tgtaccgatc	attggggatt	tctgggttca	cagcccaatg	180
tactattttc	ttggtgtttt	atcattcttg	gatgtctgct	attctacagt	tgtcactcca	240
aaaatgttgg	tcaatttcct	ggcaaaaaat	aaatctattt	catttcttgg	atgtgcaaca	300
cagatgtttc	ttgcttgtae	ttttggaacc	acagaatgct	ttctcttggc	tgcaatggct	360
tatgatcgct	atgtagccat	ctacaaccct	ctcctgtatt	cagtgaecat	gtcaccacaga	420
gtctatgtgc	cactcatcac	tgcttcctat	gttgctagca	ttttacatgc	tactatacat	480
acagtggcta	catttagcct	gtccttctgt	ggatccaatg	aaattaggca	tgtcttttgt	540
aataatgcct	cctctgcttg	ctatttcttg	ttctgacact	cacgtaatcc	agcttctatt	600
cttctacttt	gtgggctcta	ttgagatagt	cactatcctg	attgtcctga	tctcctatgg	660
ttttattctg	ttggccattc	tgaagatgca	gtctgctgaa	gggaggagaa	aagtcttctc	720
tacatgtgga	gtcaccttaa	ctggagtgc	aatttatcat	gggacaatcc	tcttcattga	780
tgtgagacca	agttccagct	acacttcgga	caatgacatg	atagtgtcaa	tattttatac	840
cattgtgatt	cccatgctga	atcccatcat	ctacagtttg	cggaacaaag	atgtaaagga	900
ggcaatcaaa	agattgcttg	tgagaaattg	gttcataaat	aagttatagt	tttaaaattg	960
agtaaagtgg	caaataatat	tg				982

&lt;210&gt; 338

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g187 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 338

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgatttggac	tttccaagcc	60
tccttgggag	atgcatcttt	ttcttttttg	gttcttctct	gtgttctaca	tggaatttat	120
cctggaaaat	ctcttcattg	tgttcacagt	aattattgac	tctcatttaa	attccccagg	180
tactgcctac	tgcccaacat	ttatcttctt	gatctgggtc	ttctcctaca	gttctgactt	240
tttactaac	tgacagcatc	tttcttttcc	aagatgcac	atacagatat	ttttcatttg	300
tgtcatgcgt	aaaaattgag	atggtgctgc	tcataaccat	ggcatagagc	aggtacactg	360
ccaatctgta	agcctcccca	ttacctgacc	acaatgaacc	ccaaaatgtg	tgtttccttt	420
gttggaggca	tcctggatag	tcaggataat	ccatgctgta	tctcagtttg	tttttgccat	480
aaacttgcc	ttttgtggcc	ctaataagag	aggtagtgtt	cactgtgatt	ttccttatgt	540
catgaaactt	gcttggttag	acacttacaa	actagagggt	gtagtcactg	ctaacagtgg	600
gcttatatcc	atagctacct	gtttcttatt	aataatatcc	tatattttca	tttcggtaac	660
cgtctagaat	ccttcttcag	gagacttate	taaagcattt	gtgtcatgtt	agatcacatc	720
acagttagga	ttttgttttt	tatgccatgt	atatttctgt	atgtgtagcc	tttgccataa	780
acaacacatg	attaatat	gttcattggt	ccttttgcta	tcaccctgtg	ctaggatcta	840
cacattaaga	aacaaagaca	tgaacgtctc	catggaaaga	ctgggaaaat	ggattgcagg	900
ttctagcagg	atgtcataat	aaatggtgca	tatccagagt	gcaagatgat	tcagtctcac	960
ca						962

&lt;210&gt; 339

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g188 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 339

atgaccacca	taattctgga	agtagataat	catacagtga	caacacgttt	cattcttctg	60
gggtttccaa	cacgaccagc	cttccagctt	ctctttttct	ccattttcct	ggcaacctat	120
ctgctgacac	tgctggagaa	tcttcttata	atcttagcta	tccacagtga	tgggcagctg	180
cataagccca	tgtacttctt	cttgagccac	ctctccttcc	tggagatgtg	gtatgtcaca	240
gtcatcagcc	ccaagatgct	tggtgacttc	ctcagtcag	acaagagtat	ttccttcaat	300
ggctgcatga	ctcaacttta	cttttttgtg	acctttgtct	gcactgagta	catccttctt	360
gctatcatgg	cctttgaccg	ctatgtagcc	atttghtaat	cactacgcta	cccagtcata	420
atgaccaacc	agctctgtgg	cacactggct	ggaggatgct	ggttctgtgg	actcatgact	480
gccatgatta	agatgggttt	tatagcaca	cttctact	gtggcatgcc	tcagatcaat	540
cactactttt	gtgatattct	tccactcctt	aacgtctcct	gtgaggatgc	ctcacaggct	600
gagatgggtg	acttcttctt	ggccctcatg	gtcattgcta	ttcctctttg	tggtgtgggtg	660
gcctcctacg	ctgctatcct	tgccaccatc	ctcaggatcc	cttctgtcta	gggcccga	720
aaggcattct	ccacctgtgc	ctcccacctg	accgtctgta	ttctcttcta	ttccatgaca	780
cttttcacct	atgcccgtcc	caaactcatg	tatgcttaca	attccaacaa	agtggatatct	840
gttctctaca	ctgtcattgt	tccactcctc	aaccccatca	tttactgtct	gaggaaccat	900
gaagtaaaag	cagccctcag	aaagaccata	cattgcagag	gaagtgggcc	ccagggaaat	960
ggggctttca	gt					972

&lt;210&gt; 340

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g189 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 340

atgatgggac	aaaatcaaac	cagcatctca	gacttcctgc	tcctgggcct	gcccatacaa	60
ccagagcagc	aaaacctgtg	ctatgccctg	ttcttggcca	tgtatcttac	cacctctctg	120
gggaacctcc	tcatcattgt	cctcattoga	ctggactccc	atctccacac	gcctgtgtat	180
ttgtttctca	gcaacttgct	cttctctgac	ctctgctttt	cctcagtcac	aatgccccaa	240
ttgctgcaga	acatgcagaa	ccaagaccca	tccatcccct	atgcagactg	cctgacccaa	300
atgtacttct	tcttgtattt	ttcggatcta	gagagcttcc	tccttgtggc	catggcctat	360
gaccgctatg	tgcccatctg	cttcccctatg	cactacaccg	ccatctgctt	cctcctgcac	420
tacaccgcca	tcatgagccc	catgctctgt	ctctccgtgg	tgccgctgtc	ctgggtgctg	480
accaccttcc	atgccatggt	acacacttta	ctcatggcca	ggttgtgttt	ttgtgcagac	540
aatgtgatcc	cccacttttt	ctgtgatatg	tctgctctgc	tgaagctggc	ctgctctgac	600
actcgagtta	atgaatgggt	gatatttata	atgggagggc	tcattcttgt	catcccatte	660
ctactcatcc	ttgggtccta	tgcaagaatt	gtctctcca	tcctcaagg	cccttcttct	720
aagggtatct	gcaaggcctt	ctctacttgt	ggctcccacc	tctctgtgg	gtcactgttc	780
tatgggaccg	ttattgggtct	ctacttatgc	ccatcagcta	atagttctac	tctaaaggac	840
actgtcatgg	ctatgatgta	cactgtgggt	accctatgc	tgacccctt	catctacagc	900
ctgaggaaca	gagacatgaa	gggagccctg	gaaagggtca	tttgtaaaag	gaaaaatccc	960
ttccttcta						969

&lt;210&gt; 341

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g190 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 341

atgggtagaa	gaaataacac	aaatgtgcct	gacttcatcc	ttacgggact	gtcagattct	60
gaagaggctc	agatggccct	ctttatacta	tttctcctga	tataccta	tactatgctg	120
ggcaatgtgg	ggatgatatt	gataatccgc	ctggacctcc	agcttcacac	tcccatgtat	180



tttttcctta	ctcacttgtc	at ttattgac	ctcagttact	caactgtcat	cacacctaaa	240
accttagcga	acttactgac	ttccaactat	atttccttca	tgggctgctt	tgcccagatg	300
ttcttttttg	tcttcttggg	agctgctgaa	tgttttcttc	tctcatcaat	ggcctatgat	360
cgctacgtag	ctatctgcag	tcctctacgt	taccagttta	ttatgtccaa	aaggctgtgt	420
tgcgctcttg	tcactggggc	ctatgtgatt	agctttatca	actcctttgt	caatgtgggt	480
tggtatgagca	gactgcattt	ctgcgactca	aatgtagttc	gtcacttttt	ctgcgacacg	540
tctccaattt	tagtctctgc	ctgcatggac	acatacgaca	ttgaaatcat	gatacacatt	600
ttagctgggt	ccaccctgat	gggtgtccct	atcacaaat	ctgcatccta	tgtgtccatt	660
ctctctacca	tcctgaaaat	taattccact	tcaggaaagc	agaaagcttt	gtctacttgt	720
gcctctcatc	tcttgggagt	caccatcttt	tatggaacta	tgattttttac	ttatttaaaa	780
ccaagaaagt	cttattcttt	gggaagggat	caagtggctt	ctgtttttta	tactattgtg	840
attcccatgc	tgaatccact	catttatagt	cttagaaaca	aagaagttaa	aaatgctctc	900
attagagtca	tgcagagaag	acaggactcc	agg			933

&lt;210&gt; 342

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g191 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 342

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttccta	60
tttatgttgt	ttttgtatt	ctatggagga	atcggtgttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggtctg	cttggtcaga	tatttctcct	tcacttcttt	300
gggtgggagt	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aagcccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
acatggggaa	ttggctttct	ccattcgggt	agccagttgg	cgtttgccgt	gcacttactc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgtctact	600
gtgtgtttct	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgtgtgatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

&lt;210&gt; 343

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g192 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 343

atggagcggg	tcaatgagac	tgtggtgaga	gaggtcatct	tcctcggctt	ctcatccctg	60
gccaggctgc	agcagctgct	ctttgttata	ttcctgctcc	tctacctgtt	cactctgggc	120
accaatgcaa	tcattcatttc	caccattgtc	ctggacaggg	cccttcataat	ccccatgtac	180
ttcttccttg	ccatccctct	ttgtctgtgag	atttgtctaca	ccttcacat	tgtacccaag	240
atgtctggtg	acctgctgtc	ccagaagaag	accatttctt	tcctgggctg	tgccatccaa	300
atgttttctt	tcctcttctt	tggctgctct	cactcctttc	tgctggcagt	catgggttat	360
gatcggtaca	tagccatctg	taaccactg	cgctactcag	tgctaattgg	acatgggggtg	420
tgatggggac	tagtggtgtc	tgctgtgccc	tgtggcttca	ctgttgacac	gatcatcaca	480
tccttggtat	ttcacctgcc	tttttattcc	tccaataaac	tacatcactt	cttctgtgac	540
attgctcctg	tcctcaagct	ggcatctcac	cataaccact	ttagtcagat	tgtcatcttc	600
atgtctctga	cattggtcct	ggctatcccc	ttattgttga	tcttgggtgtc	ctatgttcac	660
atcctctctg	ccatacttca	gtttccttcc	acactgggta	ggtgcaaagc	tttttctacc	720

tgtgtatctc	acctcattat	tgtcactgtc	cactatggct	gtgcctcctt	tatctactta	780
aggcctcagt	ccaactactc	ctcaagccag	gatgctctaa	tatcagtatc	ctacactatt	840
ataactccat	tgttcaaccc	aatgatttat	agcttgagaa	ataaagagtt	caaactcagct	900
ctttgtaaaa	ttgtgagaag	aacaatttcc	ctgttg			936

&lt;210&gt; 344

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g193 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 344

atgatgattt	cctcagatga	agaaaatgat	acaaatatga	tggaatttat	tctggtagga	60
ctgtccagac	agcctgcac	tcagctactc	ttcttttagg	caatattgtt	catctactct	120
gtcaccctgg	ttggtaatat	tctcatcatt	gttattatcc	agattgattc	ccatcttcaa	180
acccccatgt	acttctttct	catacaagta	tccttcttag	atatctgctc	cacaccacg	240
gttctgggtga	actgctagaa	ggactttcca	agtgtatcct	atagtggctg	cttattctaa	300
atgactatct	ttctttactt	aggggtgacg	gagtgtgttt	ttttttgtt	ctgttttgag	360
tgttttctta	ttgctgttat	ggcctatgac	aggtttgttg	ccatctcaaa	acccttgtgt	420
taccattca	ttatcaatag	caatgtttgc	atctggatgg	tggcaggagt	ttggggccat	480
cctggctcgca	ccaatccaat	tctgtggcca	caatgtagtc	aacattttac	atgtgagctc	540
caagtaattt	tcaaactcac	ttgctctcct	gtactagtca	aagagatcca	gtgattcatg	600
attccaggtt	gtacattata	ggcattgtat	cagcattaag	tgtgctccta	cagttaagct	660
cgccagcaaa	cccattccag	gagctgagag	gcatacaatt	agggcataag	gtgagggtatt	720
atcggggtac	ac					732

&lt;210&gt; 345

&lt;211&gt; 919

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g194 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 345

acagctggca	gcaatttcac	tgagggtgact	gtcttcatcc	tctctggata	tgcaaatcac	60
cctgaattac	aagtcagttt	tttcttgatg	tttctcttca	tttatctatt	cactattttg	120
ggaaacctgg	gactgatcat	gttaatcaga	atggattctc	agcttcacac	ccctatgtac	180
tttttctctca	gcaatttagc	attcattgac	atattttact	cctcttccgt	aacacctaag	240
acattggcga	atttccaatc	caatcagaga	tccatctcct	ttgttggctg	ctttgttcaa	300
atgtactttt	ctgttggtat	ggtgtgtact	gagtgtttcc	tgctgggac	aatggcctat	360
gattgctatg	tagcaatctg	gaatccctca	ttcagtagtc	atttcttaga	aagcgtgcaa	420
ctggctggga	gtaatgtcat	acacgatagg	tttcacaaat	tctctgggat	ctgtctgtgt	480
gataagtggg	tttggttctgt	gattccagca	tcaatctttt	ttttctgtga	caccacagct	540
cttttagcac	tgtctgtgt	agatgcattc	agcacagaaa	tggtgagctt	tgcttagct	600
ggattcactc	ttcttggctc	tatccttata	atcacagtca	cttatatcgc	catcacctca	660
gccatctctga	agaaccagtg	ggcagcagga	tggcagaagg	ccttctccac	ctgcgcattc	720
cacctcatgg	gttaactatc	ttctatgggt	ccctgatttt	cacctatttg	caactggata	780
aaacatcatc	cctgatccac	gcacagttgg	catttgtatt	ctatatgact	gtcattccca	840
tgctgaatcc	actcatctag	agtctgagga	acaaagatgt	aaaaaatgct	ctttgagagt	900
catacataga	aaacttttt					919

&lt;210&gt; 346

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g195 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

```

<400> 346
atggccaatt cttcctctgt cactgagttc ttagtgctgg gcttctctag ccttggggaa 60
ttgcagcttg tccctcttgc agtctttctc tgcctctatt tgattatctt gagtggaaac 120
atcatcatca tctcagtcac tcatttggat cacagcctcc acacacccat gtacttcttt 180
ctagggtattc tttctatctc tgaaatcttc tacacaactg ttattctgcc caagatgctt 240
atcaacttat tctctgtatt caggacactc tcccttgtga gttgtgccac ccaaatgttc 300
ttcttctctg gttttgctgt cactaactgt ctgcttctgg gagtgatggg ttatgatcgt 360
tatgctgccca tctgtcagcc tttgcaatac gctgttctca tgagctggag agtatgtgga 420
caactgatag caacttgtat tattagtggc ttcctaatat ctctgggtggg aacaactttt 480
gtcttttagcc tccctttctg tggctccaac aaggctcaacc actacttttg tgatatttca 540
ccagttatcc gtctcgctg tgetgacagc tacatcagtg aactgggtcat cttcatcttc 600
gggggtcttg tgettggtgt gcccttgata tttatctgca tttctatgg cttcattgtc 660
cgcaccatcc tgaagatccc atcagctgaa ggcaaacaaa aagccttctc cacctgtgct 720
tcccatctca ttgtagtcac tgtccattat ggt 753

```

<210> 347

<211> 941

<212> DNA

<213> Unknown (H38g196 nucleotide)

<220>

<223> Synthetic construct

```

<400> 347
atgggtggtc taaaaagaga caatgcctct gagatgactg aactcatcct tgttggattt 60
gcccaacacc ctgaaatcca gactgccttc ttcttggaaac tactgttttt ctactagtca 120
cagcgtttga gaacatcctt atcgttgctg tagtgagatg agattctcga cttcatactc 180
ctatgggatt ttttttctct cagtacctta tctcctcttg aaatgtgtta ctccatcagc 240
tgaggagctat aagtcttggc tcaatgcac aaggacttcc ccaccatctc ctataacagc 300
tgttctgttc agatgatcac acacctcttt ctggggatga cagtgtctcc tcttgtctgg 360
catggcttac aacaggtttg ttgaaatctc ttatctcctc cattacacta ttattatgag 420
caatcgggtc tgtatacagt tggccttggg aatctggacc catgccttct tagtagcagt 480
cacactaatc attgcaattc ctgctagtta ttatggacac aatgtcatca accattttac 540
cttgagatcc aggcctgct gaagctcgtc tgctcagaca cccttgtcag cctgattcag 600
ggctctggta tcagtgtgtt cacactgccc ctgcccttca cattcatcct catctcctaa 660
ttttgcattt ttgttgtgct gtggaggcta ggctgaagc tttctccacc tgtggatctc 720
atctgactgg agtcaccata ttttatgggg cagccatctg catgtacttg aaacctcagt 780
caaagggaac caggaagagc gataaagtgt tctcaaaaact ttatggagca gttactccca 840
tgttaaatcc cccaatttac attcagagaa ataaggatat aaaagggtgca cttagaaagt 900
tagccaaagg aatgaaaaa tcttaacagt tctctttaa c 941

```

<210> 348

<211> 957

<212> DNA

<213> Unknown (H38g197 nucleotide)

<220>

<223> Synthetic construct

```

<400> 348
atgaatcatg tggtaaaaca caatcacacg gcagtgacca aggtgactga atttattctc 60
atggggatta cagacaaccc tgggctgcag gctccactgt ttggactctt cctcatcata 120
tatctggtca cagtgatagg caatctgggc atgggttatct tgacctactt ggactccaag 180
ctacacaccc ccatgtactt tttccttaga catttgtcaa tcactgatct tggttactcc 240
actgtcattg ccccgaaagat gttagtaaac ttcatagtgc acaaaaacac aatttcttac 300
aattggatg ccactcagct agcattcttt gagattttca tcatctctga gctctttatt 360
ctatcagcaa tggcctatga tcgctacgta gccatctgta aacctcttct gtacgtgatc 420
atcatggcag agaaagtact ttgggtgctg gtaattgttc cctatctcta tagcagttt 480
gtgtcactat ttctcacaat taagttattt aaactgtcct tctgtggctc aaacataatc 540
agctattttt actgtgactg tatccctctg atgtccatac tctgttctga cacaatgaa 600

```

ttagaattaa taattttgat cttctcaggc tgtaatttgc tcttctccct ctcaattgtt	660
ctcatatcct acatgtttat tctagtggcc attctcagaa tgaactcaag gaaagggagg	720
tacaaagcct tctccacctg tagctctcat ctgacagtgg tgatcatgtt ctatgggaca	780
ttgttattta tttacttgca acccaagtcc agtcatactt tggctattga taaaatggcc	840
tcagtgtttt ataccctgtt gattcctatg ctgaatccgt tgatctacag cctaaggaac	900
aaagaagtaa aagatgctct aaagagaact ttaaccaatc gattcaaaat tcccatt	957

&lt;210&gt; 349

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g198 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 349

tttttaaaaa tgagattaaa ggaattaatg taagatagaa ccataatgga ttattggagg	60
gaaggtaggc acatttaggg gatgttcttg gcctttccgt ttggctgacc tatcccaaaa	120
cttttcctct gggctctctat cagagacatg gcagtaacct ggatggacca taggcacgag	180
tcctgtagcc cattcctccc gaagctgcag cctttttcat cctgccatgt atctgagtta	240
tgacagtgcc ttgacacctt cactaaatca tatataactt gaatccgggg actcaagggt	300
ttcaaccatc tttgttttct tctccattac tgtcactgtg ctagagccca agtctcctga	360
aatgcgcctt ggagccttgc tcaaagatgt caaccaca tgctgatcag gtagctattt	420
tgtctgaagc tggtagttca tgacaggctc tgacatgtgc tgagcttgct c	471

&lt;210&gt; 350

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g199 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 350

atgggccaaa agaactaac agtgcttact gaattaattc tgatggaaat cacaaggcgg	60
cttgagctgc agctctccct tttttgggtc ttcctcatca tctgcacatt cacagtgggtg	120
agcaaagagt gcataatcat tttgaacaat gtggacttgg gtctacacaa catttgtgta	180
tttttttaaat cagggtacctg aatttttatta atcttggtaa ttctatggtc atttatccca	240
agatactggg aaactttgtt gtggctcaaa atgccattcc ctggtatgca tgtaccatgc	300
agatggcctt cttcattatg ttcattatct gtgaactttt cgtctcatca gccatggcct	360
atgaccacta tgtggacatc catagccttc tgccataaaa tgttatgtct cagggaacttt	420
gtcatgtgct ggtgggtattc cataccttta tagtaccttt caagctctga tggtcactat	480
aaagattttt atattggcct tctatggctc caatgtcata agttatttct actgttaaga	540
tgtttctttg ttagccatgg tggactcaaa tgcattgagg atagaaatgt tgatcacact	600
attttccagta cttaatttga tattctttct tctggtagtc ctaatgtcct ccatgctgat	660
tctattaact gtttgttgaa tgcattctgc agagagcagt aaaaaacttt cttcacgtat	720
gtttcttgtc tgatagtggg ggttgtgttc tgtgggtttc tatactttat gtacttgcag	780
ctcaaattca gttccttttt ttttgataat aataaaatga cctccatgtt ttctctttta	840
gtgattacca tgctttacca tttgggtctgt agtgtaaaga acaaagggag taaaaaaaaat	900
gccttctata gtttttttat gaagcagtga aaactttgta atttaattgt c	951

&lt;210&gt; 351

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g200 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 351

atgacgaact tgaatgcac acaggccaac caccgtaact tcattctgac aggtatccca	60
--	----

ggaacgccag	acaagaaccc	atggttggcc	tttcccctgg	gatttctcta	cacactcaca	120
ctcctgggaa	atggtacat	cctagctgtc	atcaagggtg	agccaagtct	ccatgagccc	180
acgtattact	tcctttctat	cttggtcttc	actgaagtta	gtctctccat	gtccaccttg	240
ccctccatgc	tcagcatcta	ctggtttaat	gcccctcaga	ttgtttttga	tgcatgcatc	300
atgcagatgt	tcctcatcca	tgtatttggg	atagtagaat	caggagtcct	agtgtccatg	360
gcctttgaca	gatttgtggc	catccgaaac	ccattacact	atgtttccat	cctcactcac	420
gatgttattc	gaaagactgg	aatatctgtc	ctcaccgggg	cagtctgtgt	ggatttcctt	480
gtgcccttcc	ttataaagt	cctacccttc	tgccattcca	atgtcttgtc	tcattcatac	540
tgtcttcacc	aaaacatgat	gcggctagct	tgtgccagca	ccgcacataa	cagcctctac	600
ggcctcatcg	tcgtcatctt	cacactgggg	ctcgatgttc	tcctcactct	actgtcttat	660
gtactcacc	tgaagactgt	gctgggcatt	gtctccagag	gtgaaaggct	gaaaaccctc	720
agcacatgcc	tctctcacat	gtctaccgtg	ctcctcttct	atgttccttt	tatgggtgct	780
gcctccatga	tcacagatt	ttgggagcat	ttatcaccag	tagtgacat	ggcatggct	840
gatatatacc	tactgtctcc	gcctgtgcta	aaccccatg	tctacagtgt	gaagaccaag	900
caaatt						906

&lt;210&gt; 352

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g201 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 352

cacacagagc	cacggaatct	cacagggtgc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tcagccgggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggc	120
acagtgtgta	ggaacctgct	cagcatcccg	gctgtcagct	ctgactccca	cctccacacc	180
cccacgtact	tcttctcttc	catcctgtgc	tgggctgaca	tcgggtttcac	ctcggccacg	240
gttcccaaga	tgattgtgga	catgcagtg	tatagcagag	tcattctctca	tcggggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcattgtatag	aaggcatgct	cctgactgta	360
atggcctatg	actgctttgt	aggcatctat	cgcctctctg	actaccagct	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctggt	ggattcccag	480
ctgcacagtt	ggattgtggt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaactt	gcctcttatg	acagcgtcat	caatagcata	600
ttcatatatt	tcgatagtac	aatgtttggt	tttcttccca	tttcagggat	cctttcatct	660
tactataaaa	ttgtcccctc	cattctaagg	atgtcatcgt	cagatgggaa	gtataaaact	720
ttctccacct	atggctctca	cctagcattt	gtttgcgtat	tttatggaac	aggcattgac	780
atgtcctatg	cttcagctat	gtcaccaacc	cccaggaatg	gtgtgggtgt	gtcagtgatg	840
taagctgtgg	tcaccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tcgggaggct	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttctgggt	t					971

&lt;210&gt; 353

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g202 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 353

ttctctgtta	caggatcag	cgttgtggat	tgtgttttct	agtccacagt	tattcctgaa	60
atgtctttca	gttgccagg	acagcacttg	gtccataacc	caaaggggat	actattatta	120
ttattattat	tattattatt	attattatta	acattttttt	aaaaatttct	tttcatagaa	180
tgcatttttt	tattagagat	tcctctagtg	ggaaaataac	agttttattac	ttatagttct	240
atatttgtgg	acagatcggt	ttagaacaag	taaaacacat	ttgagaatga	agtctcagtt	300
tagaatttgt	aatttttga	tacttctaca	agggggacct	tgcccttaaa	cagaactttg	360
ctatactcag	aagcattcca	agcttttctt	cctaggattt	agaaattcat	aatgtgagat	420
atcagcattt	c					431

<210> 354  
 <211> 938  
 <212> DNA  
 <213> Unknown (H38g203 nucleotide)

<220>

<223> Synthetic construct

<400> 354  
 actcatggat acacttttag cttgaggctt tttctgcatt gccttaccta tgtttaggtt 60  
 agtcattgcc tattaatttg gttaatcctt tctccccatt taatttgta tttaaataaa 120  
 atttataatt tactatttaa cttatcactt aaattgaatc cagatattca aaacactggc 180  
 cattctttct actatgatgt ttttgtaatg ttttattcca ccttgactgt gatagtcccg 240  
 tttgtaatac caagaggatc agatcatttt ttgttctaga aagataaaaa agttcctgaa 300  
 agagtggaaa aatacacttt tgaacccgaa acaaagtctc attttctaag attttggcat 360  
 aaaatatacc gtgtaccttt tgctcttaaa acacttcggtt gttaatacat tcaattttaa 420  
 ggtacttatg agtggcaggc tatgggacta gttagttctt gtctagaatc tcctctataa 480  
 cctcaagaa ataatatgta ttttaaaaaa atcttaccat ttttccagt tacaatatac 540  
 aatttcttac attgatccat ttattaactc attagtattt ttgtgggttt cactgctttt 600  
 atacaagctt ttgcttttat gatcatcata gtttcttata cccaagtcct ctttgcctta 660  
 ctgaaaaaga attctgagaa gggcagaagc aaaagcttcc tcatgtgcag tgcccacctg 720  
 ctctctgtct ctttgttcta tagcagtgtc ttcttcatgt atgggtgccc cagggtctggc 780  
 ccagattaac agtggaatga aatgtatttt ccgttctaca tgattataat tcctctgcag 840  
 actcctttat ttacagtatg aaaaacaaag aagttttagg tacacttaga acaatgataa 900  
 agaaatattt ttggagaaca ctttcataat tctttcca 938

<210> 355

<211> 759

<212> DNA

<213> Unknown (H38g204 nucleotide)

<220>

<223> Synthetic construct

<400> 355  
 atgtgcttgt tcctgtgtca cctctccttc ttggacatga ccatttcttg tgctattgtc 60  
 cccaagatgc tggctggctt tctcttgggt agtaggatta tctcctttgg gggctgtgta 120  
 atccaactat tttctttcca tttcctgggc tgtactgagt gcttccttta cacactcatg 180  
 gcttatgacc gtttccttgc catttgtaag cccttacact atgctacat catgaccac 240  
 agagtctgta actccctggc tttaggcacc tggctgggag ggactatcca ttcacttttc 300  
 caaacaagtt ttgtattccg gctgcccttc tgtggcccca atcgggtcga ctacatcttc 360  
 tgtgacattc ctgccatgct gcgtctagcc tgcgccgata cggccatcaa cgagctggtc 420  
 acctttgcag acattggctt cctggccctc acctgcttca tgctcatcct cacttccat 480  
 ggctatattg tagctgcat cctgcgaatt ccgtcagcag atgggcgccg caatgccttc 540  
 tccacttggt ctgccacct cactgttgct attgttact atgtgccctg caccttcatt 600  
 tacctgcggc cttgttcaca ggagccctg gatgggtgg tagctgtctt ttacactgtc 660  
 atcactccct tgcttaactc catcatctac acactgtgca acaaagaaat gaaggcagca 720  
 ttacagaggc tagggggcca caaggaagtg cagcctcac 759

<210> 356

<211> 933

<212> DNA

<213> Unknown (H38g205 nucleotide)

<220>

<223> Synthetic construct

<400> 356  
 atgggaagtt tcaacaccag ttttgaagat ggcttcattt tgggtgggatt ctcagattgg 60  
 ccgcaactgg agcccatcct gtttgtcttt atttttattt tctactccct aactctcttt 120  
 ggcaacacca tcatcatcgc tctctcctgg ctagaccttc ggctgcacac acctatgtac 180

ttctttctct	ctcatctgtc	cctcctggac	ctctgcttca	ccaccagcac	cgtgccccag	240
ctcctgatca	accttttgcg	ggtggaccgc	accatcaccc	gtggagggtg	tgtggctcag	300
ctcttcatct	acctagccct	gggtccaca	gagtgtgtgc	tcctggtggt	gatggccttt	360
gaccgctatg	ctgctgtctg	tcgtccactc	cactacatgg	ccatcatgca	ccccatctc	420
tgccagaccc	tggctatcgc	ctcctggggt	gcgggtttcg	tgaactctct	gatccagaca	480
ggtctcgcaa	tggccatgcc	tctctgtggc	catcgactga	atcacttctt	ctgtgagatg	540
cctgtatttc	tgaagtggc	ttgtgcggac	acagaaggaa	cagaggccaa	gatgtttgtg	600
gcceagtgca	tagtcgtggc	tgttcctgca	gcacttattc	taggctccta	tgtgcacatt	660
gctcatgcag	tgctgagggt	gaagtcaacg	gctgggcgca	gaaaggcttt	tgggacttgt	720
gggtcccacc	tcctagtagt	tttccttttt	tatggctcag	ccatctacac	atatctccaa	780
tccatccaca	attattctga	gcgtgaggga	aaatttgttg	ccctttttta	tactataatt	840
acccccattc	tcaatcctct	catttatata	ctaagaaaca	aggacgtgaa	gggggctctg	900
tggaaagtac	tatggagggg	cagggactca	ggg			933

&lt;210&gt; 357

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g206 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 357

atgaagataa	agaatcacac	tccagtaact	gaggtccccc	tgatgggaat	ccctcataca	60
aaggggatgg	aaaatgtgct	ttttgtctta	tttctggcct	tctacctctt	caccttgctg	120
gggaacctac	tcattcttct	ggcgtcctc	actttctcca	acctccacac	ccccatgtat	180
ttcttctctg	gaaacctgtc	tgtgtttgac	atatttttcc	cttcagttag	ttcccccaaa	240
atgatgctct	gcttagtggg	acaaagctgc	accatctctt	tccagggttg	tgctctccag	300
ctcttctttc	accatttcct	gggttgccac	gagtgtttcc	tgtacactgt	gatggcctat	360
gaccgatatt	cagccatctg	ccaccctttg	ccatacacgg	tcacatgaa	acgcagggtg	420
tgtgccctcc	tgacgctagg	cacctggacg	gggagctgtc	tgcatgcac	tgtcctcaca	480
ctcctcatct	ttaagttatc	ctactgtggc	cccaatgaag	tggacaattt	ttttctgtga	540
tattccgggt	gtgtgcccc	tggcctgcgc	agacacctct	ctagcacgga	cagtgaagtt	600
catcaacgta	ggtgttgttg	cgctcatgtg	ttttcttctt	atcctcacct	cttatgcttg	660
cattgttatc	tctatactga	aaatcagttc	ctcagaaggt	aggcgcagag	ccttctcaac	720
ctgcagtgcc	catctgacgt	ccatcctgct	cttctatgga	ccaatagtc	tcatttatct	780
ccgacctgcc	tccagccctt	ggctggactc	tgtggttcag	gtgttgaata	atattgttat	840
cccttccctg	aatcctttga	tatatacttt	gagaaacaaa	ggtgtaaagc	tggcactgag	900
aaaggtgctc	attcaaggag	tacataattg	tgg			934

&lt;210&gt; 358

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g207 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 358

gtgcgtgggt	ccaagcagct	gcggaatggg	accctagtgt	cccagtttct	tctgaaaggc	60
ctgaggggaca	gcaaggcttg	gaggcccctg	ctgttcacca	cctttctgct	aatctacata	120
gtggttgggt	ttgggagcca	catgttcaca	gtggactacc	gacgccacac	tcccatgtac	180
ttcttcttgg	gcggccactc	gctgatggat	gccgcctgta	tctccaacat	ggtgactcag	240
gtgctgggtg	atttgcctgg	tcgggtaggg	cccgtacttt	attgtgcttg	tctcatccag	300
atatgctttc	tccacttcct	ggcaccctag	gagtccttcc	tcctcacagc	cgtggcctat	360
gattctatgc	agctatctgc	cagccattgc	actactttgt	cctcgtgggc	cgactgaccc	420
acacgggcct	cacttccatc	tcctgcctgc	tggccttggc	caacgcattc	acctacagca	480
tcctcacagc	tctacccaag	ttctgcaggc	cttgcttcac	caccttctc	ttctgcgacc	540
tcctgcactg	ctcagactct	cttgcttcag	cacacgtacc	aatgaacttg	ccctgttctt	600
cagttttctg	gtggctcttg	cacactgcgt	cctggctcgt	gtctcctatg	gacacgttgt	660
ggctgctgtt	caggattcat	tcacccagg	gctgaagaaa	agccttttct	acctgtgttg	720

cccatctcgc	tatgatcggt	cttttctacg	tcacttcagt	cccctgctac	atccttccca	780
actctgcata	ctctggcttg	ggcgactggg	tgctctctgt	gctatgtgtg	gtcctcactc	840
acatgctaaa	ccccatcttc	cccagcatgc	tgggatgaca	ggcatgagcc	ac	892

&lt;210&gt; 359

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g208 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 359

atgggtgtaa	aaaaccattc	cacagtgact	gagtttcttc	tttcaggatt	aactgaacaa	60
gcagagcttc	agctgcccct	cttctgcctc	ttcttaggaa	tttacacagt	tactgtgggtg	120
ggaaacctca	gcatgatctc	aattattagg	ctgaatcgtc	aacttcatac	ccccatgtac	180
tatttctctga	gtagttttgtc	tttttttagat	ttctgtctatt	cttctgtcat	taccctaaa	240
atgctatcag	ggtttttatg	cagagataga	tccatctcct	attctggatg	catgattcag	300
ctgttttttt	tctgtgtttg	tggtatttct	gaatgctaca	tgctggcagc	catggcctgc	360
gatcgctacg	tggccatctg	cagcccactg	ctctacaggg	tcacatgtc	ccctagggtc	420
tgttctctgc	tggtggctgc	tgtcttctca	gtaggtttca	ctgatgctgt	gatccatgga	480
ggttgtatac	tcaggttgtc	tttctgtgga	tcaaacatca	ttaaaccatta	tttctgtgac	540
attgtccctc	ttattaaact	ctcctgctcc	agcacttata	ttgatgagct	tttgattttt	600
gtcattgggtg	gatttaacat	gggtggccaca	agcctaacaa	tcattatttc	atatgctttt	660
atcctcacca	gcacctcgcg	catccactct	aaaaagggca	ggtgcaaagc	gtttagcacc	720
tgtagctccc	acctgacagc	tggtcttatg	ttttatgggt	ctctgatgtc	catgtatctc	780
aaacctgctt	ctagcagttc	actcaccag	gagaaagtat	cctcagtatt	ttataccact	840
gtgattctca	tggtgaatcc	cttgatatat	agtctgagga	acaatgaagt	aagaaatgct	900
ctgatgaaac	ttttaagaag	aaaaatatct	ttatct			936

&lt;210&gt; 360

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g209 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 360

atgtactatt	tcctcagcca	cctggccttt	gttgaccttt	gttactcctc	tgctattaca	60
ccgaagatga	tggtgaattt	tggtgtggaa	cgcaacacca	ttcctttcca	tgcttgtgca	120
acccaactgg	gttggtttct	caccttcacg	atcactgagt	gtttccttct	agcctccatg	180
gcctacgatt	gctatgtcgc	catctgtagt	cccctgcatt	attcaacact	gatgtcaaga	240
agagtctgca	ttcaactggg	ggcagttcca	tatatataca	gcttcttggt	tgccctcttc	300
cacaccgtta	tcactttccg	tctgacttac	tgtggcccaa	acttaattaa	ccatttctat	360
tgtgatgacc	tccccttctt	agctctgtcc	tgctcagaca	cacacatgaa	ggaaattctg	420
atatttgcct	ttgctggctt	tgatatgac	tcttctctct	ccattgtcct	cacctcctac	480
atctttatta	ttgccgctat	cctaaggatc	cgctctactc	aggggcaaca	caaagccatt	540
tccacctgtg	gtcccatat	ggtgactgtc	actattttct	atggcacact	gatctttatg	600
tacctacagc	ccaaatcaaa	tcactccttg	gacacagaca	agatggcttc	tgtattttac	660
acagtgggtga	tcccatgtt	aaacccccta	atctatagtc	taaggaacaa	agaagtgaag	720
gatgcctcaa	agaaagcctt	ggataaagggt	tgt			753

&lt;210&gt; 361

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g210 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



<400> 361  
 atgtccaacg ccaccctact gacagcgttc atcctcacgg gccttcccca tgccccaggg 60  
 ctggagcccc cctcttttgg aatcttcctg gtggtttacg tgctcactgt gctggggaac 120  
 ctcctcatcc tgctggtgat caggggtgat tctcacctcc acaccccat gtactacttc 180  
 ctaccaacc tgtccttcat tgacatgtgg ttctccactg tcacgggtgcc caaaatgctg 240  
 atgaccttgg tgtccccaag cggcaggact atctccttcc acagctgcgt ggctcagctc 300  
 tattttttcc acttcctggg gagcaccgag tgtttcctct acacagtcac gtcctatgat 360  
 cgctacctgg ccatcagtta cccgctcagg tacaccaaca tgatgactgg gcgctcgtgt 420  
 gccctcctgg ccaccggcac ttggctcagt ggctctctgc actctgctgt ccagaccata 480  
 ttgactttcc atttgcccta ctgtggaccc aaccagatcc agcactactt ctgtgacgca 540  
 ccgccatcc tgaaactggc ctgtgcagac acctcagcca acgagatggg catctttgtg 600  
 aatattgggc tagtgacctc gggctgcttt gtctgatag tgctgtccta tgtgtccatc 660  
 gtctgttcca tcttgccgat ccgcacctca gaggggaggg acagagcctt tcagacctgt 720  
 gcctcccaact gtatcgtggg cctttgcttc ttggccctg gtcttttcat ttacctgagg 780  
 ccaggctcca gggacgcctt gcatggggtt gtggccgttt tctacaccac gctgactcct 840  
 cttttcaacc ctgttgtgta caccctgaga aacaaggagg taaagaaagc tctgttgaag 900  
 ctgaaaaatg ggtcagtatt tgctcagggt gaa 933

<210> 362

<211> 827

<212> DNA

<213> Unknown (H38g211 nucleotide)

<220>

<223> Synthetic construct

<400> 362  
 cactcctcac tctcttttgc tgtcttctctg ctgacctact ccgtgactct ggtgggcaac 60  
 ctgggcatga cagatctgat ctgccaatct gcaccagctc tgccctccac acccccatgt 120  
 gcttctctct gagcgtattc tcttccctag acatctgcag ttctcccatg tgcacccag 180  
 gctgctgac cactttctca ccactaacca tccatctcct ttgcagggtg tataatccag 240  
 atggccctca tgaccttcta tggcacaggg gaatgtctgc tgctggccat cgtagcctat 300  
 gactgagttg tggccatttg ccaccctttc ccctagcata tcatcatgtc caaggggact 360  
 gtgtgcccag ctggtgggtg ttacctctgc tgtgggggtg ctcatctcag ctctagacag 420  
 gatgcattca tctgcacctc ccgtggccta acatcattga tcattactat gttctgttac 480  
 attccccacc cccatgctcc aactggcctg ctcatatgcc actgtggcca acatgatcct 540  
 gtttgtctct tctgccttga tcaactatccc taccatctca gtcattcttg tctcttacac 600  
 ttacatcctg gttaatcagt gggatgaggt cccctgcatc ccagtgcata gctttctcca 660  
 ctctgacctc ccacctcact gctcactgcc tgttttatgg gtttgtgttc cttgtataca 720  
 ttccacccaa ccctgaaatg gcctcagcct ataacaaaat cctcttcacc gttgtgatcc 780  
 ccatgctgaa cctcctggtc taaggcctga gaaataaaga tgtcaaa 827

<210> 363

<211> 937

<212> DNA

<213> Unknown (H38g212 nucleotide)

<220>

<223> Synthetic construct

<400> 363  
 tcagtggcca aaggcaatca ttcaacagtg tatgaattta tctctttggg gctcacagat 60  
 aatgcagagc ttcaagtcac tctcttttgg atattccttg tagtatactt agctagcttt 120  
 atgggtaatt tgggtttgat tatgctaatt caaatcagtc ctgagcttca tacacccatg 180  
 tattttttcc tcagccatct ggcttttggg gatttttctt ttacttcac tggtgcccc 240  
 aataccttgg taaattttct gtgtgaagtt aaaagtataa cattttatgc atgtgccatt 300  
 caggtatgct gcttcatcac attttagtgg tgtgaattat atttgcctc aatcatggca 360  
 tatgatcggg atgttgccat ctgtaaccct ttactttatg tcattctcat tcttagaaaa 420  
 ctgtattaaa ctgattgcta gcacgtatgt gtatggattc actgtgggac ttgtacagac 480  
 agtggcgaca tctacttgt ctttttgtga ttccaacgtg atcaaccact tctaccatga 540  
 tgatgttcca ttagtggtc tggcctgttc tgacactcat gtcaaagagc tgatgttgtt 600

aatcattgct	gggttcaata	ctctctgctc	tctagtaatt	gtgctgattt	cttatggttt	660
cattttcttt	gccatcctga	ggatacattc	tgctgaaggg	agacagaaag	cattttctac	720
cagtgtctcc	catctgacct	ccatcacaaat	attttatgga	acaatcattt	ttatgtaccc	780
gcagcccaag	tcaagccatt	ccctgaatat	ggataaagtt	gcttctgtgt	ttaatgtggt	840
agtgtattct	acattaaacc	cactgatcta	tagtttaaga	aatcaggagg	taaaaaatgc	900
actaaagaga	attatagaaa	agttatgttt	ggctgtc			937

&lt;210&gt; 364

&lt;211&gt; 697

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g213 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 364

tctggttttg	tccccaaaag	tttccctggc	tgtctcacc	aattattctt	tctgcactat	60
agctttgtgt	tggaactcagc	tatactgctg	gccatggcat	ttgaccgcta	tatggccatt	120
tgctcaccct	tcgagataca	ctactattct	gactcccaaa	accattgtca	aaattgctgt	180
gggaatatgt	ttccgaagtt	tctgtgtttt	tgtcccatgt	gttttccttg	tgaatcgttt	240
acccttctgc	aggacacata	tcatttctca	cacatactgt	gagcacatag	gtgttgccca	300
gcttgctgtg	gctgatatct	ccatcaatat	ctgggtgtga	ttttgtgttc	ccatcatgac	360
ggtgatgaca	gacgtgatcc	tcattgctgt	ctcctacacc	ctcatcctct	gtgctgtctt	420
ttgcctcccc	tcccaagatg	cccgctcagaa	ggccctttgc	tcctgtgggt	cccatgtctg	480
tggtatcctc	atattctata	taccagcatt	cttctccatt	cttgcccat	gctttgggca	540
taatgtccct	catacctttc	atattatgtt	tgccaacctt	tatgtaatca	ttccacctgc	600
tctcaactct	attgtctaca	gaataaagac	caagcaaatc	cagaacagaa	tccttttgct	660
ctttcccaag	gggtcccagt	gataggtgcc	tgagctc			697

&lt;210&gt; 365

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g214 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 365

atgtccaacg	ccagcctact	gacagcgttc	atcctcatgg	gccttcccca	tgccccagcg	60
ctggacgccc	ccctcttttg	agtcttctcg	gtggtttacg	tgctcactgt	gctggggaac	120
ctcctcatcc	tgctggtgat	cagggtggat	tctcacctcc	acaccaccat	gtactacttc	180
ctcaccaacc	tgctgttcat	tgacatgtgg	ttctccactg	tcacggtgcc	caaattgtctg	240
atgacttttg	tgttcccaag	tggcagggct	atctccttcc	acagctgcat	ggctcagctc	300
tattttcttc	acttcctagg	gggcaccgag	tgtttctctt	acagggtcac	gtcctgtgat	360
cgtacctg	ccatcagtta	cccgtcagg	tacaccagca	tgatgactgg	gcgctcggtg	420
actcttctg	ccaccagcac	ttggctcagt	ggctctctgc	actctgctgt	ccaggccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aactggatcc	agcactattt	gtgtgatgca	540
ccgcccaccc	tgaactggc	ctgtgcagac	acctcagcca	tagagactgt	catttttgtg	600
actgttggaa	tagtggcctc	gggctgcttt	gtcctgatag	tgctgtccta	tgtgtccatc	660
gtctgttcca	tcctgcggt	ccgcacctca	gaggggaagc	acagagcctt	tcagacctgt	720
gcctcccact	gtatcgtggt	cctttgcttc	tttggccctg	gtcttttcat	ttacctgagg	780
ccaggctcca	ggaaagctgt	ggatggagtt	gtggccgttt	tctacactgt	gctgacgccc	840
cttctcaacc	ctgttgtgta	cacctgagg	aacaaggagg	tgaagaaagc	tctgttgaag	900
ctgaaagaca	aagtagcaca	ttctcagagc				930

&lt;210&gt; 366

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g215 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 366

atgagaagaa	actgcacgtt	ggtgactgag	ttcattctcc	tgggactgac	cagtcgccgg	60
gaattacaaa	ttctcctctt	cacgctgttt	ctggccattt	acatgggtcac	ggtggcaggg	120
aaccttggca	tgattgtcct	catccaggcc	aacgcctggc	tccacatgcc	catgtacttt	180
ttctgagacc	acttatcctt	cgtggatctg	tgtctctctt	ccaatgtgac	tccaaagatg	240
ctggagattt	tcctttcaga	gaagaaaagc	atttcctatc	ctgcctgtct	tgtgcagtgt	300
taccttttta	tcgccttggg	ccatgttgag	atctacatcc	tggctgtgat	ggcctttgac	360
cggtagatgg	ccatctgcaa	ccctctgctt	tatggcagca	gaatgtccaa	gagtgtgtgc	420
tccttcctca	tcacgggtgcc	ttatgtgtat	ggagcgctca	ctggcctgat	ggagaccatg	480
tggacctaca	acctagcctt	ctgtggcccc	aatgaaatta	atcacttcta	ctgtgcggac	540
ccaccactga	ttaagctggc	ttgttctgac	acctacaaca	aggagtgtgc	aatgtttatt	600
gtggctggct	ggaacctttc	ttttctcttc	ttcatcatat	gtatttctta	cctttacatt	660
ttccctgcta	ttttaagat	tcgctctaca	gagggcaggg	aaaaagcttt	ttctacctgt	720
ggctcccatc	tgacagctgt	cactatatcc	tatgcaaccc	ttttcttcat	gtatctcaga	780
ccccctcaa	aggaatctgt	tgaacagggt	aaaatggtag	ctgtatttta	taccacagta	840
atccctatgc	tgaaccttat	aatttatagc	cttagaataa	aaaatgtaaa	agaagcatta	900
atcaaagagc	tgtaaatgaa	gatatacttt	tct			933

&lt;210&gt; 367

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g216 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 367

atgtctctat	ccaacattac	tcagtttagc	cccatattct	atctcaccag	ctttcctgga	60
ttggaaggca	tcaaacactg	gatttttcac	ccctttttct	ttatgtacat	ggttgccatc	120
tcaggcaatt	gtttcattct	gatcattatt	aagaccaacc	ctcgtctgca	cacacccatg	180
tactatctac	tatccttgct	ggccctcact	gacctggggc	tgtgtgtgtc	cacgttgccc	240
accactatgg	ggatcttctg	gtttaactcc	cagagtatct	actttggagc	gtgtcaaadc	300
cagatgttct	gcateccact	tttttcttcc	atggagtcct	cagtgtctct	catgatgtcc	360
tttgaccgct	ttgtggccat	ctgccaccct	ctgagggtatt	cggtcattat	cactggccag	420
caagtgggtca	gagcaggcct	aattgtcatc	ttccggggac	ctgtggccac	tatccctatt	480
gtctctctcc	tgaaggcttt	tcctactgtt	ggatctgttg	tcctctccca	ctcattttgc	540
ctgcaccagg	aagtgtatca	gctggcctgc	acagatacca	ccttcaataa	tctgtatgga	600
ctgatgggtg	tagttttcac	tgtgatgctg	gacctgggtc	tcacgcact	gtcctatgga	660
ctcatcctgc	acacagtagc	aggcctggcc	tcccaagagg	agcagcgccg	tgcctttcag	720
acatgcaccg	ctcatctctg	tgtgtgtgta	gtattctttg	tgcctatgat	ggggctgtcc	780
ctggtgcacc	gttttgggaa	gcatgccccca	cctgctattc	atcttcttat	ggccaatgtc	840
tacctttttg	tgcctcccat	gcttaacccta	atcatataca	gcattaagac	caaggagatc	900
caccgtgcca	ttatcaaact	cctaggtctt	aaaaaggcca	gtaaa		945

&lt;210&gt; 368

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g217 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 368

atgaaccctg	aaaactggac	tcaggtaaca	agctttgtcc	ttctgggttt	ccccagtagc	60
cacctcatat	agttcctggg	gttcctgggg	ttaatgggtg	cctacattgt	aacagccaca	120
ggcaagctgc	taattattgt	gctcagctgg	atagaccaac	gcctgcacat	acagatgtac	180
ttcttctctc	ggaatttctc	cttctctggg	ctgttgctgg	taactgttgt	ggttcccaag	240
atgcttctgc	tcacctcac	gggggatcac	accatctcat	ttgtcagctg	catcatccag	300
tcctacctct	acttctttct	aggcaccact	gacttcttcc	tcttggccgt	catgtctctg	360

```

gatcgttacc tggcaatctg ccgaccactc cgctatgaga ccttgatgaa tggccatgtc 420
tggtcccaac tagtgctggc ctcttggtta gctggattcc tctgggtcct ttgccccact 480
gtcctcatgg ccagcctgcc tttctgtggc cccaatggta ttgaccactt ctttcgtgac 540
agttggccct tgctcaggct ttcttgtggg gacaccacc tgctgaaact ggtggctttc 600
atgctctcta cgttggtgtt actgggtctc ctggtcttga cctcagtttc ctatgcctgc 660
attcttgcca ctgttctcag ggcccctaca gctgctgagc gaaggaaagc gttttccact 720
tgcgccctgc atcttacagt ggtgggtcatc atctatggca gttccatctt tctctacatt 780
cgtatgtcag aggtctcagc caaactgctc aacaaagggt cctccgtcct gagctgcac 840
atcacacccc tcttgaaccc attcatcttc actctccgca atgacaaggc gcagcaagca 900
ctgagagaag ccttgggggtg gccagggtc actgctgtga tgaaactgag ggtcacaagt 960
caaaggaaa

```

&lt;210&gt; 369

&lt;211&gt; 1016

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g218 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 369

```

atgatgggag aagcaaggaa caggacagta gtccaggaat ttatcctgga gggatttctc 60
gctgtccagc atctggggaa tgctcttttc ctggtgcacc tgctggcata cctggcctcc 120
atcatggcaa acatgctcat aatcaccatc acctgggtg accatcacct ccagacacct 180
atgtatttct tctcaacag ttttctcttc tgtgaatgct gttttatcac cacagttatt 240
cctaaacttc tggtcacatt tctttcaggc aggcataata tcccctttac tacttgcttc 300
atgcagtcct tttcattttt atttcttggg tcaacagttt tcttccttat ggctgtgatg 360
tccttggatt gatacctggc catttgcaag cctctgcatt actccaccat catgagcctg 420
aggactagct tccacctggt cactgtctgc tttgtcgtgg gcttccactc catcactggt 480
ctcatggtga aggtttccca gttatctttc tgtggacccc atgtcatccc tcaattcttc 540
cgtgacctcg gccctctgat ccaactctcc tgttctgaca ccagatctac tgaaacgttg 600
gcctttgtcc ttgtttcatt cgttcttttt acatccctca ttataacat cattgcata 660
ggcaacatag tggtcacaat tgtacgactc ccatcgcca aggagcggca gaaagctttc 720
tccacctgct cctctcacct cattgtcttc tctctggtgt atggcagctg tgtcttcata 780
tatgtgaagc cgaagcaaat ggacaggctg gactccaaca gaatggctgc tcttgtgaac 840
acagtgtgta cccactgct gaaccgatc atttacactc tgcggaacaa gcaggtccac 900
caggctctga gggatgctca gtccagaatg aaattgtaaa aacagaatca caacctccca 960
gtgaaggaat gcaccttctc cttgatctaa tccaatcttt ctctgtttc tggaat 1016

```

&lt;210&gt; 370

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g219 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 370

```

atggccagta caagtaatgt gactgagttg attttctctg gccttttcca ggatccagct 60
gtgcagagtg tatgctttgt ggtgtttctc cccgtgtacc ttgccacggg ggtgggcaat 120
ggcctcatcg ttctgacggg cagtatcagc aagagtctgg attctcccat gtacttcttc 180
cttagctgcc tgtccttggg ggagatcagt tattcttcca ctatcgcccc taaattcatc 240
atagacttac ttgccaaagt taaaaccatc tctctggaag gctgtctgac tcagatattc 300
ttcttccact tctttggggg tgctgagatc cttttgattg tgggtgatggc ctatgattgc 360
tacgtggcca tttgcaagcc tcttcattat atgaacatta tcagtcgtca actgtgtcac 420
cttctggtgg ctggttctcg gctggggggc ttttgtcact ccataattca gattctcggt 480
atcatccaat tgcccttctg tgggtccaat gtgattgacc actatttctg tgacctccag 540
cctttattca agcttgctcg cactgacacc ttcatggagg gggttattgt gttggccaac 600
agtggattat tctctgtctt ctccttcttc atcttgggtg cctcttatat tgtcattctg 660
gtcaacttga ggaaccattc tgcaaggggg aggcacaaag ccctctccac ctgtgcttct 720
cacatcacag tggtcacatt gtttttttga cctgctatct tctctacat gcgaccttct 780

```

tccactttca	ctgaagataa	acttgtggct	gtattctaca	cggatcatcac	ccccatgctg	840
aaccccatca	tttacacact	caggaatgca	gaggtgaaaa	tcgccataag	aagattgtgg	900
agcaaaaagg	agaatccagg	gagggag				927

&lt;210&gt; 371

&lt;211&gt; 965

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g220 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 371

atggcaaaag	gcaatcattc	atcagtgact	gagttcatcc	tcctagggct	cacagataat	60
caggaacttc	aagtcattct	ctttgggtga	ttcctactga	tttacttagt	tactgtgttg	120
ggtaatcttg	gtttgattgt	gctaatacat	atcagtcctc	agcttcacac	acctatgtat	180
tttttcctca	gccatctggc	ttttgtggat	ttttacggta	cctctgctat	cactccaaac	240
acccttgtea	actctttgca	tgaaattaaa	agcatgtcat	tttatgcatg	tgccactcaa	300
gtgtgctgct	tcattacact	ttcagtcctg	gaattattgt	tgctctcatg	gcataatgat	360
ggtagtgggc	catctgcaac	cctttactct	atgtagttct	catgcctagg	agactctgca	420
ttcaaatggg	cactggctta	tatatattat	gtttcaccat	gggactcata	caagcagtgg	480
ccacattcca	catgtcgttt	tgtgactcta	atgtgggtcaa	ccagttctac	tgtgatgatg	540
ttcctctgat	tgctctggct	tggtctgata	cacaagtcaa	ggaattgatg	ttgttcatac	600
ttgtgcggtt	caatgttttt	tggtctctta	tcattgttct	catctcctat	gtattcatcg	660
tctttgctat	ctaaggatcc	actctgccgt	aggaagacag	aaagcctttt	ctacctgtgc	720
ttctcacatg	ttttctatct	ccatatatta	tgggaccctc	agttttatgt	acctacagcc	780
taagtcaagc	cactcactag	ataaagacaa	atttgcctca	gtattctatg	cagtgggtgat	840
tcccatgcta	aacccattga	tctatagctt	gaggaatcaa	gaggtaaaaa	aatgctatga	900
aaaaaattat	tgaaaaaatg	tggtctagta	atcaacagta	aaatttggtg	gtactaaaag	960
aaata						965

&lt;210&gt; 372

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g221 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 372

atgtcccagg	tgactaacac	cacacaagaa	ggcatctact	tcacccctac	ggacatccct	60
ggatttgagg	cctcccacat	ctggatctcc	atcccgcgtc	gctgtctcta	caccatctcc	120
atcatgggca	ataccacat	cctcactgtc	attcgacacag	agccatctgt	ccaccagcgc	180
atgtatctgt	ttctctccat	gctggccctg	acggacctgg	gtctcaccct	caccacccta	240
cccacagtca	tcagcttct	ctggttcaac	gttcgtagaa	tcagctctga	ggcctgtttt	300
gctcagtttt	tcttccttca	tggattctcc	tttatggagt	cttctgtcct	cctggctatg	360
tccgttgact	gctatgtggc	catctgctgt	cccctccatt	atgcctccat	cctcaccaat	420
gaagtcattg	gtagaactgg	gttagccatc	atgtgctgct	gtgttctggc	ggttcttccc	480
tcccttttct	tactcaagcg	actgcctttc	tgccactccc	accttctctc	tcgctcctat	540
tgccctccac	aggatatgat	ccgcctggtc	tgtgctgaca	tcagggtcaa	cagctgggat	600
ggatttgctc	ttgccttgct	cattattatc	gtggatcctc	tgtcatttgt	gatctcctat	660
acacttatte	tgaaaaatat	cttgggcaca	gccacctggg	ctgagcgact	ccgtgccctc	720
aataactgcc	tgtcccacat	tctagctgtc	ctggctctct	acattcccat	ggttgggtga	780
tctatgactc	atcgctttgc	caagcatgcc	tctccactgg	tccatgttat	catggccaat	840
atctacctgc	tggcaccccc	ggtgatgaac	cccatcattt	acagtgtaaa	gaacaagcag	900
atccaatggg	gaatgttaaa	tttcctttcc	ctcaaaaata	tgcatccaag	a	951

&lt;210&gt; 373

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g222 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 373

atgaatccag	caaatcattc	ccaggtggca	ggatttggtc	tactggggct	ctctcagggt	60
tgggagcttc	ggtttggttt	cttcactggt	ttctctgctg	tgtattttat	gactgtagtg	120
ggaaaccttc	ttattgtggt	catagtgacc	tccgaccac	acctgcacac	aaccatgtat	180
tttctcttgg	gcaatctttc	tttcctggac	ttttgctact	cttccatcac	agcacctagg	240
atgctgggtg	acttgctctc	aggcaaccct	accatttcct	ttgggtgatg	cctgactcaa	300
ctcttcttct	tccacttcat	tggaggcatc	aagatcttcc	tgctgactgt	catggcgat	360
gaccgctaca	ttgccatttc	ccagcccctg	cactacacgc	tcattatgaa	tcagactgtc	420
tgtgcactcc	ttatggcagc	ctcctgggtg	gggggcttca	tccactccat	agtacagatt	480
gcattgacta	tccagctgcc	attctgtggg	cctgacaagc	tggacaactt	ttattgtgat	540
gtgcctcagc	tgatcaaatt	ggcctgcaca	gatacctttg	tcttagagct	tttaatgggtg	600
tctaacaatg	gcctgggtgac	cctgatgtgt	tttctgggtg	ttctgggac	gtacacagca	660
ctgctagtca	tgctccgaag	ccactcacgg	gagggccgca	gcaaggccct	gtctacctgt	720
gcctctcaca	ttgctgtggt	gaccttaatc	tttctgcctt	gcactctacg	ctatacaagg	780
ccttttcgga	cattccccat	ggacaaggcc	gtctctgtgc	tatacacaat	tgtaaccccc	840
atgctgaatc	ctgccatcta	tacctgaga	aacaaggaag	tgatcatggc	catgaagaag	900
ctgtggagga	ggaaaaagga	ccctattggt	cccctggagc	acaga		945

&lt;210&gt; 374

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g223 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 374

atgtcatttc	taaatggcac	cagcctaact	ccagcttcat	tcatacctaaa	tggcatccct	60
ggtttggaag	atgtgcattt	gtggatctcc	ttcccactgt	gtaccatgta	cagcattgct	120
attacagga	acttcggcct	tatgtacctc	atctactgtg	atgaggcctt	acacagacct	180
atgtatgtct	tccttgccct	tctttccttc	acagatgtgc	tcattgtcac	cagcaccctt	240
cccaacactc	tcttcatatt	gtggtttaat	ctcaaggaga	ttgattttaa	agcctgcctc	300
gccagatgt	tctttgtgca	caccttcaca	gggatggagt	ctgggggtgt	catgctcatg	360
gccctggacc	actgtgtggc	catctgcttc	cctctgcgtt	atgccaccat	cctcactaat	420
tcagtcatgt	ctaaagctgg	gttcctcact	tttcttaggg	gtgtgatgct	tgttatccct	480
tccactttcc	tcaccaagcg	ccttcacata	tgcaagggca	acgtcatacc	ccacacctac	540
tgtgaccaca	tgtctgtggc	caagatatct	tgtggtaatg	tcagggttaa	cgccatctat	600
ggtttgatag	ttgccctgct	gattgggggc	tttgatatcc	tgtgcattac	aatctcctac	660
actatgattc	ttcaagcagt	tgtgagtcta	tcatacagcag	atgctcgaca	gaaggccttc	720
agcacctgca	ctgcccactt	ctgtgccata	gtcctcacct	atgttccagc	cttctttacc	780
ttctttacac	accatttttg	gggacacacc	attctcttac	acatacatat	tattatgggt	840
aatctctacc	tactaatgcc	tcccacaatg	aaccctattg	tgtatggggg	gaaaaccagg	900
caggtacgag	aaagtgtcat	taggttcttt	cttaagggaa	aggacaattc	tcataacttt	960

&lt;210&gt; 375

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g224 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 375

atggttgcta	caaacaatgt	gactgaaata	attttcgtgg	gattttccca	gaattggagt	60
gagcagaggg	tcattttctgt	gatgtttctc	ctcatgtaca	cagctgttgt	gctgggcaat	120
ggcctcattg	tggtgaccat	cctggccagc	aaagtgtctc	cctcccccat	gtattttctt	180
ctcagctact	tatcctttgt	ggagatctgc	tactgttctg	tcattggccc	caagcttacc	240

tttgactcct	ttatcaagag	gaaagtcatt	tctctcaagg	gctgcctcac	acagatgttt	300
tcctccatt	tctttggtgg	cactgaggcc	tttctcctga	tggtgatggc	ctatgaccgc	360
tatgtggcca	tctgcaagcc	cttgactac	atggccatca	tgaaccagcg	aatgtgtggt	420
ctcctcgtga	ggatagcatg	gggcgggggc	ctgctgcatt	ctggtgggca	aaccttctctg	480
attttccagc	tcccgttctg	tggccccaac	atcatggacc	actacttctg	tgatgtccac	540
ccagtgtgg	agctggcctg	cgcagacacc	ttcttcatta	gcctgctgat	catcaccaat	600
ggcggctcca	tctccgtagt	cagttttctc	gtgctgatgg	cttctacct	gatcatcctg	660
cacttctcga	gaagccacaa	cttggagggg	cagcacaagg	ccctctccac	ctgtgcctct	720
catgtcacag	ttgtcgacct	gttcttcata	ccttgctcct	tggtctatat	taggccctgt	780
gtcacctcc	ctgcagacaa	gatagttgct	gtattttata	cagtggtcac	acctctctta	840
aacctgtga	tttactcctt	caggaatgct	gaagtgaaaa	atgccatgag	gagatttatt	900
gggggaaaag	taatt					915

&lt;210&gt; 376

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g225 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 376

atggctcctg	aaaatttcac	cagggtcact	gagtttattc	ttacaggtgt	ctctagctgt	60
ccagagctcc	agattccctt	cttctcgtgc	tttctggtgc	tctatgggct	gaccatggca	120
gggaacctgg	gcatcatcac	cctcaccagt	gttgactctc	gacttcaaac	ccccatgtac	180
tttttctcgc	aacatctggc	tctcattaat	cttggttaact	ctactgtcat	tgcccctaaa	240
atgctgatta	acttttttagt	aaagaagaaa	actacctcat	tctatgaatg	tgccacccaa	300
ctgggagggt	tcttggttctt	tattgtatcg	gaggtaatca	tgctggcttt	gatggcctgt	360
gaccgctatg	tggtattttg	taaccctctg	ctgtacatgg	tggtgggtgc	tcggcgggctc	420
tgcctcctgc	tggtctccct	cacatacctc	tatggctttt	ctacagctat	tgtggtttca	480
tcttatgtat	tctctgtgtc	ttattgtctc	tctaataata	tcaatcattt	ttactgtgat	540
aatgttcctc	tgtagcatt	atcttgctct	gatacttact	taccagaaac	agttgtcttt	600
atatctgcag	caacaaatgt	ggttggttcc	ttgattatag	ttctagtatc	ttatttcaat	660
attgttttgt	ctatttttaa	aatatgttca	tcagaaggaa	ggaaaaaagc	cttttctacc	720
tgtgcttcac	atatgatggc	agtcacaatt	ttttatggga	cattgtctatt	catgtatgtg	780
cagccccgaa	gtaaccattc	actggatact	gatgataaga	tggtctctgt	gttttacacg	840
ttggtaattc	ctatgtgtaa	tcccttgatc	tacagcctga	ggaataagga	tgtgaagact	900
gctctacaga	gattcatgac	aaatctgtgc	tattccttt			939

&lt;210&gt; 377

&lt;211&gt; 979

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g226 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 377

atgaaaattt	ctaataactc	tttggggttt	ttacctacga	cattcatttt	ggttggcatc	60
ccagggtcgg	agtcagagca	cctctggata	tccgtcccct	tctctctgat	atacatcatc	120
attttccttg	ggaatggcat	cattcttcac	gtcatcagaa	cagatattgc	cctacatcaa	180
cccatgtacc	tcttctctgc	catgttggca	ctggccgagg	ttcgtgtctc	tgcatccacc	240
ctgcctacag	tgtaggcat	attccttttt	ggaaatactg	aaattagtct	tgaagcttat	300
ctttttccag	atgttctcca	tccattcttt	atccatgatg	gagtcagctg	tgctgctggc	360
catgtctttg	gaccgcttta	tagccatcta	cagccactg	agctatacag	ctatcctgac	420
actgccagg	gtctttggca	caggagctat	tatcgtactg	aaaagcatta	tgctcatggc	480
tccgttgccc	attctcttat	ggcgtctgcc	cttctgtggc	cacaatgccc	tctcacatc	540
ctattgtctg	caccccaate	ttatctatct	atcttgtggg	aacatttctg	ttacaatat	600
ctatgggatt	ttcattgtta	cctctacttt	tgggctggat	tcgttctgta	ttgtgatctc	660
ctatgggctc	atactccaca	ccgtgttggg	tattgccact	ggagaagggc	ggaagaaggc	720
actcaacacg	tgtggctcac	acgtctgtgc	tgtgcttgct	tactatgtgc	ctatgattgg	780

cttgtctata	gtgcaccgcc	ttggacatcg	tgtgtccct	ctgctgcaag	ccatgatggc	840
caatgcctac	ctcttcttcc	cacctgtgtg	caatcctatt	gtctacagca	ttaagaccaa	900
ggagatccat	ggtgccattg	tccgaatgct	attagagaaa	agacgcagag	tgtagccaaa	960
aaccatagta	ggaagaaat					979

&lt;210&gt; 378

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g227 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 378

atgtccaaga	ccagcctcgt	gacagcgctc	atcctcacgg	gccttcccca	tgccccaggg	60
ctggagcccc	cactctttgg	aatcttcctg	gtggtttacg	tgctcactgt	gctgggggaa	120
ctcctcatcc	tgctggtgat	caggggtgat	tctcacctcc	acaccccat	gtactacttc	180
ctcaccaacc	tgctcttcat	tgacatgtgg	ttctccactg	tcacgggtgc	caaaatgctg	240
atgaccttgg	tgcccccaag	cggcagggct	atctccttcc	acagctgcgt	ggctcagctc	300
tattttttcc	acttcttggg	gagcaccgag	tgtttctct	acacagtcac	gtcctatgat	360
cgctacttgg	ccatcagtta	cccgtcagg	tacaccagca	tgatgagtgg	gagcagatgt	420
gccctcctgg	ccaccagcac	ttggctcagt	ggctctctgc	actctgctgt	ccagaccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aaccagatcc	agcactatct	gtgtgatgca	540
ccgcccaccc	tgaaactggc	ctgtgcagac	acctcagcca	acgagatggg	catctttgtg	600
gacattgggc	tagtggcctc	gggctgcttt	ctcctgatag	tgctgtctta	tgtgtccatc	660
gtctgtttca	tcctgcggat	ccacacctca	gaggggaggg	acagagcctt	tcagacctgt	720
gcctcccact	gcctcgtggg	cctttgcttt	ttgtttccct	gtgttttcat	ttacctgaga	780
ccaggctcca	gggacgtcgt	ggatggagtt	gtggccattt	tctacactgt	gctgacaccc	840
cttctcaacc	ctgttgtgta	caccttgaga	aacaaggagg	tgaagaaagc	tgtgttgaaa	900
ctgagagaca	aagtagcaca	ttctcaggga	gaa			933

&lt;210&gt; 379

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g228 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 379

atgccttcta	tcaatgacac	ccactttctat	cccccttct	tcctcctgct	aggaatacca	60
ggactggaca	ctttacatat	ctggatttct	ttccattct	gtattgtgta	cctgattgcc	120
attgtgggga	atatgaccat	tctctttgtg	atcaaaactg	aacatagtct	acaccagccc	180
atgttctact	tcctggccat	gttgtctatg	attgatctgg	gtctgtccac	atccactatc	240
cccaaaatgc	taggaatctt	ctggttcaac	ctccaagaga	tcagctttgg	gggatgcctt	300
cttcagatgt	tctttattca	catgtttaca	ggcatggaga	ctgttctgtt	ggtgggtcatg	360
gcttatgacc	gctttgttgc	catctgcaac	cctctccagt	acaccatgat	cctcaccaat	420
aaaaccatca	gtatcctagc	ttctgtgggt	gttggaagaa	atttagttct	tgtaacccca	480
tttgtgtttc	tcattctgcg	tctgccattc	tgtgggcata	acatcgtacc	tcacacatac	540
tgtgagcaca	gggtctggc	cgggttggcc	tgtgcaccca	taaagatcaa	cataatctat	600
gggtcatgg	tgatttctta	tattattgtg	gatgtgatct	taattgcctc	ttcctatgtg	660
cttatcctta	gagctgtttt	tcgccttccc	tctcaagatg	tccgactaaa	ggccttcaat	720
acctgtgggt	ctcatgtctg	tgttatgctg	tgcttttaca	caccagcatt	tttttctttt	780
atgacacatc	gttttggcca	aaacattccc	cactatatcc	atattctttt	ggctaacctg	840
tatgtgggtg	tcccacctgc	ccttaaccct	gtcatttatg	gagtcaggac	caagcagatc	900
cgagagcaaa	ttgtgaaaat	atttgtacag	aaagaa			936

&lt;210&gt; 380

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g229 nucleotide)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 380

atgactgaat	tcatttttct	ggtactttct	cccaaccagg	agggtgcagag	ggtttgcttt	60
gtgatatttc	tggtcttgta	cacagcaatt	gtgctgggga	atttcctcat	tgtgctcact	120
gtcatgacca	gcagaagcct	tggttcccc	atgtacttct	tcctcagcta	cctctccttc	180
atggagatct	gctactcctc	cgctacagcc	cccaaactca	tctcagatct	gctggctgaa	240
aggaaagtca	tatcttggtg	gggctgcatg	gcacagcttt	tcttcttgca	cttctttggt	300
ggcactgaga	ttttcctgct	cactgtgatg	gcctatgacc	actatgtggc	catctgcaag	360
cccctcagct	acaccacat	catgaactgg	cagggtgtgta	ctgtccttgt	aggaatagca	420
tgggtgggag	gcttcatgca	ttcctttgca	caaatccttc	tcattctcca	cctgctcttc	480
tgtggcccca	atgtgatcaa	tcaacttttc	tgtgacctag	ttccccctct	caaacttgcc	540
tgtctgaca	ccttcctcat	tggtctgctg	attggtgcca	atggaggcac	cctgtctgtg	600
atcagttttg	gggtcctctt	agcatcctat	atgggtcatct	tgctccatct	gagaacctgg	660
agctctgaag	gggtggtgca	agccctctcc	acctgtgggt	cccatttcgc	tgtggttatc	720
ttgttctttg	ggccctgctg	cttcaactct	ctgaggcctt	ctaccactct	gcccatagac	780
aagatggtgg	ctgtgttcta	cacagtgata	accgcgatcc	tgaaccctgt	catctactct	840
ctgagaaatg	ctgaaatgag	gaaggccatg	aagaggctgt	ggattaggac	attgagacta	900
aatgagaaa						909

&lt;210&gt; 381

&lt;211&gt; 947

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g230 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 381

cttatagcta	caggaaactg	gacaagaata	agtgagttta	tcctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctggtcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	accccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatctttc	ctggagattg	gcttcaacct	agtcattgtg	240
cccaaaatgc	tggggaccct	gcttgcccag	gacacaacca	tctccttctt	tggctgtgcc	300
actcagatgt	atttcttctt	cttctttgga	gtggctgaat	gcttcctcca	ggctaccatg	360
gcataatgacc	gctatgtggc	catctgcagt	cccttgcact	acccagtcac	catgaaccaa	420
aggactcgtg	ccaaactggc	tgctgcctcc	tggttcccag	gctttcctgt	agctactgtg	480
cagaccacat	ggctcttcag	ttttccattc	tgtggcacca	acaagggtgaa	ccacttcttc	540
tgtgacagcc	cacctgtgct	gaggctggtc	tgtgcagaca	cagcactgtt	tgagatctac	600
gccatcgctg	gaaccattct	ggtggtcatg	atccccctgt	tgctgatctt	gtgttcctat	660
actcgatttg	ctgtgcccat	cctcaagatc	ccatcagcta	aagggaagaa	taaagccttt	720
tctacatgtt	cctcacacct	ccttgttgtc	tctcttttct	atatatcatt	aagcctcacc	780
tacttccggc	ctaaatcaaa	taattcacct	gagggcacga	agctgctatc	attgtcctac	840
actgttatga	ctcccatggt	gaaccccat	atctacagcc	tgagaaataa	cgagggtgaag	900
aatgccctca	gcaggacggg	ctctaaggcc	ctagccctca	gaaactg		947

&lt;210&gt; 382

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g231 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 382

atgcctaatt	tcacggatgt	gacagaattt	actctcctgg	ggctgacctg	tcgtcaggag	60
ctacagggttc	tcttttttgt	ggtgttcccta	gcggtttaca	tgatcactct	gttgggaaat	120
attgggatga	tcattttgat	tagcatcagt	cctcagcttc	agagtcccat	gtactttttc	180
ctgagtcatc	tgtctttttg	ggacgtgtgc	ttctcctcca	acgttaccac	caaaatgctg	240

gaaaacttat	tatcagagac	aaaaaccatt	tcctatgtgg	gatgcttggt	gcagtgtctac	300
tttttcattg	ccgttggtcca	cgtggagggtc	tatatcctgg	ctgtgatggc	ctttgacagg	360
tacatggccg	gctgcaaccc	tctgctttat	ggcagtaaaa	tgtctaggac	tgtgtgtgtt	420
cggctcatct	ctgtgcctta	tgtctatgga	ttctctgtca	gcctaataatg	cacactatgg	480
acttatggct	tatacttctg	tggaaacttt	gaaatcaatc	acttctattg	tgcagatccc	540
cctctcatcc	agattgcctg	tgggagagt	cacatcaaag	aaatcacaat	gattgttatt	600
gctggaatta	acttcacata	ttccctctcg	gtggctctca	tctcctacac	tctcattgta	660
gtagctgtgc	tacgcattgc	ctctgccgat	ggcaggagga	aggcgttctc	cacctgtggg	720
tcccacttga	cggctgtttc	tatgttttat	gggaccccca	tcttcattgta	tctcaggaga	780
cccactgagg	aatccgtaga	gcagggcaaa	atgggtggctg	tgttttacac	cacagtaatt	840
cctatgttga	atccccatgat	ctacagtctg	agaaataagg	atgtaaaaga	agcagtcaac	900
aaagcaatca	ccaagacata	tgtgagg				927

&lt;210&gt; 383

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g232 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 383

atgcttcata	ccaacaatac	acagtttcac	ccttcacact	tctcgtagt	gggggtccca	60
gggctggaag	atgtgcatgt	atggattggc	ttccccttct	ttgcgggtgta	tctaacagcc	120
cttctaggga	acatcattat	cctgtttgtg	atacagactg	aacagagcct	ccaccaaccc	180
atgttttact	tcctagccat	gttggccggc	actgatctgg	gcttgtctac	agcaaccatc	240
cccaagatgc	tgggaatttt	ctggtttaaat	cttgagagaga	ttgcatttgg	tgcctgcatc	300
acacagatgt	ataccattca	tatatgcact	ggcctggagt	ctgtggtact	gacagtcacg	360
ggcatagatc	gctatattgc	catctgcaac	cccctgagat	atagcatgat	ccttaccac	420
aaggtaatag	ccattctggg	catagtcac	attgtcagga	ctttggtatt	tgtgactcca	480
ttcacatttc	tcaccctgag	attgccttct	tgtggtgtcc	ggattatccc	tcataacctat	540
tgtgaacaca	tgggcttggc	aaagttagct	tgtgccagta	ttaatgttat	atatggattg	600
attgccttct	cagtgggata	cattgacatt	tctgtattg	gattttccta	tgtccagatc	660
ctccgagctg	tcttccatct	cccagcctgg	gatgccgggc	ttaaggcact	cagcacatgt	720
ggctctcacg	tctgtgttat	gttggcttct	tacctgccag	ccctcttctc	cttcatgaca	780
caccgctttg	gccacaacat	ccctcattac	atccacattc	ttctggccaa	tctgtatgtg	840
gtttttcccc	ctgctcttaa	ctctgttatc	tatgggtgca	aaacaaaaca	gatacgagag	900
caggtactta	ggataactcaa	ccctaaaagc	ttttggcatt	ttgaccccaa	gaggatcttc	960

&lt;210&gt; 384

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g233 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 384

atggaacaac	acaatctaac	aacggtgaat	gaattcattc	ttacgggaat	cacagatatac	60
gctgagctgc	aggcaccatt	atttgcatgt	ttcctcatga	tctatgtgat	ctcagtgtatg	120
ggcaatttgg	gcatgattgt	cctcaccaag	ttggactcca	ggttgcaaac	ccctatgtac	180
ttttttctca	gacatctggc	tttcatggat	cttggttatt	caacaactgt	gggacccaaa	240
atgttagtaa	attttgttgt	ggataagaat	ataatttctt	attatttttg	tgcaacacag	300
ctagctttct	ttcttgtgtt	cattggtagt	gaacttttta	ttctctcagc	catgtcctac	360
gacctctatg	tggcctatctg	taaccctctg	ctatacacag	taatcatgtc	acgaagggtta	420
tgtcaggtgc	tggtagcaat	cccttacctc	tattgcacat	tcatttctct	tctagtccac	480
ataaagattt	ttactttatc	cttctgtggc	tacaacgtca	ttagtcatct	ctactgtgac	540
agtctccctt	tgttaccttt	gctttgttca	aatacacatg	aaattgaatt	gataattctg	600
atctttgcag	ctattgattt	gatttcatct	cttctgatag	ttcttttatac	ttacctgtctc	660
atccttgtag	ccattctcag	gatgaattct	gctggcagac	aaaaggcttt	ttctacctgt	720
ggagccacc	tgacagtggg	catagtgttc	tatgggactt	tgcttttcat	gtacgtgcag	780

cccaagtcca	gtcattcctt	tgacactgat	aaagtggctt	ccatatttta	caccctgggt	840
atccccatgt	tgaatccctt	gatctatagt	ttacgaaaca	aagatgtaaa	atatgcccta	900
cgaaggacat	ggaataaactt	atgtaaatatt	tttgtt			936

&lt;210&gt; 385

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g234 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 385

atgatgtggg	aaaactggac	aattgtcagt	gaatttggtc	tcgtgagctt	ctcagccctg	60
tccactgagc	ttcaggctct	actgtttctc	cttttcttga	ccattttactt	ggttacttta	120
atgggcaatg	tcctcatcat	cctggtcact	atagctgact	ctgcactaca	aagtcctatg	180
tacttcttcc	tcagaaactt	gtccttcctg	gagatagggt	tcaacttggg	cattgtgccc	240
aagatgctgg	ggaccctgat	cattcaagac	acaaccatct	ccttccttgg	atgtgccact	300
cagatgtatt	tcttcttctt	ttttggggct	gctgagtget	gcctcctggc	caccatggca	360
tatgaccgct	acgtggccat	ctgtgacccc	ttgcactacc	cagtcatcat	gggccacata	420
tcctgtgccc	agctggcagc	tgccctcttg	ttctcagggt	tttcagtggc	cactgtgcaa	480
accacatgga	ttttcagttt	ccctttttgt	ggccccaaca	gggtgaacca	cttcttctgt	540
gacagccctc	ctgttattgc	actgggtctgt	gctgacacct	ctgtgtttga	actggaggct	600
ctgacagcca	ctgtcccatt	cattctcttt	cctttcttgc	tgatcctggg	atcctatgtc	660
cgcatectct	ccactatctt	caggatgccg	tcagctgagg	ggaacatca	ggcattctcc	720
acctgttccg	cccacctctt	ggttgtctct	ctcttctata	gcactgccat	cctcacgtat	780
ttccgacccc	aatccagtgc	ctcttctgag	agcaagaagc	tgctgtcact	ctcttccaca	840
gtggtgactc	ccatgttgaa	ccccatcatc	tacagctcaa	ggaataaaga	agtgaaggct	900
gcactgaagc	ggcttatcca	caggaccctg	ggctctcaga	aacta		945

&lt;210&gt; 386

&lt;211&gt; 931

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g235 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 386

atggccaaaa	ccaataattc	agaagttact	gaattcatcc	tcttgggact	cacagacaat	60
ccagagctcc	aagccctttt	ttagggggat	ctttctagt	atcaatttaa	gtagtgtcat	120
gggtagcctt	gggttaatta	tgctaattca	tatcagtcct	cagcttcaca	cagctatgta	180
tttttttctc	agccacgtag	cttttggtta	tttttgctac	acctcctcta	tcacccctaa	240
cagcctagt	aacctcctcc	aagaaactaa	aagaatatcc	ttacctactt	gtgcctctca	300
gttgcatgtc	tttatcatgt	ttgtgggttg	tgacatgtat	gtgctctcag	ccatggcata	360
tgacaggat	gtggccatct	gcaacccttt	actctatagt	atcatcatga	acagaagggt	420
ctgtattcaa	atgggtggtaa	gtacatattt	gtatggcttt	tctgtgagac	tcctacaggc	480
aattcttaca	ttccacttgt	ctttctgaga	ttcaaataata	ataaataatt	cctattgtga	540
tgatgttccc	ctagcatgtc	taccctatca	taaaaacat	tacaaagatg	taaaagaact	600
gatattgttc	acacttgctg	gtttcaatac	acttttctcc	cttcttatca	tcctcatctc	660
ctacatatca	gtactgtctg	ccattctgag	aattaattca	gctgaaagta	gacaaaaggc	720
attttctact	tgtgactccc	acctgacttc	tatcatcata	ttttatggta	taattacctt	780
catgtatatg	cagtgaaaaa	caaataattc	tctggataca	gacaaaatag	cttctgtttt	840
ctgtattgtg	aaaattcctt	caatatatag	cctgaggaac	cacgaagtca	aagatgcttt	900
gaagatgatt	atggaaaatc	tatgtcttac	t			931

&lt;210&gt; 387

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g236 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 387

ttagttaagg	taaaaaaaaa	ctagaatatt	tttctctcaa	cagcatatca	ctttttcccc	60
acactttctg	taaataataa	caaatttcta	taaataataa	ataataattt	ctaggataaa	120
tttaatttac	atagtgaac	aagccattct	taggtatatt	ccttagttct	gtcttcgaaa	180
gtctgcatcc	tgtagcagc	tggcgtagtt	ggtgggatac	ttagcagaag	gattgtatgt	240
gtgtcctact	gtttcactgt	cctcctccag	gtccaatgcc	atcaatcact	ttttctgtaa	300
taaatcccta	gggcttggtc	tttcatgcta	caacatttat	atcagcacag	cagtccctgc	360
ctttgctggag	tttgagtgtc	gcattcattg	ccatatttgg	tcacatgtt	ctcctggaca	420
tatatcctgg	ttgctatcaa	gaggatgtcc	tcagtgggga	gaaaagaatt	gtctatttgt	480
gtctcccacc	tgaaaactag	caccattttt	catacagccc	tcttttatgt	gtacttacag	540
cctgattttt	tt					552

&lt;210&gt; 388

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g237 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 388

atgtctgggg	acaacagctc	cagcctgacc	ccaggattct	ttatcttgaa	tggcgttcct	60
gggctggaag	ccacacacat	ctggatctcc	ctgccattct	gctttatgta	catcattgct	120
gtcgtgggga	actgtgggct	catctgcctc	atcagccatg	aggaggccct	gcaccggccc	180
atgtactact	tcctggccct	gtctctcttc	actgatgtca	ccttgtgcac	caccatggta	240
cctaatatgc	tgtgcatatt	ctggttcaac	ctcaaggaga	ttgacttta	cgctgcctg	300
gcccagatgt	tttttgtcca	tatgtgaca	gggatggagt	ctgggggtgt	catgtcatg	360
gccctggacc	gctatgtggc	catctgtctc	cccttacgct	atgccaccat	ccttaccac	420
cctgtcatcg	ccaaggctgg	tcttgccacc	ttcttgagga	atgtgatgct	catcatcca	480
ttcactctcc	tcaccaagcg	cctgccctat	tgccggggga	acttcatccc	ccacacctac	540
tgtgaccata	tgtctgtggc	caaggtatcc	tgtggcaatt	tcaaggtaaa	tgctatttat	600
ggtctgatgg	ttgctctcct	gattgggtgt	tttgatatct	gctgtatctc	tgtatcttac	660
actatgattt	tgcaggctgt	tatgagcctg	tcacagcag	atgctcgtca	caaagccttc	720
agcacctgca	catctcacat	gtgttccatt	gtgatcacct	atgttgctgc	ttttttcact	780
tttttcactc	atcgttttgt	aggacacaat	atcccaaacc	acatacacat	catcgtggcc	840
aacctttatc	tgctactgcc	tcctaccatg	aaccctaatg	tttatggagt	caagaccaag	900
cagattcagg	aagggtgta	taaattttta	cttgagagaca	aggttagttt	tacctatgac	960
aaa						963

&lt;210&gt; 389

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g238 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 389

tgtttctgtg	gctttgtgtg	tctcaccagt	tgctgtttct	gtctaacccc	ggagaggtaa	60
ataacaccct	gagaatggcc	ctaggctcac	acaggtttcc	cagttagcca	atcaagaaga	120
attacaaatg	gccacactat	cagccagagc	tgctgcctca	ctggagtccc	aaaacggaga	180
ggatctgctc	ccctgcaccc	tcaggcttgg	aaatgctgag	aaatgctaag	ccactggggg	240
ttcaattata	cctaatttaa	aacgagcaaa	gtagacttgc	cccccaagg	gttccacaaa	300
aaacttaaag	cctggcagct	cagccctgag	ttcatactgc	ttaaaagaca	ccggggggagg	360
aggtaagtga	tcagggtgaga	gaagttcggt	ccccagagag			400

&lt;210&gt; 390

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g239 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 390

atgaagccaa caatacaaat ggcttcagga aatctcacat gggtgacgga gttcattctt	60
gtgggagctc cagatgatcc ggagctccag attccccctc tcctgggtctt cctgggtgctc	120
tatttgctga ccggtggcagg gaacctgggc atcatcaccc tcaccagtgt tgacctcaa	180
cttcaaacc ccatgtactt ttctctctga cacttggcta ttattaatct ttgcaattct	240
actgtcggtg cccctaaaat gctgggtaac ttcttgggta ccaagaaaac catatcatac	300
tatggatgtg cagcccaact gggtggattc ttggttttca ttgtggctga gattttcacg	360
ctggctgcaa tggcctatga ccgctatgtg gctatttggg gccctctgct ctacgccgta	420
gtgggtgtctc caaagggtgtg tegtctgctg gtgtccctca cataccttca gagtcttctc	480
acagcactga ctgtctcttc ctgtgtgttc tctgtgtcat actgttcttc caacattatc	540
aaccattttt actgtgatga tgtccctttg ctagcattgt cctgttctga tacctacatt	600
ccagaaacag cagtctttat cttttcaggg accaacttgc ttttctccat gatcggttgtt	660
ctgatatcct acttcaaat ctttattacc attttgagga tacgttcctc agaaggacga	720
caaaaagcct tttccacctg tgcttctcac atgatagctg tgggtgtgtt ctatgggact	780
ctccttttca tgtatttgca accaaggagt aatcattcat tagatactga caaaatggct	840
tcgggtctct acaccctggg gataccagtg ctgaaccctc taatctacag cctcaggaac	900
aagaacgtga aggatgcact aaagagggtc ctagataacc catgccgac actc	954

&lt;210&gt; 391

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g240 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 391

atgttgctccc caaaccacac catagtgcac gaattcattc tcttaggact gacagacgac	60
ccagtgtctag agaagatcct gtttgggggtg ttcttggcga tctacctaat cacactggca	120
ggcaacctgt gcatgatcct gctgatcagg accaattccc aactgcaaac acccatgtat	180
ttcttctctg gtcacctctc cttttagagac atttgetatt cttccaatgt tactccaaat	240
atgctgcaca atttctctc agaacagaag accatctcct acgctggatg cttcacacag	300
tgctctctct tcatcgccct agtgatcact gagttttact tccttgcttc aatggcattg	360
gatcgctatg tagccatttg cagcccttta cattacagtt ccaggatgtc caagaacatt	420
tgcactctctc tggctactgt gccttacatg tatggcttcc ttaatgggct ctctcagaca	480
ctgctgacct ttcacttctc cttctgtggc tcccttgaaa tcaatcattt ctactgcgct	540
gatcctcctc ttatcatgct ggcttgcctc gacaccctg tcaaaaagat ggcaatgttt	600
gtagtgtcag gctttactct ctcaagctct ctcttcatca ttcttctgtc ctatcttttc	660
atttttgcag cgatcttcag gatccgttct gctgaaggca ggcacaaagc cttttctacg	720
tgtgcttccc acctgacaat agtcactttg ttttatggaa ccctcttctg catgtacgta	780
aggcctccat cagagaagtc tgtagaggag tccaaaataa ttgcagtctt ttatactttt	840
ttgagcccaa tgcagaacct attgatctat agcctacgga acagagatgt aatccttgcc	900
atacaacaaa tgattagggg aaaatccttt tgtaaaattg cagtt	945

&lt;210&gt; 392

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g241 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 392

atgcctatag ctaacgacac ccagttccat acttcttcat tctactgct gggtatocca	60
gggctagaag atgtgcacat ctggattgga ttcccttttt tctctgtgta tcttattgca	120

```

ctcctgggaa atgctgctat cttctttgtg atccaaactg agcagagtct ccatgagccc 180
atgtactact gcctggccat gttggattcc attgacctga gcttgtctac ggccaccatt 240
cccaaaatgc tgggcatctt ctggttcaat atcaaggaaa tatcttttgg aggtacatt 300
tctcagatgt tcttcacca tttcttcaact gtcattggaga gcatcgtatt ggtggccatg 360
gcctttgacc gctacattgc catttgcaaa cctctttggt acaccatgat cctcaccagc 420
aaaatcatca gcctcattgc aggcatgtct gtcctgagga gcttgtacat ggtcattcca 480
ctggtgtttc tcctcttaag gttgcccttc tgtggacatc gtatcatccc tcatacttac 540
tgtgagcaca tgggcattgc ccgtctggcc tgtgccagca tcaaagtcaa cattatgttt 600
ggtcttggca gtatttctct cttgttattg gatgtgtctc ttattattct ctcccatatc 660
aggatcctct atgctgtctt ctgcctgcc tcctgggaag ctgcactcaa agctctcaac 720
acctgtggct ctcacattgg tgttatctta gccttttcta caccagcatt tttctcttct 780
tttacacact gctttggcca tgatattccc caatatatcc acattttctt ggctaattca 840
tatgtggttg ttctccac cctcaatcct gtaattctatg ggtcagaac caaacatatt 900
agggagacag tgctgaggat tttcttcaag acagatcac 939

```

&lt;210&gt; 393

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g242 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 393

```

atgcatatct tcaagtttgt tctagatttc aacatgaaga atgtcactga agttacctta 60
tttgtactga agggcttcac agacaatctt gaactgcaga ctatcttctt cttcctgttt 120
ctagcaatct acctcttcac tctcatggga aatttaggac tgattttagt ggtcattagg 180
gattccagc tccacaaacc catgtactat tttctgagta tgttgtcttc tgtggatgcc 240
tgctattcct cagttattac cccaaatatg ttagtagatt ttacgacaaa gaataaagtc 300
atttcattcc ttggatgtgt agcacagggtg tttcttgctt gtagttttgg aaccacagaa 360
tgctttctct tggctgcaat ggcttatgat cgctatgtag ccatctacaa cctctctctg 420
tattcagtga gcatgtcacc cagagtctac atgccactca tcaatgcttc ctatgttgct 480
ggcattttac atgtactat acatacagtg gctacattta gcctatcctt ctgtggagcc 540
aatgaaatta ggcgtgtctt ttgtgatata cctcctctcc ttgctatttc ttattctgac 600
actcacacaa accagcttct actcttctac tttgtgggct ctatcgagct ggctactatc 660
ctgattgttc tgatctccta tggtttgatt ctggtggcca ttctgaagat gtattctgct 720
gaagggagga gaaaagtctt ctccacatgt ggagctcacc taactggagt gtcaatttat 780
tatgggacaa tcctcttcat gtatgtgaga ccaagttcca gctatgcttc ggaccatgac 840
atgatagtgt caatatctta caccattgtg attcccttgc tgaatcccgat catctacagt 900
ttgaggaaca aagatgtaaa agactcaatg aaaaaaatgt ttgggaaaaa tcagggttatc 960
aataaagtat attttcatac taaa 984

```

&lt;210&gt; 394

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g243 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 394

```

atgaatggag ccaacagctc cagcctgaca ccaagatatt tcattctcag tggcgcttct 60
gggctggaag ctgcacacat ctggatctcc ctgccttctt gcttcattgta catcattgtt 120
gttttggga actgtggact tatatacctc attagccatg aggaggccct gcaccaaccc 180
acctactact tcctagactt gctgtctctt acagatgtta ctggatgcac ctcatattgtt 240
cccaatatgt tatgtatttt ttggtttggc ctcaaggaaa ttgactttaa tgctgcctt 300
gtgcagatgt ttttcacca catgctgaca ggcattggagt ctggggcgct catgcttatg 360
gctctagacc gctatgtggc catttgctac cctctacact attccaccat cttcaccaac 420
actgtaatta ccaaagtggg gcttgtcacc ttcattcaaa gtgtgttgct tatgattcca 480
tttgctttcc tgatcaagtg tcttccctat tgcaggggca acctcatcca ccacacctat 540
tttaacatat gtctgtggcc aaattatcct gtggtaatgt ccagattaat gccatctatg 600

```

gtctcatagc	tgccatattg	attggggggg	ttgacatgtt	ctgtatctcc	atgtcttaca	660
ccatgattat	ccgtgctgta	gtgaatttgt	catctgcaga	tgctgccaca	aagccttcag	720
tacctgtaca	gcacatatat	gtgctatgtt	catcacttat	gtcccagcct	ttttcaactt	780
cttcactcac	cgctttgggg	gacacaccat	acctcatcat	gttcacattt	ttatagccaa	840
cctttacctg	atgctgcctc	ccaccttaaa	tccaattgtc	tatggagtga	agaccaagca	900
gatccgtgaa	ggagtgatca	aattgttttt	tagagagaaa	ggatatttaa	gtatgacata	960
aatctatgat	atagaagtct	gaat				984

&lt;210&gt; 395

&lt;211&gt; 903

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g244 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 395

atggccagta	caaataatgt	gactgagtca	atgatcacca	gccttttcca	ggatccagca	60
gtgcagagag	tgtgctttgt	gggtgttctc	cccggtgtact	ggccatggag	gtgggcaatg	120
gcctcatcgt	tctgacggtc	agtatcagca	agagtctgca	ttcccctgtg	tacttcttcc	180
tgagctacct	gtcattgatg	gagatcagtt	acttcactgt	tgccctaaa	ttcatcacag	240
acttacttgc	caagattaaa	gccatctctc	tggagggtca	tctggctcag	atattcttgc	300
acttctttgg	catcccctgg	atctttctgc	tcccactgat	gaccaatgac	caatatatgg	360
ccaactgcaa	actttattac	tacacaacca	tcatgagctg	cctgtctgtc	accttctggg	420
ggctggttcc	tggctgaggg	gcataattca	ctcaatgggt	cagatccctg	tctctgtcca	480
attgttcttc	tgtggtccca	acatgattga	ccactcattc	tgtgacctcc	aggtcttatt	540
caagcttgcc	tgactgaca	cctttgtgga	gggggttatt	gtgttgcca	acagtgaatt	600
agtatctgtc	tcttctctta	tcttgggtgc	ctcttaatat	catcatccta	gtcaacttga	660
ggaaccattc	tgagagggg	aggtgcaaag	ccctctccac	ctgtgcctct	tatcttgtat	720
tttgaacttg	ccattttcct	ctacgtgtga	ctctctcca	cctttactaa	agataaactc	780
gtggctgtat	tttacgtggg	catcaccccc	atgctgaacc	ccttcatcta	cacgcttggg	840
aatgcagaga	tgaaaatcac	catgaggaga	ttgttgggca	ggacagtga	ctcaggaatg	900
gaa						903

&lt;210&gt; 396

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g245 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 396

gggagctgaa	agcaatgaaa	gtcttgacct	cctatctgtc	ttcctgactg	gcatcccagg	60
actggaggcc	caacatgggt	ggctctccat	ccctttcttc	accatgtaca	ttgtggccat	120
tgtgggaaac	atcctaatta	tggcagcagt	gcagggaagac	tctgccctac	atgagcccat	180
gtacttattt	ctctccatgt	tggctgtcac	tgagggtggc	gtctctgtgt	ctacactgct	240
actgttacag	gcattctttg	gtttgatgcc	cacagagttg	actttgatgg	ctgcctggcc	300
cagatgttct	tcattcacac	cttctctctg	atggagtcag	gggtcctact	agccatgagc	360
tatgaccgct	ttgtagccat	ctacaacctc	ctgcgctata	cagccatcct	gacctgccc	420
cgtattatct	gcatgggtct	gggcattaca	ctgaagagtg	tggcactcat	ggccccactt	480
ccaatccttt	tgaggcaact	gccctattgc	cacactaatg	tcctctcaca	ctcctactgc	540
ctccactcag	atctgatcca	gctgccttgt	gcagatacta	aactcaacag	catcctgggc	600
ttagccattg	ttctcgcaaa	tttcgggctg	gactcattgc	ttatcgtggg	ctcttatgtc	660
ttgattcttt	atacagtgat	gggcattgct	tctggagagg	gacgggtgaa	ggctctcaac	720
acatgtgtgt	cacatatttg	tgcagtgtct	atatattatg	tgcccatgat	tgggggtgtct	780
gtgatgcac	gtgctgcaaa	acatgcttct	cccattgtcc	acacacttat	gtctagcatc	840
tgccttttgg	tgccacctgt	acttaatccc	atcatctata	gtgttaagac	ccagacaata	900
agacagggaa	ttctcacctt	gttttctctg	aagagggaat	tgctctgaat	cactgcaagg	960
agtcaggaac	tg					972

<210> 397  
 <211> 874  
 <212> DNA  
 <213> Unknown (H38g246 nucleotide)

<220>  
 <223> Synthetic construct

<400> 397  
 actttgttta ttatttcaaa atttcaaggc tgctgaaagg taggtcttta tacacagtca 60  
 ctttatttgc tagctgagta. ttttcatcgg gggcaactga tgaaaaatgtt gacttccact 120  
 aacctaaagcc tgtccgttgt tactatcgta tcttccagtt caacgtcagg gaaatagttt 180  
 ttggtgcttt ccttgtttat atacagatgt ttatgactta tctatgcact ggcctggaat 240  
 ctgggggtact gataatcctg gccatagacc actatgtcgt aattcgcaat ccactgagat 300  
 ataccatgat tctcatgaac aatgtggttag ccacccagg aagtcagat aattagatct 360  
 ttaatcttta tcatcccttt tgagtttctc atcttgcgtg tgctattctg tgctgcccac 420  
 atcatccccc acaccaaagt tgagcacatg ggcattgccc atctttcctg tgccagtgtc 480  
 agagccaata atatgtttgg gatggttgcc tttttgtggg atttattgac cttattgcaa 540  
 ttggtttctc ctatgtaaag aaactacaca ctgtttcact taccaccatg gaatggccag 600  
 ttcgaggctc tcaatacctg tgggtcccat gtttgcctg ctcatcttct acatcccagt 660  
 atttttttct tgatacactg cttggtgaaa gcacccctgc tatattcgta tatttctggc 720  
 caatgtatat acggtgttct tacctgtatt caacctgtt atctatggga tcaggaaaaa 780  
 acagatccca gactagggtg tagacctaaa gacatttgat gatcagtcac ttctagtcac 840  
 gatgatatat atattgggat atatatgcaa atat 874

<210> 398  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g247 nucleotide)

<220>  
 <223> Synthetic construct

<400> 398  
 atggatgaag ccaatcactc tgtggtctct gagtttgtgt tcttgggact ctctgactcg 60  
 cggaagatcc agctcctcct ctctcctttt ttctcagtggt tctatgtatc aagcctgatg 120  
 ggaaatctcc tcattgtgct aactgtgacc tctgaccctc gtttacagtc ccccatgtac 180  
 ttctctgctgg ccaacctttc catcatcaat ttggtatttt gtctctccac agctcccaag 240  
 atgatttatg accttttcag gaagcacaag accatctctt ttgggggctg tgtagttcag 300  
 atcttcttta tccatgcagt tgggggaact gagatggtgc tgctcatagc catggctttt 360  
 gaccgatatg tggccatatg taagcctctc cactacctga ccatcatgaa cccacaaagg 420  
 tgcattttgt ttttagtcat ttcttggtat ataggtatta ttcactcagt gattcagttg 480  
 gcttttggtg tagacctgct gttctgtggc cctaataaat tagatagttt cttttgtgat 540  
 ctctctcgat ttatcaaact ggcttgcata gagacctaca cattgggatt catggttact 600  
 gccaatagtg gatttatttc tctggcttct tttttaatte tcataatctc ttacatcttt 660  
 attttggtga ctgttcagaa aaaatcttca ggtgtatat tcaaggcttt ctctatgctg 720  
 tcagctcatg tcattgtggt gggtttgtgc ttggggccat taatcttttt ctatattttt 780  
 ccatttccca catcacatct tgataaattc cttgccatct ttgatgcagt tatcactccc 840  
 gttttgaatc cagtcactta tacttttaga aataaagaga tgatggtggc aatgagaaga 900  
 cgatgctctc agtttgtgaa ttacagtaaa atcttt 936

<210> 399  
 <211> 503  
 <212> DNA  
 <213> Unknown (H38g248 nucleotide)

<220>  
 <223> Synthetic construct

<400> 399  
 aagcagtcca gtggtgacag tgggaaccag accacctggc tgatcctagt gggcttcggg 60



gagctgcaat	acctgggctt	ccttcccttc	actctcttcc	tggccatcta	tgtggtgaca	120
gttggggcaa	tgcctcctc	atgctggctg	tggcctctag	tcggacactg	caccaccaa	180
tgtacttctt	cctctgccac	ttctccctgc	tggagattgg	ctatacctcc	aacgtcatac	240
tatggtctgt	gcagagtttc	ttggagggga	aggaagtcac	ctctctagtc	agctgtctgg	300
ctcagttcta	cgtgttttcc	tcgctggctg	cagctgagtg	cctcctgcta	tctgccgtgt	360
cctatgactg	ttacttggcc	atctgctgcc	cccttcaacta	tcctgccttg	atgagcacct	420
ggttttgtca	ctgcctggcc	gctggtgctt	ggttcagtg	cttcttctcc	tctgccttca	480
ctatggccct	ggcagcacct	ctg				503

&lt;210&gt; 400

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g249 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 400

atgctaacac	tgaataaaac	agacctaata	ccagcttcat	ttattctgaa	tggagtccca	60
ggagtgaag	acacacaact	ctggatttcc	ttcccattct	gctctatgta	tgttgtggct	120
atggtaggga	attgtggact	cctctacctc	attcactatg	aggatgcctt	gcacaaaccc	180
atgtactact	tcttggccat	gctttccttt	actgaccttg	ttatgtgctc	tagtacaatc	240
cctaaagccc	tctgcatctt	ctggtttcat	ctcaaggaca	ttggatttga	tgaatgcctt	300
gtccagatgt	tcttcatcca	caccttcaca	gggatggagt	ctgggggtgct	tatgcttatg	360
gccctggatc	gctatgtggc	catctgctac	cccttacgct	attcaactat	cctcaccaat	420
cctgtaattg	caaagggttg	gactgccacc	ttcctgagag	gggtattact	cattattccc	480
tttactttcc	tcaccaagcg	cctgccctac	tgcagaggca	atatacttcc	ccatacctac	540
tgtgaccaca	tgtctgtagc	caaattgtcc	tgtggtaatg	tcaagggtcaa	tgccatctat	600
ggctctgatg	ttgccctcct	gattgggggc	tttgacatac	tgtgtatcac	catctcctat	660
accatgatcc	tccgggcagt	ggtcagcctc	tcctcagcag	atgctcggca	gaaggccttt	720
aatacctgca	ctgccacacat	ttgtgccatt	gttttctcct	atactccagc	tttcttctcc	780
ttcttttccc	accgcttttg	ggaacacata	atcccccttt	cttgccacat	cattgtagcc	840
aatattttatc	tgtccttacc	acccactatg	aaccttattg	tctatggggg	gaaaaccaa	900
cagatacgag	actgtgtcat	aaggatcctt	tcaggttcta	aggataccaa	atcctacagc	960
atg						963

&lt;210&gt; 401

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g250 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 401

atgacaacac	accgaaatga	caccctctcc	actgaagctt	cagacttcct	cttgaattgt	60
tttgtcagat	ccccagctg	gcagcactgg	ctgtccctgc	ccctcagcct	ccttttcttc	120
ttggccgtag	gggccaacac	caccctcctg	atgaccatct	ggctggaggc	ctctctgcac	180
cagccctgtg	actacctgct	cagcctcctc	tcctgtctgg	acatcgtgct	ctgcctcact	240
gtcatcccca	aggctcctgac	catcttctgg	tttgacctca	ggcccatcag	cttccctgcc	300
tgttctctcc	agatgtacat	catgaattgt	ttcctagcca	tggagtcttg	cacattcatg	360
gtcatggcct	atgatcgta	tgtagccatc	tgccaccac	tgagatatcc	atcaatcatc	420
actgatcact	ttgtagtcaa	ggctgccatg	tttattttga	ccagaaatgt	gcttatgact	480
ctgccatccc	ccatcctttc	agcacaactc	cgttattgtg	gaagaaatgt	cattgagaac	540
tgcattctgtg	ccaatatgtc	tgtttccaga	ctctcctgcg	atgatgtcac	catcaatcac	600
ctttaccaat	ttgtctggagg	ctggactctg	ctaggatctg	acctcatcct	tatcttcttc	660
tcctacacct	tcattctgcg	agctgtgctg	agactcaagg	cagaggggtgc	cgtggcaaag	720
gccctaagca	catgtggctc	ccacttcatg	ctcatcctct	tcttcagcac	catccttctg	780
gtttttgtcc	tcacacatgt	ggctaagaag	aaagtctccc	ctgatgtgcc	agtcttgctc	840
aatgtttctcc	accatgtcat	tcctgcagcc	cttaacccca	tcatttacgg	ggtgagaacc	900
caagaaatta	agcagggaat	gcagaggttg	ttgaagaaag	ggtgc		945

<210> 402  
 <211> 906  
 <212> DNA  
 <213> Unknown (H38g251 nucleotide)

<220>  
 <223> Synthetic construct

<400> 402  
 ttgagctcta tgtgtctcac cattgtgatg cattgtgaat tcttctcat ggacttgact 60  
 gatgatcctc agcttcatcc cacccttctct gccctcttcc tccccatcta tgtagtcatg 120  
 gtgatggaaa cctgggcttc cttgccttca ttgtggcag tccccaatc ctcaccccca 180  
 tgtatttctt cctcagcaac tggctctctg ttgacttctg ttattcttca gtaacagtcc 240  
 caaaaatata aatgggggttc ttttctgact gccaaagtct ctccttctct gggtgcatgg 300  
 cccagttaag ctgcttttaa aatatttgct gacaccgagt tcttctctct ggctcccatg 360  
 gtctattacc gctaagagge cgtctgcaat cctctgctct accatatcac catgtcccca 420  
 aagctctgct tgcagctggg ggccaccagc tatgaacatg gtgctcccta gtagcacaat 480  
 ctttcatctg atcttctgta agtctgtgcc atcattcatt aattctgtta tttctctccc 540  
 caccgaggct ttaaaaactc tcctgctctg acatgcaagg ccttcaactt cttacctttg 600  
 cctctagtag ctttaatgta tcgggtgccc ggacaatctt ccttgtctcc atttaattat 660  
 gagaatgccc tcggtttgag gcaaacactt gtgcttcca cctgacagca gtcagcctgt 720  
 gctatggaac cacagtgttc cttcacctgc acctatcctt gaagtgttca ccagacagag 780  
 atatgctggg ctctgtttta cacagtggct attctcatgc tcaaccccat ggtccaaagt 840  
 ctgaggaaca aggatgtgaa gaaaacattt gggacttctt catgaagggt tacaattcct 900  
 ctctct 906

<210> 403  
 <211> 972  
 <212> DNA  
 <213> Unknown (H38g252 nucleotide)

<220>  
 <223> Synthetic construct

<400> 403  
 atgcctctat ttaattcatt atgctgggtt ccaacaattc atgtgactcc tccatctttt 60  
 attcttaatg gaatacctgg tctggaaaga gtacatgtat ggatctccct cccactctgc 120  
 acaatgtaca tcatcttctt tgtggggaat cttggtcttg tgtacctcat ttattatgag 180  
 gagtctttac atcatccgat gtattttttt tttggccatg ctctctccct cattgacctc 240  
 cttacctgca ccaccactct acccaatgca ctctgcatct tctggttcag tctcaaagaa 300  
 attaacttca atgcttgctt ggcccagatg ttctttgttc atgggttcac aggtgtggag 360  
 tctgggggtgc tcatgctcat ggctctagac cgctatgtag ccatttgcta ccctttgcgt 420  
 tatgtacca cactcaccaa ccctatcatt gccaaaggct agcttgccac cttctgagg 480  
 ggtgtattgc tgatgattcc tttccattc ttggttaagc gtttgccctt ctgccaaagc 540  
 aatattatct cccatacgta ctgcgaccac atgtctgtag taaagctatc ttgtgccagc 600  
 atcaagggtca atgtaatcta tggctaatg gttgctctcc tgattggagt gtttgacatt 660  
 tgttgatat ctttgtctta cactttgatc ctcaaggcag cgatcagcct ctcttcatca 720  
 gatgctcggc agaaggcttt cagcacctgc actgcccata tatctgccat catcatcacc 780  
 tatgttccag cattcttcac tttctttgcc caccgttttg ggggacacac aattccccct 840  
 tctcttcaca tcaatgtggc taatctttat cttcttcttc ccccaactct aaacctatt 900  
 gtttatggag taaagacaaa acagatacgc aagagtgtca taaagttctt ccagggtgat 960  
 aaggggtgcag gt 972

<210> 404  
 <211> 821  
 <212> DNA  
 <213> Unknown (H38g253 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 404

gagagaaatc	ccagtgtagc	agaaaagtgc	cttcaagga	tgactgattc	ctctcaccat	60
tatcttttagc	ttaactccct	ctcttcaggc	tgtaatcct	cttgatact	atcattacga	120
tagggaattt	gggcacggc	attctcattg	ggatcagtct	cggtttatat	gtctgtctcg	180
cctagatttc	tgctattcac	ttttcccatg	ctcagagtc	tagtaaaatg	tttttgaagt	240
acagtgtctg	ccttctcttt	ctggagtctt	gaagcacaga	ttaacttctt	cagcatcttg	300
tgtatcacag	agttctttcc	cttggccaca	atggcctatg	atgacaatgt	tgccacttgt	360
gaacctttat	tccacccttt	caccagtttg	agactcaact	ggcatttggt	tgagaaaaac	420
tgtatcttag	agccttcacc	tcagccctcc	cctcaactct	tccgttccac	ctccccttct	480
tcaattccca	cttgtgtctc	cttcagtgc	attactttct	gggtcaagtt	gtcctctgaa	540
acatgactcc	caactttaaa	ctccctgatt	tctctaactc	caatgtgaac	ttagtaagcc	600
tgtgtgtg	aacctctg	tgctacccca	tcattttaag	gtcattatca	tcccataact	660
aattctgaaa	acaaattatt	gataatcatt	ttttttcaga	attccactca	ttgtctctta	720
ttttctgttc	agatgaaaat	gtttattaaa	ccatttgagg	tatcactgac	tagttcatta	780
aaagtaaaaa	ttgtgtacat	attcccttaa	tgagattctt	t		821

&lt;210&gt; 405

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g254 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 405

atgtcttctc	tcaatgtcac	tgaacccac	ctctcttctc	tctgtttggt	taggaattcc	60
aggattggaa	gctgcacaac	gctggctagg	cttcccttc	tgtgttgat	atctgattgc	120
tcttgttgg	aatcttatca	ttctatttgt	tatctggact	gataaaaacc	ttcaccaacc	180
catgttctac	tttctggcca	tgctgtcagt	catgacctga	gtctttctac	atctactatc	240
ccaagatgt	tgggcatctt	ctggttcagc	cttcaggagt	tgtgtttgg	gtgctgtgtt	300
gctcaagtct	tttttatcca	tttttttgc	agtcattggag	agcattgtac	ttcttgtcat	360
gggattttgat	cgctatgtgg	ctatttgcaa	cccttcagg	tagaccaaga	tcctcaccaa	420
cagaattact	ggtgtgattg	ctatggttgt	ggttcttaga	agcttatgta	tgattgctcc	480
catcattttt	ctctcatga	ggctgcctta	ctgtggacat	agaatcatcc	cttataccta	540
ttgtgagcac	atgggagtgg	ctcgtctggc	ttgtgccagc	atcagtgatc	atgtctctca	600
tggctcttgg	aatattttta	tcttgtttct	ggatatgttt	cttatcatca	tctcctatgc	660
tagaatttta	tgcacagtct	ttcacctccc	ttcccaagag	gcccacctga	aggctcttaa	720
tacctgtagc	tcccatatct	gtgtcatctt	agcatttttt	ggcccagctc	tcttctcctt	780
tctcactcat	cgctttggtc	atggcatccc	acagtatata	catattctcc	tggctaattct	840
ctatatatag	tcattccccc	tgctcttaac	ccagtcattt	atggagttag	gaccaagcaa	900
atccaggagc	gggtagaaag	tctctttact	aaaaattgat	tgaat		945

&lt;210&gt; 406

&lt;211&gt; 970

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g255 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 406

gtggaaaatt	cacccatggt	gactgacttc	atctttctcg	gcatgacaga	taactctcag	60
cttgaagtcc	tgctatttgg	agtctttctt	attgcttaca	tcatcactgt	gttggagaat	120
ctaggccttg	tggttctgat	cagagtcagc	tcccgcctcc	acaccccatg	tactttttcc	180
tctctaatac	gtccttccct	gatgtctgtt	tctcttccat	tacaattcca	cagaattttag	240
cacatttgtt	ttctaagctg	cagtatgttt	ctttcccttt	cccgtataac	ttaaagtggc	300
ttgtttgtaa	tctttgcctc	tgctgaatgc	aattttttaa	acttgcatgg	cctatgaccg	360
ctttactgcc	atctgtcacc	cactgttcta	ccacattacc	atgtcaagag	gccattatct	420
tttcttggta	gcaggatgct	accttgggtg	gttagttaag	atggtcactg	tgacaacttc	480
catcacacaa	ctatcgcttt	gtcaacccatg	tgctctccct	gccttcttct	gtgacattcc	540

ctcattgttg	gtactgggtt	gctcagatcc	ttggatcacc	tcccgatctt	gggtggtggc	600
tgtgggggat	tcaccctggt	cacctctgtt	gtgggtgatcc	ttgtctccta	catgtcttcc	660
ctcatgacta	tcctaggaat	tcccttagct	tctggaaaac	agagagcctt	ctccacctgt	720
gcctccact	tgactgctgt	tagcctgtac	tatgaaacaa	ctatgtacac	ttacttggcc	780
gcctcgcgac	atggatccgg	ggcaggaaat	cagattgtgt	cagtatttta	tacaatgggtg	840
atccccatgt	taaatcctct	catctatagt	ttgagaaatg	aggaagtgaa	agttggcccta	900
tgaaaaacat	tgagacatag	tccttaatct	tctattgagt	gtctcaaaaa	tgcaaaatat	960
tctgtgaaga						970

&lt;210&gt; 407

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g256 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 407

tggcttgatg	aaaaaaaaa	agattctaac	gtgacagAAC	ttgttcttct	gggcctatca	60
tcttcttggg	agctgcagct	atttctctta	ttactatttt	tgttttttta	cattgctatt	120
gtcctgggaa	acctcttgat	agtggtaaca	gtgcaagccc	atgctcatct	gctccaatct	180
cctatgtatt	attttttagg	tcatctctct	ttcattgacc	tatgcctaag	ctgtgttact	240
ctgccaaga	tgtagggga	tttctacag	cagggcaaga	gcatctcttt	ttcaggatgc	300
ctggcccaga	tctacttct	ccactttcta	ggagccagtg	agatgttttt	gctgacagtt	360
atggcctatg	acaggatgt	tgccatctgt	aaccctttgc	gctaccttat	aagtcagaa	420
ccccagcta	tgcttttgg	tggttcttgc	ctgctgggtg	gggggtttta	tccactctat	480
catgcaggtc	atactagtca	tccagctgcc	tttctgtggc	cccaatgaac	tggacaactt	540
ctactgtgat	gtcccacagg	tcatcaagct	ggcctgcagt	gacacctatg	tggtagaggt	600
gctgatgata	gccaacagtg	gtctgctctc	tcttgtctgc	ttcttgggtc	tactattctc	660
ttatgctgtc	atcctgatca	ccctgagaac	acacttcggc	cagggccaga	acaagttcct	720
ctctacctgt	gcttctcacc	tgacagtgg	cagcctgac	ttcatgccat	gtatattcat	780
ctatttgagg	cctttctgca	gcttctctgt	ggataagata	ttctccatgt	ttacacaggt	840
gatgacacct	atggttagcc	ccctcatcta	cacactcaga	aatgctgata	tgaagacagc	900
tatgaagaag	ctgaggataa	aaccatgtga	catt			934

&lt;210&gt; 408

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g257 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 408

atgatgggtg	atcccaatgg	caatgaatcc	agtgtacat	acttcacct	aataggcctc	60
cctgggttag	aagaggctca	gttctggttg	gccttcccat	tgtgtccct	ctaccttatt	120
gctgtgctag	gtaacttgac	aatcatctac	attgtgcgga	ctgagcacag	cctgcatgag	180
cccatgtata	tatttctttg	catgctttca	ggcattgaca	tcctcatctc	cacctcatcc	240
atgcccacaa	tgctggccat	cttctgggtc	aattccacta	ccatccagtt	tgatgcttgt	300
ctgtacaga	tgtttgccat	ccactcctta	tctggcatgg	aatccacagt	gctgtgtggc	360
atggcttttg	accgctatgt	ggccatctgt	cacccactgc	gccatgccac	agtacttacg	420
ttgcctcgtg	tcacaaaaat	tggtgtggct	gctgtgtgct	ggggggctgc	actgatggca	480
cccttccctg	ttctcatcaa	gcagctgcc	ttctgceget	ccaatatcct	ttcccatcc	540
tactgcctac	accaagatgt	catgaagctg	gcctgtgatg	atatccgggt	caatgtcgtc	600
tatggcctta	tcgtcatcat	ctccgccatt	ggcctggact	cacttctcat	ctccttctca	660
tatctgctta	ttcttaagac	tgtgttgggc	ttgacacgtg	aagcccaggc	caaggcattt	720
ggcacttgcg	tctctcatgt	gtgtgctgtg	ttcatattct	atgtaccttt	cattggattg	780
tccatgggtc	atcgcttttag	caagcggcgt	gactctccgc	tgcccgctcat	cttggccaat	840
atctatctgc	tggttccctc	tgtgtctcaac	ccaattgtct	atggagtgaa	gacaaaggag	900
attcgacagc	gcaccttcg	acttttccat	gtggccacac	acgcttcaga	gccc	954

<210> 409  
 <211> 959  
 <212> DNA  
 <213> Unknown (H38g258 nucleotide)

<220>  
 <223> Synthetic construct

<400> 409  
 atgtcttcca gactaatgaa tgtgttcagc atggaaacta tcaattttgt tagctgcctt 60  
 atcctcatgg gctttccctc aagcccagaa atgcagctcc tctacttcgg tctcttctca 120  
 gtagcctata ctctcaccac gatgggaaat gcagccattg tctgtgctgt gtggtaggac 180  
 cagcaccttc acaactccat gtacaccctc ttgggaaatt tctctctcct ggaaatatgt 240  
 tatgttactg caactaaact gctggccaac ttcctctcca caagcaagtc catctcatc 300  
 atgagttgtt ttgcacagtt ctactcttct tctttggggg atgatgaggg cttcttctct 360  
 tgcatacagg cctttgacag gtatcttgcc atctgccgcc ctctacgtta tccatgcac 420  
 atgactaaac aagtatgcac tggcctcatc atttttgcat ggatcatgtg ctttgtaac 480  
 ttctaaactc tgggtgattct catttcacag ctatcctact gtggcccaaa tattatcaac 540  
 cattttattt gtgatcccggt cccattgaag atgctgtcct gttctgaaga catcatcatc 600  
 acccagctca tttactccac attcaattct gtcttcataa ttggcacctt tctctttatc 660  
 ctttgttcct atgctctggg gattctgggt ataatacggg tgccttcaga ggctggcaaa 720  
 cgaaaagctt tctccacttg tgcctctcat ttggcagttg tcaccttatt ttatggctct 780  
 atcatgggta tgtatgtag tcttgatca gcacaccag taaaaatgaa aaaatcatta 840  
 ccttgttctt ttctgtgata acaccactct gtaatcctct aatataatag ctccaggaaca 900  
 aagagatgaa agattatctg aggaaaatct tcaggactgg aaaagatgtt aataaaata 959

<210> 410  
 <211> 926  
 <212> DNA  
 <213> Unknown (H38g259 nucleotide)

<220>  
 <223> Synthetic construct

<400> 410  
 atgctgaata caacctcagt cactgaattt ctcttttgg gagtgacaga cattcaagaa 60  
 ctgcagcctt ttctcttcgt tgttttctt accatctact tcatcagtggt ggctgggaat 120  
 ggagccattc tgatgattgt catctctgat cctagactcc attcccctat gtattttctt 180  
 ctgggaaacc tgtctgcct ggacatctgc tactccagcg taacactgcc aaaaatgctg 240  
 cagaacttcc tctctgcaca caaagcaatt tctttcttgg gatgcataag ccaactccat 300  
 ttcttccact tcctgggcag cacagaggcc atgttggttg ccgtgatggc atttgaccgc 360  
 tttgtggcta tttgcaagcc acttcgctac actgtcatta tgaacctca gctctgtacc 420  
 cagatggcca tcacaatctg gatgattggg tttttccatg ccctgctgca ctccctaattg 480  
 acctctcgct tgaacttctg tggttctaac cgtatctatc acttcttctg tgatgtgaag 540  
 ccattgctaa agctgagctt aatcagtggc tgctcagtac tgtcacaggg acaatcgcca 600  
 tgggcccctt ctttctcaca ttactctcct atttctacat tatcaccat ctcttcttca 660  
 agactcattc ttttagcatg ctccgcaaag cactgtccac ttgtgcctcc cacttcatgg 720  
 tagttattct tttgtatgca cctgttctct tcacctatat tcatcatgcc tcagggacct 780  
 ccatggacca ggaccggatc actgccatca tgtatactgt ggctactcca gtactaaacc 840  
 cactgatcta cactttgagg aacaaggaag tgaaaggggc ctttaataga gcaatgaaaa 900  
 ggtggctttg gcctaaagaa atctttg 926

<210> 411  
 <211> 994  
 <212> DNA  
 <213> Unknown (H38g260 nucleotide)

<220>  
 <223> Synthetic construct

<400> 411

atggaaagcg	agaacagaac	agtgataaga	gaattcatcc	tccttcgttt	gacccagttt	60
cgagatat	agctcctggt	ctttgtgcta	gttttaatat	tctacttctt	catcctccct	120
ggaaattttc	tcattatttt	caccataagg	tcagaccctg	ggctcacagc	ccccctctat	180
ttatttctgg	gcaacttggc	cttcctggat	gcacccctact	ccttcattgt	ggctcccagg	240
atgttggtgg	acttcctctc	tgagaagaag	gtaatctcct	acagaggctg	catcactcag	300
ctctttttct	tgcacttctt	tggaggagg	gagggattac	tccttggtgt	gatggccttt	360
gaccgtaca	tcaccatctg	cctgcctctg	cagtattcaa	ctgtcatgaa	ctctagagcc	420
tgctatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatca	tccgcttgcc	ttttgtggc	ccaaaccagc	tggacaactt	cttctgtgat	540
gtccgacagg	tcacaaagct	ggcttgacc	gacatgtttg	tgggtgagct	tctgatggtc	600
ttcaatagtg	gcctgatgac	actcatgtgc	tttctgggac	ttctggcctc	ctatgcagtc	660
attctttgtc	gcatacgagc	gtcttcttct	gaggcaaaaa	acaaggccat	gtccacatgc	720
accaccata	tcattgttat	attcttcatg	tttggacctg	gcattctcat	ctacacgtgc	780
cccttcagg	ctttccagc	cgacaagggtg	gtttctctct	tccacacagt	gattcttctt	840
ttgttgaatc	ctgtcattta	tacccttcat	aaccagggaag	tgaagcttc	catgaaaaag	900
gtgtttaata	aacacatagc	ctgaaaaagg	gcaaaaaaaa	aaagaagaaa	aatagactgt	960
agaattttat	ctgaaattga	ttgttttatt	tcca			994

&lt;210&gt; 412

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g261 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 412

atggaaattg	tctccacagg	aaacgaaact	attactgaat	ttgtcctcct	tggcttctat	60
gacatccctg	aactgcattt	cttgtttttt	attgtattca	ctgtgtgcta	tgtcttcate	120
atcataggga	atatgctgat	tattgtagca	gtggtagct	cccagaggct	ccacaaacct	180
atgtatat	tcttggcgaa	tctgtccttc	ctggatattc	tctacacctc	cgcagtgatg	240
ccaaaaatgc	tggagggtct	cctgcaagaa	gcaactatct	ctgtgggtgg	ttgttgtctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgtggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgtaccaca	ctccactacc	cactcctgat	ggggccaga	420
cggtagatgg	ggctgggtgt	cacaacctgg	ctctctggat	ttgtggtaga	tggactgggt	480
gtggccctgg	tggcccagct	gaggttctgt	ggccccaacc	acattgacca	gttttactgt	540
gactttatgc	ttttcgtggg	cctggcttgc	tcggatccca	gagtggctca	ggtgacaact	600
ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgct	gagagttcct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgctctc	cccacctagc	tgtagtgacc	acattctatg	gaacgctcat	gatcttttat	780
gttgcaccct	ctgctgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcaccc	ctctcttcaa	tcctgtgac	tataccatga	ggaacaagga	ggtgcacag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

&lt;210&gt; 413

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g262 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 413

atgagtgc	aaacacctccat	ggtgactgag	tttcttcttc	tgggttctc	ccacctggcc	60
gacctccagg	gcttgccttt	ctctgtcttt	ctcactatct	acctgctgac	cgtggcaggc	120
aatcttctca	ttgtggtgct	ggtctccact	gatgtgccc	tccagtccc	tatgtacttc	180
ttcctgcgca	ccctctcggc	cttgagatt	ggctatacgt	ctgtcacgg	ccccctgcta	240
cttcaccacc	tccttactgg	cggcgccac	atctctcgt	ctggatgtgc	tctccagatg	300
ttcttcttcc	tcttctttgg	cgccacggag	tgtgctctcc	tggcagccat	ggcctatgac	360
cgctatgcag	ccatctgtga	acccctccgc	taccactgc	tgtgagcca	cgggtgtgt	420
ctacagctag	ctgggtcggc	gtgggcctgt	ggggtgctgg	tggggtcggg	ccacaccctt	480

ttcatcttct	ctttgccctt	ctgcggcccc	aataccatcc	cgcagttctt	ctgtgagatc	540
cagcctgtcc	tgcagctggg	atgtggagac	acctcgctta	atgaactgca	gattatcctg	600
gcaacagccc	tcctcaccct	ctgccccctt	ggcctcatcc	tgggctccta	cgggcgtatc	660
ctcgtttacca	tcttccggat	cccattctgt	gcgggcccgc	gcaaggcctt	ctccacctgc	720
tcctcccacc	tgatcgtggg	ctccctcttc	tatggcaccg	cactctttat	ctatatctgc	780
cctaaggcca	gctacgatcc	ggccactgac	cctctgggtg	ccctcttcta	tgctgtgggc	840
acccccatcc	tcaaccccat	catctacagc	ctgcggaaca	cagagggtcaa	agctgcccta	900
aagagaacca	tccagaaaac	ggtgcctatg	gagatt			936

&lt;210&gt; 414

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g263 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 414

atgggttaacc	aaagctcccc	catgggcttc	ctccttcttg	gcttctctga	acaccagca	60
ctggaaagga	ctctctttgt	ggttgtcttc	acttcctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tcctgtgtgc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
ctctctgacc	tctccttctt	ggacctctgc	tttaccacaa	gttgtgtccc	ccagatgctg	240
gtcaacctct	ggggcccaaa	gaagaccatc	agcttctctg	gatgctctgt	ccagctcttc	300
atcttctctg	ccctggggac	cactgagtgc	atcctcctga	cagtgtggc	ctttgaccga	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccacccccg	cctgtgtctg	420
cagctggcat	ctgtggcctg	ggttatgagt	ctggttcaat	cgatagtcca	gacaccatcc	480
accctccact	tgcccttctg	tccccaccag	cagatagatg	actttttatg	tgagggtcca	540
tctctgatcc	gactctcctg	tggagatacc	tctacaatg	aaatccagtt	ggctgtgtcc	600
agtgtcatct	tcgtgggtgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
caggcagtgc	tgaggattaa	ctctgccaca	gcattggagaa	aggccttttg	gacctgtctc	720
tcccatctca	ctgtggtcac	cctcttctac	agctcagtc	ttgtgtctca	cctccagccc	780
aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcact	840
ccttacttta	accctctcgt	atacaccctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaag	agactccagg	gaaagctgga	gagctgct		948

&lt;210&gt; 415

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g264 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 415

atgaagagcg	aactgaacag	gaattactca	gaggtgacag	agttttattct	gctgggattc	60
agaacatcgc	cagaagcaca	gattctctta	ttcttcctgt	tcttgcttat	ctacatgggc	120
attgtgttga	gaaatctcag	catgttagtt	gtcattgaaa	tagactccag	acttcacaca	180
cctgtgtatt	tctttctcag	aaatttgtcc	tatttggatc	tccgctactc	cacagttatt	240
gcttccaaaa	ctgactactt	tattttccaa	ggaaaagaaa	atttcttaca	atggttgagc	300
aacacagttg	tttttctttg	ctctctttgt	tgggactgaa	ggtttttttc	tggatatgat	360
ggcatatgat	cgcttctcag	ctatttgttc	acctttcttc	tatactgtat	gtatgtctca	420
gcaagcttgt	gtttgtttgg	tggttggctc	ctctatctgt	ggatgcatca	actccatgat	480
acaacaggt	tttaccttca	gtttgcattt	ctgtggagaa	aacagattag	agcacttttt	540
ctgtgatgtc	tcagtcatga	tcaagatctc	atgtattgac	atccttgtga	atgaggtagt	600
actgtttatt	ctctctgtgc	tcataccacc	caccacaact	gtcattctgg	cttcctatgt	660
gcatactctc	tcactgtgcc	tgaagattct	ctcaaccacc	ggcagaagga	agactttctc	720
cacttgcagc	tctcacatca	ctgtgggtgag	tttattctat	ggaactgtat	tcttcatgta	780
tgcccaacct	ggggccatct	ccaaagagca	aggttatagt	tgtattctaa	actcttgtca	840
tcctcatgtt	aaatatctga	tttatagtct	aagaaatagg	tgcaaaatgc	tttgaaaagg	900
acattgataa	gaaaaatatc	ttttcattgg	cctctagcca	tctataaaac	tata	954

<210> 416  
 <211> 531  
 <212> DNA  
 <213> Unknown (H38g265 nucleotide)

<220>  
 <223> Synthetic construct

<400> 416  
 atgagcccaa gaatgtgcct ttcatttctg gctgttgcct ggacccttgg tgtcagtcac 60  
 tccctgttcc aactggcatt tcttgttaat ttacccttct gtggccctaa tgtgttggac 120  
 agcttctact gtgaccttcc tcggcttctc agactagcct gtaccgacac ctacagattg 180  
 cagttcatgg tcaactgtta cagtgggttt atctgtgtgg gtactttctt catacttcta 240  
 atctcctaca tcttcactct gtttactgtt tggaaacatt cctcaggtgg ttcattccaag 300  
 gccctttcca ctctttcagc tcacagcaca gcggtccttt tgttctttgg tccacccatg 360  
 tttgtgtata catggccaca ccctaattca cagatggaca agtttctggc tatttttgat 420  
 gcagttctca ctcttttct gaatccagtt gtctatacat tcaggaataa ggagatgaag 480  
 gcagcaataa agagagtatg caaacagcta gtgatttaca agaagatctc a 531

<210> 417  
 <211> 965  
 <212> DNA  
 <213> Unknown (H38g266 nucleotide)

<220>  
 <223> Synthetic construct

<400> 417  
 atggaagcag aaaaccttac agaattatca aaatttctcc tcctgggact ctcagatgat 60  
 cctgaactgc agcccgctct ctttgggctg ttctgtcca tgtacctggg cagcgtgctg 120  
 gggaacctgc tcatcattct ggccgtcagc tctgactccc acctccacac ccccatgtac 180  
 ttcttctct ccaacctgtc ctttgttgac atctgtttca tctccaccac agtccccaag 240  
 atgctagtga gcatccaggc acggagcaaa gacatctcct acatgggggtg cctcactcag 300  
 gtgtattttt taatgatgtt tgctggaatg gatactttcc tactggccgt gatggcctat 360  
 gaccggtttg tggccatctg ccaccactg cactacacgg tcatcatgaa cccctgcctc 420  
 tgtggcctcc tgggtctggc atcttgggtc atcattttct ggttctcctt ggttcatatt 480  
 ctactgatga agaggttgac cttctccaca ggcactgaga ttccgcattt cttctgtgaa 540  
 ccggctcagg tcctcaagggt ggctgtctct aacaccctcc tcaataacat tgtcttgat 600  
 gtggccacgg cactgtctggg tgtgttctct gtactgtgga tcctcttctc ctactctcag 660  
 attgtctcct ccttaatggg aatgtcctcc accaagggca agtacaagc cttttccacc 720  
 tgtggatctc acctctgtgt ggtctccttg ttctatggaa caggacttgg ggtctatctg 780  
 agttctgtctg tgaccattc ttccagagc agtccaccg cctcagtgat gtacgccatg 840  
 gtcaccccca tgctgaaccc cttcatctac agcctgagga acaaggatgt gaagggggcc 900  
 ctggaaagac tcctcagcag ggccgactct tgtccatgac aaatcagggc ctcagaacta 960  
 agagg 965

<210> 418  
 <211> 967  
 <212> DNA  
 <213> Unknown (H38g267 nucleotide)

<220>  
 <223> Synthetic construct

<400> 418  
 tacacagagc cagagaatct cacaggtgtc ttagaattcc tgctcctggg actcccagat 60  
 gatccagaac tgcagcccgt cctcttttggg ctgttctctg ccatgtacct ggtcatgggtg 120  
 ctggggaacc tgctcatcat tctggccgtc agctctgact cccatctcca cagccccatg 180  
 tacttcttcc tctccaacct gtcttggct gacatcgggt ttgcctctac tactgtcccc 240  
 aagatgattg tggacatcca ggctcatagt agactcatct cttacgtggg ctgctgact 300  
 cagatgtctt ttttgatctt tttcgcattg atggaaagtc tgctcctgat tgtgatggcc 360



tatgaccggt	tcggtggccat	ctgtcacccc	ctgcactacc	aagtcacat	gagcccacga	420
ctctgtgggt	tcttagtttt	gggtgtcttt	tttcttagcc	ttttggactc	tcagctgcac	480
aatttgattg	tgttacaact	tacctgttc	aacgatgtgg	aaatctctaa	ttttttctg	540
tgacccttct	taacttctca	agctggcctg	ttctgacacc	tccattaata	acatgggtgt	600
atattttatt	ggtgccatat	ttggttttct	ccctctctta	gggatccctt	tctcttacta	660
taaaattggt	tcctccattc	tgagagtctt	ctcttcagg	gggaagtata	aagccttctc	720
cacctgcagc	tctcacctgt	cagttgtttg	cttactttat	ggaacagccc	ttggagggtg	780
cctcagttca	gctgtgtccc	tttctccag	gaagggtgca	gtggcctcag	taatgtacat	840
gggtgtcacc	cccatgtga	accccttcat	ctacagcctg	agaaacaggg	acattcaaag	900
tgccctgcag	aggctgcacg	gcagaataat	gtaatctctt	tatctgttgc	atcttttttg	960
tagtatt						967

&lt;210&gt; 419

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g268 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 419

atgagacaga	taaatcagac	acaagtgaca	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atttatcgta	ttattgggtg	tctacctggg	cactgtgctt	120
ggaaatctgc	ttctaattct	ccttggtcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgct	tctggctgac	ctctgtttct	ctaccaacat	agttcctcag	240
gcactagtcc	acctgctttc	cagaaagaag	gtcattgcat	tcacactttg	cgcagctcga	300
cttctctttt	tcctcatttt	tgggtgtacc	cagtgcgccc	ttcttgcagt	gatgtcctat	360
gatcgctatg	ttgcaatctg	caatcctctg	cgttaccctg	acatcatgac	ctggaaagtg	420
tgtgtccagc	tggcaacagg	atcatggacc	agtggcattc	tgggtgtctg	ggtagacacc	480
accttcacac	tgaggctacc	ctaccgaggc	agtaacagca	ttgctcattt	cttttgtgag	540
gcccctgcac	tattgatctt	agcatccaca	gacacccatg	catcagagat	ggccattttt	600
cttacggggg	ttgtgattct	cctcatacct	gtttttctga	ttctggatc	ctatggccgt	660
atcatagtaa	ctgtgggtcaa	gatgaagtca	actgtgggga	gtctcaaggc	attttctacc	720
tgtggctccc	acctcatggt	ggtcatactt	ttttatggat	cagcaattat	cacttacatg	780
acacccaagt	cttccaaaca	gcaggaaaaa	tcggtgtctg	ttttctatgc	aatagtgact	840
cccatgctga	atccctcat	ctatagcctg	agaaacaagg	atgtgaaggc	agctctgagg	900
aaagtagcca	caaggaattt	ccca				924

&lt;210&gt; 420

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g269 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 420

atgcccatac	ttatggctat	aggaaactgg	acagaaataa	gtgaatttat	cctcatgagc	60
ttctcttccc	tacctactga	aatacagtca	ttgctcttcc	tgacatttct	aactatctat	120
ttggttactc	tgaagggaaa	cagcctcatc	attctgggta	ccctagctga	cccatgcta	180
cacagcccca	tgtacttctt	cctcagaaac	ttatctttcc	tggagattgg	cttcaacctg	240
gtcaattgtc	ccaaaatgct	ggggaccctg	cttgcccagg	acacaacccat	ctccttctct	300
ggctgtgcca	ctcagatgta	tttcttcttc	ttcttggggg	tagctgaatg	cttctcctg	360
gctaccatgg	catatgaccg	ctatgtggcc	atctgcagtc	ccttgcaact	cccagtcac	420
atgaacaaaa	ggacacgggc	caaactggct	gctgtcttct	gggtcccagg	ctttcctgta	480
gctactgtgc	agaccacatg	gctcttcagt	ttccattctt	gtggcaccaa	caagggtgaac	540
cacttcttct	gtgacagccc	gcctgtgctg	aagctggctt	gtgcagacac	agcactgttt	600
gagatctacg	ccatcgctcg	aaccattctg	gtggctcatg	tcccctgctt	gctgatcttg	660
tgttcctata	ctcgcattgc	tgtgtctatc	ctcaagatcc	catcagctaa	agggaagcat	720
aaagccttct	ctacgtgctc	ctcacacctc	cttggtgtct	ctcttttcta	tatatcttct	780
agcctcacct	acttctggcc	taaatcaaat	aattctcctg	agagcaagaa	gttggttatca	840

ttatcctaca ctgttgtagac tcccatgttg aaccccatata tctacagctt gagaaatagc 900  
gaggtgaaga atgccctcag caggaccttc cacaaggctc tagccctcag aaac 954

<210> 421

<211> 780

<212> DNA

<213> Unknown (H38g270 nucleotide)

<220>

<223> Synthetic construct

<400> 421

gcccaccttt ccttcctgga cctcagtttc accaccagct ccatccccc a gctgctctac 60  
aaccttaatg gatgtgacaa gaccatcagc tacatgggct gtgccatcca gctcttcttg 120  
ttcctggggtc tgggtgggtgt ggagtgcttg cttctgggctg tcatggccta tgaccggtgt 180  
gtggctatct gcaagccctt gcactacatg gtgatcatga accccagggt ctgccggggc 240  
ttgggtgtag tgacctggag ctgtgggggtg gccaaactct tggccatgtc tcctgtgacc 300  
ctgcgcttac ccgctgtgtg gcaccacgag gtggaccact tcctgcgtga gatgcccgcc 360  
ctgatccgga tggcctgcgt cagcactgtg gccatcgaag gcaccgtctt tgtcctggcg 420  
gtgggtgttg tgcgttcccc cttgtgtgtt atcctgtctt cttacagcta cattgtgagg 480  
gctgtgttac aaattcgggtc agcatcagga aggagaagg ccttcggcac ctgcggctcc 540  
catctcactg tggctcccc tttctatgga aacatcatct acatgtacat gcagccagga 600  
gccagttctt cccaggacca gggcatgttc ctcagtctct tctacaacat tgtcaccccc 660  
ctcctcaatc ctctcatcta caccctcaga aacagagagg tgaagggggc actgggaagg 720  
ttgcttcttg ggaagagaga gctaggaaag gagtaaaggc atctccacct gacttcactt 780

<210> 422

<211> 985

<212> DNA

<213> Unknown (H38g271 nucleotide)

<220>

<223> Synthetic construct

<400> 422

gaagagatat tatgaataat atcccagcat gtacacacag ggtgtgtaca gattaagaac 60  
tgcagcccat cctctttggg ctgttctctgt ccatgtgcct ggtcatgggt ctggggaacc 120  
ttctcatcat cctggccgtc agctctgact cccacctcca caccgccag tactttttcc 180  
tctccaacct gtccttggtt gacatcgggt tccccccac cactgtcccc aagatgattg 240  
tggacatcca gtctcacagc agagtcatct cctatgcggg ctgcctgact cagatatctc 300  
tttttctgtt ttttggatgc atggaagaca tgcttctgag tgtgatggct tatgaccggt 360  
ttgtggccat ctgtcaccct ctggattatc cagtcatcat gaaccatgt ttctgtgggt 420  
tcttggtttt gttgtctttt ttttctcagt ctttttagact tccagctgca caattggatt 480  
gccttacaaa ttacctgctt caaggatgtg gaaattccca gtttcttctg tgaccttctt 540  
caactcccc accttgctgt ttgtgacacc ttcaccaaca acatagtcac gtatttctct 600  
gctgccatac ttggttttct tcccatctcg gggatctttt ctcttactat aaaattgttt 660  
cctccattct gaaggtttca tcatcagggt ggaagtataa agccttctcc acctgtgggt 720  
ctcacctgtc agttgtttgc ttattttatg gaacagccct tggagggtac ctcagttcag 780  
acatgtcctc ttatcccaga aaggggtcag tggcttcagt gatgtacaca gtggctcgccc 840  
ccatgctgaa ccggttcacg tacagcctga gaaaaaggga cattaaaagt gccctgcagc 900  
agctgcatgg cagaatagtc taatctcatg atcttattat cggttccatt ctttagcatg 960  
ggttggaataa ggcagcaagg tcaaaa 985

<210> 423

<211> 963

<212> DNA

<213> Unknown (H38g272 nucleotide)

<220>

<223> Synthetic construct

&lt;400&gt; 423

atggaatctc	ctaatacacac	tgatgttgac	ccttctgtct	tcttcctcct	gggcatccca	60
ggtctggaac	aatttcattt	gtggctctca	ctccctgtgt	gtggcttagg	cacagccaca	120
attgtgggca	atataactat	tctggttggt	gttgccactg	aaccagtctt	gcacaagcct	180
gtgtaccctt	ttctgtgcat	gctctcaacc	atcgacttgg	ctgcctctgt	ctccacagtt	240
cccaagctac	tggctatctt	ctggtgtgga	gccggacata	tatctgcctc	tgcttgcttg	300
gcacagatgt	tcttcattca	tgccttctgc	atgatggagt	ccactgtgct	actggccatg	360
gcctttgatc	gctacgtggc	catctgccac	ccactccgct	atgccacaat	cctcactgac	420
accatcattg	cccacatagg	ggtggcagct	gtagtgcgag	gctccctgct	catgctccca	480
tgtcccttcc	ttattgggcg	tttgaacttc	tgccaaagcc	atgtgatcct	acacacgtac	540
tgtgagcaca	tggctgtggt	gaagctggcc	tgtggagaca	ccaggcctaa	ccgtgtgtat	600
gggctgacag	ctgcactggt	ggtcattggg	gttgacttgt	tttgacttgg	tctctcttat	660
gccctaagtg	cacaagctgt	ccttcgcctc	tcateccatg	aagctcggtc	caaggcccta	720
gggacctgtg	gttcccatgt	ctgtgtcatc	ctcatctctt	atacaccagc	cctcttctcc	780
ttttttacac	accgcttttg	ccatcacgtt	ccagtccata	ttcacattct	tttggccaat	840
gtttatctgc	ttttgccacc	tgctcttaat	cctgtggtat	atggaggtta	gaccaaacag	900
atccgtaaaa	gagttgtcag	ggtgtttcaa	agtgggcagg	gaatgggcat	caaggcatct	960
gag						963

&lt;210&gt; 424

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g273 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 424

atgacatgga	gtggcggaac	catagtggga	gagtgagtga	gtttgtgttg	ctggggcttc	60
cctgtcctcg	cgccactaca	ggtactattg	tttgcccttt	tgtgtctggc	ctatgtgttg	120
gtgctgactg	agaacacact	catcattatg	gcaattagga	accattccac	cctccacaaa	180
cccatgtact	tttttctagc	taatatgtcc	tttctggaga	tctggtatgt	actgtcact	240
attcccaaga	tgcttgctgg	ctttgttgga	tccaaacagg	atcatggaca	gctaattctc	300
tttgagggat	gcatgacaca	gctctacttt	ttccttggct	tgggctgcac	tgagtgtgtc	360
cttctcgctg	ttatggccta	tgatcgctat	atggccatct	gctatcctct	ccactaccca	420
gtcattgtca	gtggccggct	gtgtgtgcag	atggctgctg	gctcttgggc	tggagggttt	480
ggcatctcca	tgggtcaaagt	ttttcttatt	tctggcctct	cttactgtgg	ccccaacatc	540
atcaaccact	ttttctgtga	tgtctctcca	ttgtcgaacc	tctcatgcac	tgatatgtcc	600
acagcagagc	ttacagattt	catcctggcc	atttttatct	ttctagggcc	actctctgtc	660
actggggcct	cctatgtggc	cattactggt	gctgtgatgc	acataccttc	ggctgctgga	720
cgctataagg	ccttttccac	ctgtgcctct	catctcactg	ttgtgataat	cttctatgca	780
gccagtatct	tcatctatgc	tgggccaag	gcaactctcag	cttttgacac	caacaagttg	840
gtctctgtac	tgtatgctgt	cattgtacca	ttgtcgaatc	ccatcattta	ctgcctgcgc	900
aatcaagagg	tcaagagagc	cctatgctgt	actctgcacc	ctgtaccagc	accaggatcc	960
tgaccccaag	aaagctagca	ga				982

&lt;210&gt; 425

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g274 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 425

atggaagcag	gaaaccaaac	aggattttta	gagtttatcc	ttctcggact	ctctgaggat	60
ccagaactac	agccgttcat	atthgggctg	ttcctgtcca	tgtacctggt	gacgggtgctg	120
ggaaacctgc	tcatcatcct	ggccatcagc	tctgactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ctggggttgac	atctgtttca	gcacttgcat	cgtccccaag	240
atgctggtga	acatccagac	cgagaacaaa	gccatctcct	acatggactg	cctcacacag	300
gtctattttc	ccatgttttt	tcctattctg	gacacgctac	tcctgaccgt	gatggcctat	360

gaccggtttg	tggtgtctg	ccaccctctg	cactatatga	tcacatgaa	ccccacctc	420
tgtggcctcc	tggtttttgt	cacctggctc	attgggtgca	tgacatccct	cctccatatt	480
tctctgatga	tgcatcta	cttctgtaaa	gattttgaaa	ttccacattt	tttctgcgaa	540
ctgacgtaca	tcctccagct	ggcctgtctc	gataccttcc	tgaacagcac	gttgatatac	600
tttatgacgg	gtgtgctggg	cgtttttccc	ctccttggga	tcattttctc	ttattcacga	660
attgcttcat	ccataaggaa	gatgtcctca	tctgggggaa	aacaaaaagc	actttccacc	720
tgtgggtctc	acctctccgt	cgtttcttta	ttttatggga	caggcattgg	ggtccacttc	780
acttctgcgg	tgactcactc	ttcccagaaa	atctccgtgg	cctcggtgat	gtacactgtg	840
gtcacccecca	tggtgaacct	cttcatctac	agcctgagga	acaaggatgt	gaagggagcc	900
ctggggagtc	tcctcagcag	ggcagcctct	tgtttg			936

&lt;210&gt; 426

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g275 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 426

atgactgctt	gcaatgcctc	acagggccac	ccttctttct	tcattctcca	aggaattcct	60
ggcatggagg	acaaacacag	atggatatct	atccccctct	cctccatgta	tttcattatg	120
gtgcttggga	actgcacat	cctcctcacc	atctccacag	agcgtccct	gcacaaacct	180
atgttctctg	tcctctgtct	gttggccctc	acagacctgg	gcatgtctac	aaccaccatt	240
cccaagggtg	tgtgcatttt	ctggtttggc	cagagtga	tcagctatga	aggatgcctg	300
gttcagctgt	tcctcatcca	ctccatctct	gccatgcagt	cagctgtcct	gatgaccatg	360
gcctttgacc	actatgtggc	catctgcaag	cccttgcgct	atgccaccat	cctttccaat	420
agttgcactg	gactcattgg	cttagtgagt	ttggtgagag	ctatcctctt	tattctcccc	480
atgcccattc	tccttcagca	aatgccctat	catgccaatc	gtgtcatccc	caccacctcc	540
tgtgagcaca	tggtctgtgt	gaagatgggt	tgtgtagata	ctacagtcaa	caggatatat	600
ggcctggttg	tggtctgtgt	gggtgtgtgc	tagatctctc	agctattgct	tcattcttatg	660
tgctaatacat	ccaggctata	atgcatctct	cttctaagga	agcccaccac	aaagcagtc	720
acacctgcac	cacacacatc	tgtgtcatgc	ttatttctta	tactccctca	cttttctctt	780
ttctcgctca	ccgctttggc	caaggcattc	caccctatgt	ccacatcatt	cttggcaacc	840
tttacttctc	tgtacctcca	atgctcagtc	ctataattta	tggagtga	actaaggagt	900
tctgggacaa	agtgacaaaa	tagggttgct	ggaaagaaga	accacaacc	actgaccatg	960

&lt;210&gt; 427

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g276 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 427

atggagctct	ggaacttcac	cttgggaagt	ggcttcattt	tggtggggat	tctgaatgac	60
agtgggtctc	ctgaactgct	ctgtgtctaca	attacaatcc	tatacttggt	ggccctgac	120
agcaatggcc	tactgtctct	ggctatcacc	atggaagccc	ggctccacat	gcccattgtac	180
ctcctgcttg	ggcagctctc	tctcatggac	ctcctgttca	catctgttgt	cactcccaag	240
gcccttgagg	actttctgcg	cagagaaaac	accatctcct	ttggaggctg	tgcccttcag	300
atgttctctg	cactgacaat	gggtgggtgct	gaggacctcc	tactggcctt	catggcctat	360
gacaggatg	tggtcatttg	tcattcctctg	acatacatga	ccctcatgag	ctcaagagcc	420
tgtgtgctca	tggtggccac	gtcctggatc	ctggcatccc	taagtgcctt	aatatatacc	480
gtgtatacca	tgactatcc	cttctgcagg	gcccaggaga	tcaggcatct	tctctgtgag	540
atcccacact	tgtgaaggt	ggcctgtgct	gatacctcca	gatatgagct	catggtatat	600
gtgatgggtg	tgaccttctc	gattccctct	cttctgtgta	tactggcctc	ctatacacia	660
attctactca	ctgtgtctca	tatgccatca	aatgagggga	ggaagaaagc	ccttgtcacc	720
tgctcttccc	acctgactgt	gggtgggatg	ttctatggag	ctgccacatt	catgtatgtc	780
ttgccagtt	ccttccacag	caccagacaa	gacaacatca	tctctgtttt	ctacacaatt	840
gtcactccag	ccctgaatcc	actcatctac	agcctgagga	ataaggaggt	catgctgggac	900

ttgaggaggg tcctgggaaa atacatgctg ccagcacact ccacgctc

948

<210> 428

<211> 936

<212> DNA

<213> Unknown (H38g277 nucleotide)

<220>

<223> Synthetic construct

<400> 428

atgaaagcag gaaacttctc agacactcca gaattctttc tcttgggatt gtcaggggat	60
ccggagctgc agcccatcct cttcatgctg ttcctgtcca tgtacctggc cacaatgctg	120
gggaacctgc tcatcatcct ggccgtcaac tctgactccc acctccacac ccccatgtac	180
ttcctcctct ctatcctgtc cttggctgac atctgtttca cctccaccac gatgccaag	240
atgctgggtga acatccaggc acaggctcaa tccatcaatt acacaggctg cctcacccaa	300
atctgctttg tcctgggtttt tgttggattg gaaaatggaa ttctgggtcat gatggcctat	360
gatcgatttg tggccatctg tcacccactg aggtacaatg tcatcatgaa ccccaaactc	420
tgtgggctgc tgccttctgt gtccttcacg gttagtgtcc tggatgctct gctgcacacg	480
ttgatgggtgc tacagctgac cttctgcata gacctggaaa ttccccactt tttctgtgaa	540
ctagctcata ttctcaagct cgctgttctc gatgtcctca tcaataacat cctgggtgat	600
ttggtgacca gcctgttagg tgttgttctc ctctctggga tcattttctc ttacacacga	660
attgtctcct ctgtcatgaa aattccatca gctgggtggaa agtataaagc tttttccatc	720
tgcgggtcac atttaatcgt cgtttccttg ttttatggaa cagggttttg ggtgtacctt	780
agttctgggg ctacccactc ctccaggaag ggtgcaatag catcagtgat gtataccgtg	840
gtcaccacca tgctgaacct actcatttac agcctgagaa acaaggacat gttgaaggct	900
ttgaggaaac taatatctag gataccatct ttccat	936

<210> 429

<211> 984

<212> DNA

<213> Unknown (H38g278 nucleotide)

<220>

<223> Synthetic construct

<400> 429

aaaatctcca atagctccaa attccaggtc tctgagttca tcctgctggg attccccggc	60
attcacagct ggcaacactg gctatctctg cccctggcac tactgtatct ctcagcactt	120
gctgcaaaaca cctcatcct catcatcatc tggcagaacc cttctttaca gcagcccatg	180
tatattttcc ttggcatcct ctgtatggta gacatgggtc tggccactac tatcatcct	240
aagatcctgg ccattctctg gtttgatgcc aagggtatta gcctccctga gtgctttgct	300
cagatttatg ccattcactt ctttgtgggc atggagtctg gtatcctact ctgcatggct	360
tttgatagat atgtggctat ttgtcaccct cttcgctatc catcaattgt caccagttcc	420
ttaatcttaa aagctaccct gttcatgggt ctgagaaatg gcttatttgt cactccagt	480
cctgtgcttg cagcacagcg tgattattgc tccaagaatg aaattgaaca ctgcctgtgc	540
tctaaccctg gggtcacaag cctggcttgt gatgacagga ggccaaacag catttgccag	600
ttggttcttg catggcttg aatggggagt gatctaagtc ttattatact gtcatatatt	660
ttgattctgt actctgtact tagactgaac tcagctgaag ctgcagccaa ggccctgagc	720
acttgtagtt cacatctcac cctcatcctt ttcttttaca ctattgttgt agtgatttca	780
gtgactcatc tgacagagat gaaggctact ttgattccag ttctacttaa tgtgttgac	840
aacatcatcc ccccttcct caaccctaca gtttatgcac ttcagaccaa agaacttagg	900
gcagccttcc aaaagggtgct gtttgccctt acaaaagaaa taagatctta gagaccttct	960
ccatgatgta catgaacctc agct	984

<210> 430

<211> 947

<212> DNA

<213> Unknown (H38g279 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 430

atggagctcc	ggaactccac	cttgggaagc	ggcttcatct	tgggtgggat	tctgaatgac	60
agtgggtctc	ctgaactgct	ctatgctaca	tttacaatcc	tatacatgtt	ggcactgacc	120
agcaatggtc	tgtctgctct	ggccatcacc	atagaagccc	ggctccacat	gcccattgtac	180
ctcctgcttg	ggcagctctc	tctcatggac	ctcctgttca	catctgttgt	cactcccaag	240
gccttgcgga	ctttctgcgc	agagaaaaca	ctatctcctt	tggaggctgt	gcacttcaga	300
tgttcctggc	actgacaatg	ggtagcgctg	aggacctcct	actggccttc	atggcctatg	360
acaggatatg	ggccatttgt	cctcctctga	aatacatgac	cctcatgagc	ccaagagtct	420
gctggatcat	ggtggccaca	tcctggatcc	tggcatccct	gattgctata	ggacatacca	480
tgtacactat	gcacctccct	ttctgtgtgt	cctgggaaat	caggcatctg	ctctgtgaga	540
tcccaccctt	gctgaagttg	gcctgtgctg	atacctccag	gtatgagctt	ataatatacg	600
tgacaggtgt	gactttcctc	ttgctcccca	tttctgccat	tgtggcctcc	tacacactag	660
tcctattcac	tgtgcttcgt	atgccatcaa	atgaggggag	gaagaaagcc	cttgtcacct	720
gctcttccca	cctgattgtg	gtcgggatgt	tctatggagc	tgccacattc	atgtatgtct	780
tgcccagttc	cttccacagc	cccaaacaag	acaacatcat	ctctgttttc	tacacaattg	840
tcactccagc	cctgaatcca	ctcatctaca	gcctgaggaa	taaggaggtc	atgcgggcct	900
tgaggagggt	cctgggaaaa	tacatactgc	tggcacattc	cacgctc		947

&lt;210&gt; 431

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g280 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 431

atgggattcc	ctggcattca	cagttggcag	cactggctct	ccctgcccct	ggctctgctc	60
tacctcttag	ctctcagtgc	caacatcctt	atcctgatca	tcatacaaaa	agaggcagca	120
ctgcaccagc	ctatgtacta	tttctggggc	atcttggcta	tggcagacat	aggcctggct	180
accaccatca	tgctaagat	tttggccatc	ttatggttca	atgctaagac	catcagtctc	240
ctggagtgtc	ttgctcagat	gtatgccata	cattgctttg	tggccatgga	atcaagtacc	300
tttgtctgca	tggctattga	tagatatgta	gccatttgct	gaccgctacg	atatccatca	360
atcatcactg	aatcttttgt	tttcaaagca	aatgggttca	tggcactgag	aaacagcctg	420
tgtctcatct	cagtgcctct	gttggctgcc	cagaggcatt	actgctccca	gaatcaaatt	480
gagcactgtc	tttgttctaa	ccttggagtc	actagcctat	cttgtgatga	tcgaagaatc	540
aatagcatta	accaggctct	tttggcttgg	acactcatgg	gaagtgcact	gggtttgatt	600
attttatcat	atgctctaat	actttactct	gtcctgaagc	tgaactctcc	agaagctgca	660
tccaaggcct	taagtacctg	cacctcccac	ctcatcttaa	tccttttctt	ctacacagtc	720
atcattgtga	tttccattac	tcgtagtaca	ggaatgagag	ttccccctat	tccagttcta	780
cttaatgtgc	tacacaatgt	cattccccct	gcctgaacc	ccatgggtata	tgcactcaag	840
aacaaggaac	tcaggcaagg	cttataacaag	gtacttagac	tgggagtga	gggcacc	897

&lt;210&gt; 432

&lt;211&gt; 980

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g281 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 432

atgacatgga	gtggcggaac	cctagtggga	gagtgagtga	gtttgtgttg	ctgggcttcc	60
cggctcctgc	gccactacag	gtactatcgt	ttgcccgtta	gtccgcggcc	tatgcgttgg	120
tgttgactga	gaacacactc	atcattatgg	caagtaggaa	ccattccacc	ctccacaaac	180
ccatgtactt	tgttctagct	aatatgtcct	cctctggaga	tctggtatgt	cactgtcact	240
attcccaaga	tgcttgctgg	ctttgttggg	tccaaacagg	atcatggaca	gctaactctc	300
tttgagggat	gcatgacaca	gctctacttt	ttccttggct	tgggctgcac	tgagtgtgtc	360
cttctcgctg	ttatggccta	tgatcgctat	atggccatct	gctatcctct	ccactaccca	420

gtcattgtca	gtggccggct	gtgtgtgcag	atggctgctg	gctcttgggc	tggaggtttt	480
ggcatctcca	tggtcaaagt	ttttcttatt	tctggcctct	cttactgtgg	ccccaacatc	540
atcaaccact	ttttctgtga	tgtctctcca	ttgtctcaacc	tctcatgcac	tgatatgtcc	600
acagcagagc	ttacagattt	catcctggcc	atTTTTattc	ttctagggcc	actctctgtc	660
actggggcct	cctatgtggc	cattactggg	gctgtgatgc	acacttcttc	ggctgtgga	720
cgctataagg	ccttttccac	ctgtgcctct	catctcactg	ttgtgataat	cttctatgca	780
gccagtatct	tcatctatgc	tcgccaaagg	cactctcagc	ttttgacacc	aacaagttgg	840
tctctgtact	gtatgctgtc	attgtaccat	tgtctaatcc	catcatttac	tgccctgcga	900
atcaagaggt	caagagagcc	ctatgctgta	ctctgcacct	gtaccagcac	caggatcctg	960
acccaagaa	agctagcaga					980

&lt;210&gt; 433

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g282 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 433

atggatggag	agaatcactc	agtggatatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	tcagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tcacgtcat	tgggtgtgtg	gagatgggtg	tgtcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccccctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttgttgcag	tcactccctg	ttccaactgg	480
catttcttgt	taatttacc	ttctgtggcc	ctaattgtgt	ggacagcttc	tactgtgacc	540
ttcctcagct	tctcagacta	gcctgtaccg	acacctacag	attgcagttc	atggtcactg	600
ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tctaactccc	tacgtcttca	660
tcctgtttac	gttttgaaa	cattcctcag	gtggttcac	caaggccctt	tccactcttt	720
cagctcacag	cacagcggtc	cttttgttct	ttggtccacc	catgtttgtg	tatacatggc	780
cacaccctaa	ttcacagatg	gacaagtttc	tggctatttt	tgatgcagtt	ctcactcctt	840
ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaacatga	tatggcttta	tgtttctttc	tttgatat			998

&lt;210&gt; 434

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g283 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 434

atgctgctgg	gcaacctggc	catcatcagc	ttcatttgcc	ttgattcccg	ccttcactca	60
cccatgtact	tcttcctctg	caacttctcc	ctcatggaga	tgggtggcac	ctccactgtg	120
gtacatagga	tgctggcaga	cctgctatcc	actcacaaga	ccatgtccct	ggccaaatgc	180
ctaaccacgt	cttctcttta	cttctccctg	ggctctgcca	acttccctgat	actcatggtc	240
atggcctttg	atcgctacgt	ggcatctgc	cacccccctg	gctacccaac	catcacgaat	300
ggtccagtgt	gtgtgaagct	ggtggtggcc	tgttgggtgg	ttggtttcct	ctccattgtc	360
tctcccacac	tgcaaaaaac	acgactctgg	ttctgtggcc	ctaacatcat	cggccactac	420
ttctgtgact	ctgccccgct	gctcaagctt	gcctgctctg	acaccgcca	cattgagcgc	480
atggacctct	tctgtccct	gctctttgtg	ctgaccacca	tgctgcttat	catcctctcc	540
tacatcctca	ttgtggctgc	agtgtgcac	atcccttcc	cctctggatg	ccagaaggcc	600
ttctccacct	gtgcctctca	cctcacagt	gtggttctgg	gctatggcag	tgccatcttc	660
atctacgtga	ggccaggcaa	ggccactcc	acatacctca	acaaggcggg	ggccatgggtg	720
actgcaatgg	taacccttt	cctcaacccc	ttcatcttca	ccttccggaa	tgagaagggtc	780
aaggagggtca	ttgaggatgt	gactaaaagg	atcttccctg	gagaccacgc	agcctgtagg	840

<210> 435  
 <211> 939  
 <212> DNA  
 <213> Unknown (H38g284 nucleotide)

<220>  
 <223> Synthetic construct

<400> 435  
 atggaaactg caaattacac caagggtgaca gaatttggtc tcaactggcct atcccagact 60  
 ccagagggtcc aactagtcct atttggtata tttctatcct tctatttggt catcctacca 120  
 ggaaatatcc ttatcatttg caccatcagt ctagaccctc atctgacctc tcctatgtat 180  
 ttccctgttg ctaatctggc ctcccttgat atttggtact ctccattac agcccctgaa 240  
 atgctcatag acttcttctt ggagaggaag ataatttctt ttgatggatg cattgcacag 300  
 ctcttcttct tacactttgc tggggcttcg gagatgttct tgctcacagt gatggccttt 360  
 gacctctaca ctgctatctg ccgacccctc cactatgcta ccatcatgaa tcaacgtctc 420  
 tgctgtatcc tgggtggctct ctccctggagg gggggcttca ttcattctat catacagggtg 480  
 gctctcattg ttgcacttcc tttctgtggg cccaatgagt tagacagtta cttctgtgac 540  
 atcacacagg ttgtccggat tgcctgtgcc aacaccttcc cagaggagtt agtgatgatc 600  
 tgtagtagtg gtctgatctc tgtgggtgtg ttgattgtct tgtaaatgtc ctatgccttc 660  
 cttctggcct tgttcaagaa actttcaggc tcagggtgaga ataccaacag ggccatgtcc 720  
 acctgctatt cccacattac cattgtgggtg ctaatgtttg ggccatccat ctacatttat 780  
 gctcgcccat ttgactcgtt tccctagat aaagtgggtg ctgtgttcaa tactttaata 840  
 ttccctttac gtaatcccat tatttacaca ttgagaaaca aggaagtaaa ggcagccatg 900  
 aggaagtgtg tcaccaaata tattttgtgt aaagagaag 939

<210> 436  
 <211> 640  
 <212> DNA  
 <213> Unknown (H38g285 nucleotide)

<220>  
 <223> Synthetic construct

<400> 436  
 tgcttgttgt aactgtacca ggtatgacct ctcaccagag acccgatctt gcaagacctc 60  
 cattaanaagc ctgctatcta ttgttctcct tgtctctgag tctattcttt gggtttggac 120  
 aggtgagtggt gtttctcaca atgacacaga gtgtactgtg aatgagcctg tttgcttcat 180  
 gttctcctag atgcccttct gcctcagcta gatcttgccc tagacctact atgagcaagt 240  
 ggtcatgctg aatctgggtat gtgcagacat cacatatata gtccatacct gtggctctct 300  
 atggcctttt ctgtggatgg atttgatata tttggcatta ttatccacag atatcagaca 360  
 ttgcaggctg tactgtagct acctgcaaaa gaatctgtgc ccaaagtatt tagcatatat 420  
 gccttcacata tttgcgtcac cctgtacctg ctcatgatag gattctactc cttttttct 480  
 tgttgcttta gctaccatac actcacagtg attcccatct ccttgctcat ccttttactc 540  
 attagtgcct tccatgttca ataccatcac ctgtggggta aagagtaagc atatccaaga 600  
 aaacatggta cagagatttt gtgggaaaat ttcctgccat 640

<210> 437  
 <211> 989  
 <212> DNA  
 <213> Unknown (H38g286 nucleotide)

<220>  
 <223> Synthetic construct

<400> 437  
 atgtgtctct tgaccttgca ggtcactggc ccaatgaatg tctctgagcc aaattccagc 60  
 tttgcttttag taaatgaatt tatactccaa gatttatctt ttgagtggac aattcagatc 120  
 ttccctcttct cactcttcac tacaacatat gcactgacca taacaggaaa cggagccatt 180  
 gcttgccccc tgtgggtgtg ccggcgacgt cacactccca tgtacatgtt cctgggaaat 240



ttctcctttt	tagagatatg	gatatgtctt	tctacagttc	ccaagatggt	gggtcaacttc	300
ctttcagaga	aaaaaaccat	ctcctttgct	ggatgttttc	tccaatttta	tttcttcttc	360
tctttgggta	catctgaatg	cttgattttg	actgtgatgg	cctttgatca	gtaccttggt	420
atctgccatc	ccttgcaact	tcctaataaa	tcatgactgg	gcattctctg	gccaaaactgg	480
tcatactgtg	ctgggtttgt	ggattttctg	gtttcctgat	ccccactggt	ctcatctctc	540
agatgccctt	ctgtgggtcca	aacattaatg	accatgttgt	gtgtgaccca	ggggcactat	600
ttgcattggc	ttgtgtctct	gccccagaa	tccaactggt	ttgttacct	ctaagctcat	660
tagttatttt	tggtaacttc	ctctttatta	ttggatccta	tactcttggt	ctgaaagctg	720
tgttgggtat	gccttcgagc	actgggaaac	ataaagcctt	ctctacctgt	gggtctcatt	780
tggctgtggt	atcactgttc	tatggctctc	ttatgggtcat	gtgtgtgagt	ccaggacttg	840
gacactctat	ggggatgcag	aaaatcaaaa	ctttgttcta	tgctatgggt	acccactctc	900
tcaatcccct	tatctatagc	ctccagaata	aggagataaa	ggcagccctg	aggaaagttc	960
tggggagttc	caacataatc	taagccata				989

&lt;210&gt; 438

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g287 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 438

atgatggaca	accactctag	tgccactgaa	ttccaccttc	taggcttccc	tgggtcccaa	60
ggactacacc	acattctttt	tgctatatct	ttttcttctt	atttagtgac	attaatggga	120
aacacgggtc	tcattgtgat	tgtctgtgtg	gataaacgtc	tgcagtcccc	catgtatttc	180
ttcctcagcc	acctctctac	cctggagatc	ctgggtcaca	ccataattgt	ccccatgatg	240
ctttggggat	tgctcttcct	gggatgcaga	cagtatcttt	ctctacatgt	atcgctcaac	300
ttttcctgtg	ggaccatgga	gtttgcatta	cttggagtga	tggctgtgga	ccgttatgtg	360
gctgtgtgta	accctttgag	gtacaacatc	attatgaaca	gcagtacctg	tatttgggtg	420
gtaatatgtg	catgggtgtt	tggatttctt	tctgaaatct	ggcccatcta	tgccacattt	480
cagtttacct	tcgcgaaatc	aaattcatta	gaccattttt	actgtgaccg	agggcaattg	540
ctcaaactgt	cctgcgataa	cactcttctc	acagagttta	tccttttctt	aatggctgtt	600
tttattctca	ttggttcttt	gatccctacg	attgtctcct	acacctacat	tatctccacc	660
atcctcaaga	tcctgcgcag	ctctggcccg	aggaaagcct	tctccacttt	tgccctccac	720
ttcacctgtg	ttgtgattgg	ctatggcagc	tgcttgtttc	tctacgtgaa	acccaagcaa	780
acacagggag	ttgagtacaa	taagatagtt	tcctgtgttg	tttctgtgtt	aaccccttc	840
ctgaatcctt	tcctctttac	tcttcggaat	gacaaagtca	aagaggccct	ccgagatggg	900
atgaaacgct	gctgtcaact	cctgaaagat				930

&lt;210&gt; 439

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g288 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 439

atgtccaaca	caaattggcag	tgcaatcaca	gaattcattt	tacttgggct	cacagattgc	60
ccggaactcc	agtctctgct	ttttgtgctg	tttctgggtg	tttacctcgt	cacctgcta	120
ggcaacctgg	gcatgataat	gttaatgaga	ctggactctc	gccttcacac	gccccatgtac	180
ttcttctctc	ctaacttagc	ctttgtggat	ttgtgctata	catcaaattg	aaccccgag	240
atgtcgacta	atatcgatc	tgagaagacc	atttcctttg	ctgggtgtgt	tacacagtgc	300
tacattttca	ttgcccttct	actcactgag	ttttacatgc	tggcagcaat	ggcctatgac	360
cgctatgtgg	ccatatatga	ccctctgcgc	tacagtgtga	aaacgtccag	gagagtgtgc	420
atctgcttgg	ccacatttcc	ctatgtctat	ggcttctcag	atggactctt	ccaggccatc	480
ctgaccttcc	gcctgacctc	ctgtagatcc	agtgtcatca	accacttcta	ctgtgctgac	540
ccgccgctca	ttagcttttc	ttgttctgat	acttatgtca	aagagcatgc	catgttcata	600
tctgtctggc	tcaacctctc	cagctccctc	accatcgctc	tgggtgtccta	tgcttctatt	660
cttgcgtcca	tcctccggat	caaatcagca	gaggaagggc	acaaggcatt	ctccacctgt	720

ggttcccata	tgatggctgt	caccctgttt	tatgggactc	tcttttgcac	gtatataaga	780
ccaccaacag	ataagactgt	tgaggaatct	aaaataatag	ctgtctttta	cacctttgtg	840
agtccgggtac	ttaatccatt	gatctacagt	ctgaggaata	aagatgtgaa	gcaggccttg	900
aagaatgtcc	tgaga					915

&lt;210&gt; 440

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g289 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 440

atggcaaatc	tgagccagcc	ctccgaattt	gtcctcttgg	gcttctcctc	ctttggtgag	60
ctgcaggccc	ttctgtatgg	ccccttcctc	atgctttatc	ttctcgccct	catgggaaac	120
accatcatca	tagttatggt	catagctgac	accacacctac	atacaccat	gtacttcttc	180
ctgggcaatt	ttccctgct	ggagatcttg	gtaaccatga	ctgcagtgcc	caggatgctc	240
tcagacctgt	tggtcccca	caaagtcatt	accttactg	gctgcatggg	ccagttctac	300
ttccactttt	ccctggggtc	cacctccttc	ctcctcctga	cagacatggc	ccttgatcgc	360
tttgtggcca	tctgccaccc	actgcgctat	ggcactctga	tgagccgggc	tatgtgtgtc	420
cagctggctg	gggctgcctg	ggcagctcct	ttcctagcca	tggtaccac	tgctcctcctc	480
cgagctcatc	ttgattactg	ccatggcgac	gtcatcaacc	acttcttctg	tgacaatgaa	540
cctctcctgc	agttgtcatg	ctctgacact	cgctgttgg	aattctggga	ctttctgatg	600
gccttgacct	ttgtcctcag	ctccttcctg	gtgacctca	tctcctatgg	ctacatagtg	660
accactgtgc	tgcggtcccc	ctctgccagc	agctgccaga	aggctttctc	cacttgccggg	720
tctcacctca	cactggtctt	catcggtac	agtagtacca	tctttctgta	tgtaggcct	780
ggcaaagctc	actctgtgca	agtcaggaag	gtcgtggcct	tggtgacttc	agttctcacc	840
ccctttctca	atccctttat	ccttaccttc	tgcaatcaga	cagttaaaac	agtgctacag	900
gggcagatgc	agaggctgaa	aggcctttgc	aaggcacaa			939

&lt;210&gt; 441

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g290 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 441

atgaagatag	caaacaacac	agtagtgaca	gaatttatcc	tccttgggtc	gactcagtct	60
caagatatcc	agctcttggg	ctttgtgctg	atcttaattt	tctaccttat	catcctccct	120
ggaaattttc	tcattatattt	caccataagg	tcagaccctg	ggctcacagc	ccccctctat	180
ttattttctg	gcaacttggc	cttcctggat	gcctcctact	ccttcattgt	ggctcccagg	240
atgttgggtg	acttcctctc	tgagaagaag	gtaactcctc	acagaggctg	catcactcag	300
ctctttttct	tgactttcct	tgaggagggg	gagggtatcc	tccttgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggcctctg	cactgttcaa	ctgtcatgaa	ccctagagcc	420
tgctatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatcc	tcgcttgcc	tttttggggc	ccaaaccagc	tggaacaact	cttctgtgat	540
gtccgacagg	tcacaaagct	ggcttgacac	gacatgtttg	tggtggagct	tctgatgggc	600
ttcaacagtg	gcctgatgac	actcctgtgc	tttctggggc	ttctggcttc	ctatgcagtc	660
atcctctgcc	atgttcgtag	ggcagcttct	gaagggaaga	acaaggccat	gtccacgtgc	720
accactcgtg	tcattattat	acttcttatg	tttggacctg	ctatcttcat	ctacatgtgc	780
cctttcaggg	ccttaccagc	tgacaagatg	gtttctctct	ttcacacagt	gatctttcca	840
ttgatgaatc	ctatgattta	tacccttcgc	aaccaggaag	tgaaaacttc	catgaagagg	900
ttattgagtc	gacatgtagt	ctgtcaagtg	gattttataa	taagaaac		948

&lt;210&gt; 442

&lt;211&gt; 1034

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g291 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 442

atgcaccttc	ccaattcttc	tgaaattgcg	attaccacct	tctttctgat	tggaatacca	60
gggctggagc	atgccatat	atggatatct	gtcccatct	gcctcatgta	cttggtagcc	120
atcctaggca	attgcacaat	cctctttggt	atcaggactg	agccctcact	ccatgcaccc	180
atgtactatt	tcctttccat	gttggctgtc	tctgatctgg	gcctgtccct	ctcctaccta	240
cccactatgc	tgaggatctt	tgtattcaat	gccacaggaa	tctcctcaaa	tgctcgcttt	300
gctcaagaat	tctttattca	tggaattcaca	gatatggagt	cctcagtgtc	tctcgtcatg	360
tcttttgacc	ggttttggcc	atatgccacc	ctctgaggta	catatctgag	gtactgggtga	420
gctgtatcct	caccagtgtc	agagtggcca	aaatggggct	gttggtttctc	attaaaagag	480
aaacaacact	aaactcatta	aaagaaacaa	ctaactcatg	ctgttagtac	tcccatttcc	540
tttactctt	acaaggttga	catattgtag	gaaaagccta	ctctctcatt	cctattgtct	600
ccatcaggat	gtcaggaagc	tggcctgtct	cgacaacact	gtcaacttct	tctatgggtt	660
ctttcttgcc	ctctgtatga	tgtcagaaag	tgtgttcatt	actgtgtcct	atgtgtctcat	720
cctgaagacg	atcatgggaa	ttggatccca	tagggagcgg	ctcaaggccc	tcaacacctg	780
tgtctcccat	atctgtgctg	tgcttatctt	ctatgcgccc	gtcattgctt	tggcatccat	840
gcaactgctt	ggcatccatg	aactgctttg	gcaagcacag	gtccccactg	gccatgatcc	900
tcattgctga	tgttttcttg	ctagtgtccac	ctcttatgaa	tcccattgta	tattgtgtga	960
agacacagca	aattcatgaa	aaagtttttag	gaaaactggg	tctacaacaa	cggtgtcagt	1020
aaacgtggta	caag					1034

&lt;210&gt; 443

&lt;211&gt; 713

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g292 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 443

ccacttattt	gaccagatcc	attcatcttt	acacaattgt	gttcattcct	taataaatat	60
gtagcgtcaa	ctcgggttaa	tgatcataac	atagatcagg	ctccataatc	caggagcata	120
atcctaaatc	tgctccttatt	tcctttggga	ttaaaggcat	gtggagcaat	gttaattctt	180
gtttcctttc	tagccttccc	agagagaaag	agctaggatt	gaaacagcga	ggggaactac	240
tctagtgtca	ctcaattctg	tctcctgggc	ttcccaggct	ttgaggaact	gccccatttc	300
cttttggtta	acttcttctt	tcacttgatg	agattaatgg	gaaatgcagt	cattttacatg	360
gttgaattga	tgaagtcttc	agtctcccg	ggattttctt	ctcagtcaac	tcttcatctt	420
ttcacacagt	ctattaatgg	acatttccat	tgttattgct	tctttgatcc	agattgatcc	480
ctactccagt	atcccctcag	cgtctggcca	aaaaataatc	cttctccact	catgcctccc	540
atttcacctg	tgtgggggatt	gactatgaca	gctgcttggt	tctctacgtg	aaacccaagc	600
aaatttgggc	agcagaataa	aacaaggtag	ttttcctggt	tattttcctg	ttgacccctt	660
ttctgaacct	tcttacaggt	cagatttact	gacctaaatc	agtttttaggt	ggg	713

&lt;210&gt; 444

&lt;211&gt; 931

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g293 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 444

cccatgaaag	tgGCCaACAA	tgTCActGag	tttatattcc	tgggactttc	ccaagattct	60
ggaatgcaat	tgatgttctt	tgtcttattt	ctcctcttct	acgtcgtgat	catgggtggga	120
aatttgctca	ttttgcttat	ggtcttttct	gactcccgac	tacacacacc	catgtatttc	180
ttcctcagta	acctgtcttt	tgtggacatt	gcctgttcct	cagccacagc	acccaagatg	240
attgaagact	ttgtttctga	gaaaaagact	atttcctact	ggggctgtat	aactcagatg	300
tttaccttcc	acttttttgg	ttgtgctgag	atttttgttt	tgactgtcat	ggcttttcat	360

cgctatgctg	ctatctgcca	acccctccgt	tacactgtca	tcatgagtgc	taatgcttat	420
actgtgctgg	catcactgtc	ctggttgggg	gccctgggtc	attcctttgt	tcagaccctc	480
ctgaccttcc	agctgccctt	ctgtaatgct	caggttatag	accattactt	ttgtgatgtc	540
caccagtgcc	taaaacttgc	ctgtgctgat	acaactctgg	taaatatggt	ggagggtggc	600
aacagtgggc	tcattctcct	gggggttttc	ctcattcttt	tggcctccta	cacagtcatt	660
ctgtttagtc	ttcaaaaaca	gtctgcagag	agctgacaca	aagttctctc	tacctgtgga	720
tctcatctga	ctatagtaac	tttcttcttt	gttccgtgta	tctttattta	tctccatcca	780
ctactttccc	attggataaa	gctgtgtctg	tgttctatac	caccatcacc	ccaatgctga	840
acccactcat	ctatactctg	aggaatgagg	agtaaagaat	gccatgaggg	ggctatggag	900
tagcaagatc	tccttgaagg	aaaagcagag	a			931

&lt;210&gt; 445

&lt;211&gt; 968

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g294 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 445

atggaaatcc	taagcaactc	aacatctaaa	tttccaacct	tcttgttgac	cggcattcct	60
ggcctagagt	ctgcccatgt	ctggatctcc	attcctttct	gctgttttta	tgccattgcc	120
ctctctggga	acagcgtgat	cctgtttgtc	atcattaccc	agcagagtct	ccatgaaccc	180
atgtattatt	tctcttccat	gctatcagcc	actgatctgg	gcttgactgt	ttcttcattg	240
tcaacaacat	taggtatcct	ctggtttgag	gcagtgaat	cagtctatac	agctgcattg	300
tcagatggt	ttttcttcat	ggattcactt	ttatggaatc	tggagtgtctg	gtggctacag	360
cctttgaccg	ttatgtggcc	atctgtgac	ctctgaggta	cactaccatt	ctcactaatt	420
ccagaatcat	tcaaatgggt	cttctgatga	ttacacgtgc	tatagtacta	atattaccac	480
tacttttgc	ccttaagcct	ctctatttct	gtagaatgaa	tgccttttct	cactcctatt	540
gttaccatcc	agatgtgatt	caattagcat	gttcagacat	tcggggcaat	agcatctgtg	600
gattaattga	tctcatcctg	accactggaa	tagatacacc	atgcattgtc	ctgtcatata	660
tcttaattat	tcgctttgtc	ctcagaattg	cctcccctga	agaatggcac	aagggtcttca	720
gcacctgtgt	ctccccagtg	ggagcagttg	ctttcttcta	catccacatg	ctgagcctgt	780
ccttgggtga	tcgctatggt	cggtcagccc	ccagagtagt	ccattcagtg	atggctaacg	840
tatacctgct	tttaccctct	gtgctcaacc	ccatcatcta	cagtgtaaaa	acaaaacaaa	900
tccgcaaggc	tatgctcagt	ctgctgctta	caaaatgaac	agacatagtt	ttatttgata	960
caaacctg						968

&lt;210&gt; 446

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g295 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 446

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gacccagaac	tgcagcctat	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggtc	120
acgggtgctga	ggaacctgct	cagcatectg	gctgtctgct	ctgactcccc	cctccacacc	180
cccaggtact	tcttctcttc	caacctgtgc	tgggctgaca	tcgggtttcac	ctccgccacg	240
gttcccaaga	tgattgtgga	catgcagtcg	catagcagag	tcacgtctca	tgcgggctgt	300
ctgacgcaga	tgtctttctt	ggtccttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccaggt	catcgtgaat	420
cctcacctct	gtgtcttctg	tttggtgtcc	tttttcttta	gcctgttgga	ttcccagctg	480
cacagttgga	ttgtgtttaca	attcaccatc	gtctagaatt	tggaaatctc	taattttgtc	540
tgtgaccctt	ctcaacttct	caaacttgcc	tgttctgaca	gcgtcatcaa	tagcatattc	600
atatatttcg	atagtactat	gtttgggtttt	cttccatttt	cagggatcct	atgggtcttac	660
tataaaatca	tcccctccat	tctaaggatt	tcactgctag	atgggaagta	taaagccttc	720
tccacctgtg	gctctcacct	agccgttgtt	tgtgtatttt	atggaacagg	cattggcatg	780
tacctgactt	cagctgtgtc	acaaccccc	aggaatgggt	tgggtggcatc	agtgtgtat	840

gctgtggtca ccccatgct gaaccttttc atctacagcc tgagaaacag gaacatacaa	900
agtgcctctg ggaggctgca cagcagaaca gtcgaatctc atgatttggt ccatcctttc	960
tct	963

&lt;210&gt; 447

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g296 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 447

atggcaatat tcaataacac cacttcgtct tcctcaaact tcctcctcac tgcattccct	60
gggctggaat gtgctcatgt ctggatctcc attccagtct gctgtctcta caccattgcc	120
ctcttgggaa acagtatgat cttctctgtc atcattacta agcggagact ccacaaaccc	180
atgtattatt tcctctccat gctggcagct gttgatctat gtctgacct tacgaccctt	240
cccactgtgc ttggtgttct ctggtttcat gcccgggaga tcagctttaa agcttgcttc	300
attcaaatgt tctttgtgca tgctttctcc ttgctggagt cctcgggtgt ggtagccatg	360
gcctttgacc gcttcgtggc tatctgtaac ccactgaact atgctactat cctcacagac	420
aggatgggcc ttggtatagg gctggtcac tgcatagac cagcagtttt cttacttccc	480
cttctttagc ccataaacac tgtgtctttt catgggggtc acgagctttc ccatccattt	540
tgctaccacc cagaagtgat caaatacaca tattccaaac cttggatcag cagtttttgg	600
ggactgtttc ttcagctcta cctgaatggc actgacgtat tgtttattct tttctcctat	660
gtcctgatcc tccgtactgt tctgggcatt gtggcccgaa agaagcaaca aaaagctctc	720
agcacttggt tctgtcacat ctgtgcagtc actattttct atgtgccact gatcagcctc	780
tctttggcac accgcctctt ccactccacc ccaaggggtc tctgtagcac tttggccaat	840
atttatctgc tcttaccacc tgtgtgtaac cctatcattt acagcttgaa gaccaagaca	900
atccgccagg ctatgttcca gctgtccaa tccaaggggt catgggggtt taatgtgagg	960
ggtcttaggg gaaga	975

&lt;210&gt; 448

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g297 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 448

atggagacgt ggggtgaacca gtcctacaca gatggcttct tcctcttagg catcttctcc	60
cacagtactg ctgacctgt cctcttctcc gtggttatgg cggctctcac agtggccctc	120
tgtgggaatg tcctcctcat cttcctcacc tacatggacc ctcacctca ccccccatg	180
tacttcttcc tcagccagct ctccctcatg gacctcatgt tggctgtgac caatgtgcca	240
aagatggcag ccaacttcc gtctggcagg aagttccatct cctttgtggg ctgtggcata	300
caaattggcc tctttgtctg tcttgtggga tctgaggggc tcttgtggg actcatgggt	360
tatgaccgct atgtggccat tagccaccca cttcactatc ccatectcat gaatcagagg	420
gtctgtctcc agattactgg gagctcctgg gcctttggga taatcgatgg cttgatccag	480
atgggtgtag taatgaattt cccctactgt ggcttgagga aggtgaacca tttcttctgt	540
gagatgctat ccttggtgaa gctggcctgt gtagacacat ccctggttga gaaggtgata	600
tttgcttgtc gtgtcttcat gcttctcttc ccattctcca tcactgtggc ctctatgct	660
cgcattctag ggactgtgct gcaaatgcac tctgctcagg cctggaaaaa ggccctggcc	720
acctgtcctc cccacctgac agctgtcacc ctcttctatg gggcagccat gttcatctac	780
ctgaggccta ggcactaccg ggccccagc catgacaagg tggcctctat cttctacacg	840
gtccttactc ccatgtctaa cccctcatt tacagcttga ggaacaggga ggtgatgggg	900
gcaactgagga aggggctgga ccgctgcagg atcggcagcc agcac	945

&lt;210&gt; 449

&lt;211&gt; 965

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g298 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 449

atgtcaccac	tcaaccaaac	tactgagaac	caccagagct	tcttcaccct	gactgggatt	60
ccaggaatgc	cagagaaaga	cttatggatg	gccttgcccc	tctgtcttct	ttatagcacc	120
acgatcttgg	gaaatgtcac	catccttgtt	gtcatcaaag	ttgagcaaag	tctccatgag	180
cccatgtatt	tttctagcca	tgtagctgc	cactgacctc	agcctttcac	tgtcttccat	240
gcctaccatg	gtcagtgttc	actggttcaa	ctggcgttca	ataactttta	atggctgcct	300
tatccagatg	ttcttcatcc	acacatttgg	gggagtggaa	tcagggtgtc	tggtggccat	360
ggcctttgat	cgctttgtgg	ccatccgctt	tcctttgcac	tatgctacaa	ttctcactca	420
cagtgtcatc	agcaagattg	cagcagccat	cctgctacgg	agtgtggggg	ctgtgctccc	480
tgtgcctttt	ctcatcaaaa	ggttaccttt	ctgtcactcc	aatgtcctct	cccatgcata	540
ctgcctccat	caggatgcca	tgaggcttgc	ctgtgctgac	actggtgtca	atagcatcta	600
tggcctgttg	gctgtgatct	tcattcattgt	actagatgcc	ttaatacttt	tggcctctta	660
catctaaac	ctgcaggcag	tattgagcat	tgcttcccag	gaagacaggc	tcaaggctct	720
caacacctgt	ctctctcata	tctgcagtgc	tgcttttcta	tgtgcctctc	attggtatga	780
ccctaattca	tcgctatggg	aagcatttgt	caccactaat	acacacattc	atggccaata	840
tctacctgct	tctccctcct	gtgtcacaac	ccattgtgta	cagtgttagg	accaagcaga	900
tctgatagca	gattgtccag	gccttttgtg	gggctagggt	tagcccttaa	tgcatctac	960
tattt						965

&lt;210&gt; 450

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g299 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 450

atgtctgttc	tcaataactc	cgaagtcaag	cttttccctc	tgattgggat	cccaggactg	60
gaacatgccc	acatttggtt	ctccatcccc	atttgccctc	tgtacctgct	tgccatcatg	120
ggcaactgca	ccattctctt	tattataaag	acagagccct	cgcttcatga	gcccattgat	180
tatttccttg	ccatgttggc	tgtctctgac	atgggcctgt	ccctctcctc	ccttccctacc	240
atgttgaggg	tcttcttgtt	caatgccatg	ggaatttcac	ctaagcctg	ctttgctcaa	300
gaattcttca	ttcatggatt	cactgtcatg	gaatccctcag	tactttcta	tatgtctttg	360
gaccgctttc	ttgccattca	caatccctta	agatacagtt	ctatccctac	tagcaacagg	420
gttgctaaaa	tgggacttat	tttagccatt	aggagcattc	tcttagtgat	tccatttccc	480
ttcaccttaa	ggagattaaa	atattgtcaa	aagaatcttc	tttctcactc	atactgtctt	540
catcaggata	ccatgaagct	ggcctgctct	gacaacaaga	ccaatgtcat	ctatggcttc	600
ttcattgctc	tctgtactat	gctggacttg	gcactgattg	ttttgtctta	tgtgctgac	660
ttgaagacta	tactcagcat	tgcacttttg	gcagagaggc	ttaaggccct	aaataacctg	720
gtctcccaca	tctgtgctgt	gctcaccttc	tatgtgcccc	tcataccctc	ggctgccatg	780
catcactttg	ccaagcacia	aagccctctt	gttggtgatcc	ttattgcaga	tatgttcttg	840
ttggtgccgc	cccttatgaa	ccccattgtg	tactgtgtaa	agactcgaca	aatctggggg	900
aagatcttgg	ggaagttgct	taatgtatgt	gggaga			936

&lt;210&gt; 451

&lt;211&gt; 923

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g300 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 451

atgaaaataa	atgacagctc	aggggaagac	ttcatcttag	ttggcttctc	agaatatccc	60
caggctgagt	tcaccccttc	tctgtttgtc	tccgggttct	acaccatgac	attcacaggg	120
aacacagcca	tcactttggt	ctctctgctg	gactaccggc	tccgcacccc	aatgtacttc	180

tccctccgaa	agctctcatt	tctggacatg	tgtttcacca	cctgcattgt	ccttcagatg	240
ctggtgaaca	tctggggaga	gagtaagaag	gtcagctatg	taggctgcat	ggttcagtat	300
tctgtagcct	tggctcttgg	ctccacagag	tgtgtgcttc	ttgctatcat	ggctgtggac	360
cgttatgttg	ccgtccgctg	gccccttcac	tatgttacaa	tcattgcacca	acagatctgc	420
cactttctcg	cagccttgtc	ctggttttct	gggttagcca	actctctctt	tcactcttca	480
ctaaccacca	ttttgcctct	gtgtggccac	cgccgtgtgg	accatttctt	tgtgaggtec	540
tgtcatttgt	caagctgtcc	tgcgtggaca	ccggcccaac	tgaattgaag	atgttaattg	600
ctcgtgtgat	catccttgcc	cttcacagtg	gcaccatcct	cacctcctat	gcctgcattg	660
ccagggctgt	gctgaggctg	cagtcctgtg	aaggtcagca	gaaggccttt	gggacttgtg	720
cctcccacct	gatgggtggc	ttgctgttct	atggaaccat	catgttcatg	tgtcttcagc	780
tgaagagtaa	ctactctcag	attcagggaa	agctgcttcc	tcttgtttat	accattgtcg	840
ccccaccta	gaaccaccta	atctatgcac	tgaggaaaca	agttgtaaag	agggcaattg	900
gaaaattgat	ctggaaggat	tca				923

&lt;210&gt; 452

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g301 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 452

atggaaatag	ataaccagac	gtgggtgaga	gaattttatc	tccttggctt	atccagtgc	60
tggtgcactc	agatatccct	gttttccctg	ttcttgggtca	catacctcat	gacagtgcctg	120
gggaactgtc	tatttgtcct	tctgatcaga	ctggacagcc	gactccacac	tcccatgtat	180
ttctttctca	ccaacctctc	ccttgctgat	gtctcctatg	ccacaagcgt	agtccccag	240
ctgtcggcac	attttcttgc	agaacataaa	gccatcccat	tccagagctg	tgtagcccg	300
ttatttttct	ccctggcctt	gggtgggatt	gagtttgttc	tcctggcagt	gatggcctat	360
gaccgcctatg	tggtctgtgc	tgaccgcctg	cgatactcgg	ccatcatgca	tgtagggctg	420
tgtgctaggt	tggccatcac	atcctgggtc	agtggctcca	tcaactctct	tgtgcagact	480
gctatcacct	ttcagctgcc	catgtgcact	aacaagttta	ttgatcacat	atcctgtgaa	540
ctcctagctg	tggtcaggct	ggcttgtgtg	gacacctcct	ccaatgaggc	tgccatcatg	600
gtgtctagca	ttgttcttct	gatgacacct	ttctgcctgg	ttctgttgtc	ctacatccgg	660
atcatctcca	ccatccctaaa	gatccagctc	agagaaggaa	gaaagaaagc	cttccacacg	720
tgtgcctctc	acctcacggg	ggttgccctg	tgctacggca	caacgatttt	cacttacatc	780
cagccccact	ctgggtccctc	agtccttcaa	gagaagctga	tctctgtctt	ctatgccatt	840
gttatgcctc	tgctgaaccc	tgtgatttat	agtcctaagga	ataaagagggt	gaagggggcc	900
tggcataaac	tattagagaa	attctctggg	ttaacatcca	agctgggaac	t	951

&lt;210&gt; 453

&lt;211&gt; 918

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g302 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 453

atggaaggga	aaaatcaaac	caatatctct	gaatttctcc	tcctgggctt	ctcaagttgg	60
caacaacagc	aggtgctact	ctttgcactt	ttctgtgtgc	tctatttaac	agggctgttt	120
ggaaacttac	tcatcttgct	ggccattggc	tcggatcact	gccttcacac	acccatgtat	180
ttcttccctg	ccaatctgtc	cttggtagac	ctctgccttc	cctcagccac	agtccccag	240
atgctactga	acatccaaac	ccaaacccaa	accatctcct	atcccggctg	cctggctcag	300
atgtatttct	gtatgatgtt	tgccaatatg	gacaattttc	ttctcacagt	gatggcatat	360
gaccgttacg	tggccatctg	tcaccttcta	cattactcca	ccattatggc	cctgcgcctc	420
tgtgcctctc	tggtagctgc	accttgggtc	attgccattt	tgaaacctct	cttgcacact	480
cttatgatgg	cccattctga	cttctgctct	gataattgta	tccaccattt	cttctgtgat	540
atcaactctc	tcctccctct	gtcctgttcc	gacaccagtc	ttaatcagtt	gagtggtctg	600
gtacaggtgg	ggctgatctt	tgtgggtacct	tcagtgtgta	tcctgggtatc	ctatatcctc	660
attgtttctg	ctgtgatgaa	agtcccttct	gcccaggaa	aactcaaggc	tttctctacc	720

tgtggatctc	accttgccct	ggtcattctt	ttctatggag	caaacacagg	ggcttatatg	780
agcccttat	ccaatcactc	tactgaaaaa	gactcagccg	catcagtcac	ttttatgggt	840
gtagcacctg	tggtgaatcc	attcatttac	agtttaagaa	acaatgaact	gaaggggact	900
ttaaaaaaga	ccctaagc					918

&lt;210&gt; 454

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g303 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 454

atgggaccca	gaaaccaaac	agctgtttca	gaatttcttc	tcataaaagt	gacagaggac	60
ccagaactga	agttaatccc	tttcagcctg	ttcctgtcca	tgtacctggt	caccatcctg	120
gggaacctgc	tcattctcct	ggctgtcatc	tctgactccc	acctccacac	ccccatgtac	180
ttccttctct	ttaatctctc	ctttactgac	atctgtttaa	ccacaaccac	agtcccaaaag	240
atcctagtga	acatccaagc	tcagaatcag	agtatacttt	acacaggctg	cctcaccacag	300
atctgtcttg	tcttggtttt	tgctggcttg	gaaagtgtgt	ttcttgcatg	catggcctac	360
gaccgctatg	tggccatttg	ccaccacttg	aggtacacag	tcctcatgaa	tgtccatttc	420
tggggcttgc	tgattcttct	ctccatgttc	atgagcacta	tggatgccct	ggttcagagt	480
ctgatgggat	tgcagctgtc	cttctgcaaa	aacgttgaaa	tccctttgtt	cttctgtgaa	540
gtcggtcagg	tcatacaagt	cgcctgttct	gacacctca	tcaacaacat	cctcatatat	600
tttgcaagta	gtgtatttgg	tgcaattcct	ctctctggaa	taattttctc	ttattctcaa	660
atagtcacct	ctgttctgag	aatgccatca	gcaagaggaa	agtataaagc	gttttccacc	720
tgtggctgtc	acctctctgt	tttttctctg	ttctatggga	cagcttttgg	gggtgtacatt	780
agttctgtcg	ttgtgtgagc	ttcccgaaat	actgtgtgtg	cttcagtgat	gtacactgtg	840
gtccctcaaa	tgatgaaccc	cttcactctac	agcctgagaa	ataaggagat	gaagaaagct	900
ttgaggaaac	ttattggtag	gctgtttcct	ttt			933

&lt;210&gt; 455

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g304 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 455

atggaagcga	gaaaccaaac	agctatttca	aaattccttc	tcctgggact	gatagaggat	60
ccggaactgc	agcccgctct	tttcagcctg	ttcctgtcca	tgtacttggg	caccatcctg	120
gggaacctgc	tcactctctt	ggctgtcatc	tctgactctc	acctccacac	ccccatgtac	180
ttcttctctt	ccaatctctc	ctttttggac	atttgtttaa	gcacaaccac	gatcccaaaag	240
atgctgggtga	acatccaagc	tcagaatcgg	agcatcacgt	actcaggctg	cctcaccacag	300
atctgctttg	tcttggtttt	tgctggcttg	gaaaattgtc	tccttgccagc	aatggcctat	360
gaccgctatg	tggccatttg	tcaccccttt	agatacacag	tcatacatgaa	ccccgcctc	420
tgtggcctgc	tgattcttct	ctctctgttg	actagtgttg	tgaatgccct	tcttctcagc	480
ctgatgggtg	tgaggctgtc	cttctgcaca	gacctggaaa	tcccgcctct	cttctgtgaa	540
ctggctcagg	tcatacaact	cacctgttca	gacacctca	tcaataacat	cctgatatat	600
tttgacgctt	gcataatttg	tggtgttcct	ctgtctggaa	tcattttgtc	ttacactcag	660
atcacctcct	gtgttttgag	aatgccatca	gcaagtggaa	agcacaaagc	agtttccacc	720
tgtgggtctc	acctctccat	tggtctcttg	ttctatgggg	caggtttggg	gggtgtacatt	780
agttctgtgg	ttactgactc	acctaggaag	gctgcagtgg	cttcagtgat	gtattctgtg	840
ttccctcaaa	tggtgaaccc	ctttatctat	agtctgagga	ataaggacat	gaaaggaacc	900
ttgagggaag	tcatagggag	gataccttct	cttctgtgg			939

&lt;210&gt; 456

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g305 nucleotide)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 456

atggaaccaa	gaaaccaa	cagtgc	caatc	tctggg	ctcagaaa	60
ccagagcagg	agacgctt	ctttcc	ttcttgc	tgtacctg	catggctg	120
gggaacctgc	tcatc	ggccatc	atagactc	acctccac	ccccatgt	180
ttcttctg	ccaacctg	cctggtg	ttctgtg	ccaccaac	catcccta	240
atgctggtga	gccttcaa	cgggagca	gccatctt	atccctg	cctgatcc	300
atgtacttct	tccatttct	tggcatcg	gacagcgt	taatcgcc	gatggctt	360
gaccggttcg	tggccatct	ccacccatt	caactcgcc	agatcatg	cctacgcct	420
tgtcgccctg	tggcggcg	cctctggcg	tttctgct	tcatctc	cactcacat	480
ctcctgatg	ccgtctcgt	tttctggcg	agccatgag	tgcctcact	cttctgcg	540
ctcactccca	tcctccgact	ttcgtgcag	gacacctct	tgaatagg	cttcacctc	600
attgtggcag	ggatggtgat	agccacgccc	tttgtctg	tcctggcctc	ctatgctcg	660
atccttgtg	ccatcatgaa	ggtccctct	gcaggcggc	ggaagaaag	cttctccacc	720
tgcagctccc	acctgtctgt	ggttgcctc	ttctatggg	ccaccattg	cgtctatctg	780
tgtccctctc	cggctctcac	cactgtgaag	gagaaagctt	ctgcggtgat	gtacacagca	840
gtcaccccca	tgtgaatcc	cttcatctac	agcttgagg	acagagacct	gaaaggggct	900
ctcaggaagc	tgggtcaacag	aaagatcacc	tcattcttc			939

&lt;210&gt; 457

&lt;211&gt; 295

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g306 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(295)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 457

atgtcagcct	ccagtatcac	ctcaacacat	ccaacttcct	tcttggtgat	ggggattcca	60
ggcctggagc	acctgcacat	ctggatctcc	atcccttct	cagcatatac	actggccctg	120
cttggaact	gcactctcct	tctcatc	caggctgatg	cagccctcca	tgaacccatg	180
tacctctt	tggccatggt	ggcagccatc	gaccagctct	ctatctctc	agcactgccc	240
ccgggacaga	cgggtgattct	ggttcacgga	tcngaagaat	aaaccctttg	ccggg	295

&lt;210&gt; 458

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g307 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 458

atgccatctg	cctctgccat	gatcattttc	aacctgagca	gttacaatcc	aggacccttc	60
attctggtag	ggatcccagg	cctggagcaa	ttccatgtgt	ggattggaat	tcccttctgt	120
atcatctaca	ttgtagctgt	tgtgggaaac	tgcactcttc	tctacctcat	tgtgggtggag	180
catagtcttc	atgaacccat	gttcttcttt	ctctccatgc	tggccatgac	tgacctcatc	240
ttgtccacag	ctggtgtgcc	taaagcactc	agtatctttt	ggctaggggc	tcgcgaaatc	300
acattcccag	gatgccttac	acaaatgttc	ttccttcact	ataactttgt	cctggattca	360
gccattctga	tggccatggc	atttgatcac	tatgtagcta	tctgttctcc	cttgagatat	420
accaccatct	tgactcccaa	gaccatcatc	aagagtgtcta	tgggcatctc	ctttcgaagc	480
ttctgcatca	tcctgccaga	tgtattcttg	ctgacatgcc	tgcctttctg	caggacacgc	540
atcatacccc	acacatactg	tgagcatata	ggtgttgccc	agctcgccctg	tgtgatatac	600
tccatcaact	tctgggtatgg	cttttgtgtt	cccatcatga	cggctcatctc	agatgtgatt	660

ctcattgctg	tttctacgc	acacatcctc	tgtgctgtct	ttggccttcc	ctcccaagag	720
gcctgccaga	aagccctcgg	cacttggtgt	tctcatgtct	gtgtcaccct	catgttttat	780
acacctgcct	ttttctccat	cctcgcccat	cgctttggac	acaatgtctc	tcgcaccttc	840
cacatcatgt	ttgccaatct	ctacattgtt	atcccacctg	cactcaaccc	catggtttac	900
ggagtgaaga	caaagcagat	cagagataag	gttatacttt	tgttttctaa	gggtacagga	960

&lt;210&gt; 459

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g308 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 459

atgagcgagg	caaaccagtc	gagtgtctcc	gagttcctcc	tcctgggact	ctccaggcag	60
ccccagcagc	agcatctcct	ctttgtgttc	ttcctcagca	tgtacctggc	cactgtcctg	120
gggaacctgc	tcatcatcct	gtccgtaagc	atagactcct	gcctgcacac	ccccatgtac	180
ttcttctcca	gcaacctgtc	ttttgtggac	atctgtttct	ccttcaccac	cgtecccaag	240
atgctggcca	atcacatact	cgagactcag	accatctcct	tctgtggctg	tctcacacag	300
atgtatttcg	ttttcatgtt	cggtggacatg	gacaatttcc	tcctagctgt	gatggcctat	360
gaccactttg	tcgccgtgtg	ccacccctta	cattacacag	caaagatgac	ccatcagctc	420
tgtgccctgc	tggttgctgg	attatgggtg	gttgccaacc	tgaatgtcct	tctgcacacc	480
ctgctgatgg	ctccactctc	attctgtgca	gacaatgcc	tcactcactt	cttctgcgat	540
gtgactcccc	tactgaaact	ctcctgtcca	gacacacacc	tcaatgaggt	cataatcctt	600
agtgagggtg	ccctgggtcat	gatacecca	tttctttgca	tcctggcttc	ttatatgcac	660
atcacctgca	ctgtcctgaa	ggteccatcc	acaaagggaa	gggtggaaagc	cttctccacc	720
tgtgggttctc	acctggctgt	ggttctctc	ttctacagca	ccatcattgc	tgtgtatttt	780
aacctctgt	cctccactc	agctgagaaa	gacactatgg	ctactgtgtt	gtatacagta	840
gtgactccca	tgctaaaccc	tttcatctac	agcctgagga	acagggtactt	gaaaggggct	900
ctgaaaaaag	tagttggcag	gggtggtgtt	tctgtc			936

&lt;210&gt; 460

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g309 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 460

atgtacttct	tcctgcgcca	actctcagtg	gtggagctct	tctacaccac	tgacatcgtg	60
cccaggaccc	tgcccaatct	gggtctcccc	catccccagg	ccatctcttt	ccagggctgt	120
gcagcccata	tgtacgtctt	cattgtcctg	ggcatctcgg	agtgtgcct	gtcactgcc	180
atggcctatg	accgatatgt	tgccatctgc	cagccccac	gctattccac	cctcttgagc	240
ccacgggcct	gcatggccat	gggtgggtacc	tcctggctca	caggcatcat	cacggccacc	300
acccatgcct	ccctcatctt	ctctctacct	tttcgcagcc	acccgatcat	ccgcactttt	360
ctctgtgaca	tcctgccagt	actgaggctg	gcaagtgtg	ggaagcacag	gagcgagatc	420
tcctgtgatg	cagccaccat	agtcttcatt	atgatccct	tctctctgat	tgtcacctct	480
tacatccgca	tcctgggtgc	catectagca	atggectcca	cccagagccg	ccgcaaggtc	540
ttctccacct	gtctctccca	tctgtctgtg	gtctctctct	tccttggaac	agccagcatc	600
acctacatcc	ggcgcagggc	aggctcctct	gttaccacag	accgcgtcct	cagtctcttc	660
tacacagtca	tcacacccat	gctcaacccc	atcatctaca	cccttcggaa	caaggacgtg	720
aggagggccc	tgcgacactt	ggtgaagagg	cagcgccctc	ca		762

&lt;210&gt; 461

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g310 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 461

atggatggag	agaatcactc	agtggatatc	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	tcagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgtctca	300
atcttcttca	tccacgtcat	tgggtgtgtg	gagatgggtg	tgctcatagc	catggccttt	360
gacagtatat	tggccctatt	aagccctctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttgttgtcag	tactccctg	ttccaactgg	480
catttcttgt	taatttacc	ttctgtggcc	ctaagtgttt	ggacagcttc	tactgtgacc	540
ttcctcagct	tctcagacta	gcctgtaccg	acacctacag	attgcagttc	atggtcactg	600
ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tctaactctc	tacgtcttca	660
tcctgtttac	tgtttgaaa	cattcctcag	gtgggtcacc	caaggccctt	tccactcttt	720
cagctcacag	cacagcggtc	cttttgttct	ttgggtccacc	catgtttgtg	tatacatggc	780
cacacctaa	ttcacagatg	gacaagtttc	tggctatttt	tgatgcagtt	ctcactcctt	840
ttctgaaatc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaacatga	tatggcttta	tgtttctttc	tttgatat			998

&lt;210&gt; 462

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g311 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 462

atggaagagt	acaacacatc	ctctacagac	ttcactttca	tggggctgtt	caacagaaag	60
gaaacctcag	gtcttatttt	tgccatcatc	tctatcatct	tcttcaccgc	actgatggcc	120
aatgggggta	tgaatcttct	gatccaaaca	gatttgcgcc	ttcatacacc	catgtacttc	180
ctcttcagcc	acctttcctt	aattgacatg	atgtatat	ccactattgt	gcctaagatg	240
ctgggttaatt	acctgctgga	tcaaaggacc	atttcctttg	tgggggtgcac	agctcaacac	300
ttcctctacc	ttacccttgt	gggagctgaa	ttcttctctg	tgggcctcat	ggcctatgac	360
cgctatgtgg	ccatttgcaa	ccctctgaga	tacctgtccc	tcatgagccg	ccgggtctgt	420
tggatgatta	tagcaggttc	ctggtttggg	ggctcttttg	atggcttctt	cctaaccctc	480
atcaccatga	gctttccctt	ctgcaattcc	cgggagatta	accacttctt	ctgcgaggca	540
ccagcagttc	tgaagtgggc	atgtgcagac	acagccctct	acgagacagt	gatgtatgtg	600
tgctgtgttt	tgatgtgtgt	gattcctttc	tctgtagtcc	ttgcttctta	tgcccgaatc	660
ctgactacag	ttcagtgcac	gagctcagtg	gagggcagga	agaaggcatt	tgccacttgc	720
tcattcccaca	tgactgtggg	gtccttgttc	tacggggctg	ccatgtacac	ctacatgctg	780
ccacattctt	accacaagcc	agcccaggac	aaagtccctc	ctgtgtttta	caccattctc	840
acacccatgc	tgaacccctt	catctacagc	cttagaaaca	aggatgtgac	tggagctctg	900
aagagggcct	tggggagggt	caagggtcct	caa			933

&lt;210&gt; 463

&lt;211&gt; 883

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g312 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 463

atccaatgca	agggctaata	gaagtgaatt	aagacattct	ctgtaactcc	aatatttaa	60
ggaaaccggg	aaatagccag	attcctctcc	aacctgtcct	tggctggcat	cggtttcccc	120
tccaccatga	tctccaagat	gattgtggac	atccagtctc	acagcagagt	catctcctat	180
gcgggctgcc	tgactcaggt	atctcttttt	gccgtttttg	gatgcagga	agacatgctt	240
ctgagtgtga	tggcttatga	ccggtttgtg	gacatctgtc	accctctgga	ttatccagtc	300

```

atcatgaacc catgtttctg tggcttccta gttttgttgt ctttttttct cagtctttta 360
gactcccagc tgcacaattg gattgcctta caaattacct gcttcaagga tgtggaaatt 420
cccaatttct tctgtgacce ttctcaactc cccaccctt gcctgttgtg acaccttcac 480
caatgacata gtcattgtatt tcttgcctgc catatttggt tttcttccca tttcggggcc 540
ttttctctta ctataaaatt gtttcctcca ttctgagggt ttcattcatca ggtgggaagt 600
ataaagcctt ctccacctgt ggctctcacc tgtcagttgt ttgcttattt tatggaacag 660
gctttggagg ggacctcagt tcagacatgt cctcttatcc cagaaaagg gtcagtggcct 720
cagtgatgta cacggtggtt actcccatgc tgaaccatt catttacagc ctaacaggga 780
aattaaaagt gccctgcggc agctgcactg cagaatagtc taatctcatt ttcttattat 840
ctgttcatt ccttcctag tagtgagttag aaaaggcagc aag 883

```

&lt;210&gt; 464

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g313 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 464

```

atgaccctgg gatccctggg aaacagcagc agcagcgttt ctgctacctt cctgctgagt 60
ggcatccctg ggctggagcg catgcacatc tggatctcca tccactgtg cttcatgtat 120
ctggtttcca tcccgggcaa ctgcacaatt ctttttatca ttaaaacaga gcgctcactt 180
catgaacctt tgtatctctt cctgtccatg ctggctctga ttgacctggg tctctccctt 240
tgcactctcc ctacagtcct gggcatcttt tgggttgagg cactgagaaat tagccatgat 300
gcctgctttg ctacagctctt ttccattcac tgcctctcct tcctcgagtc ctctgtgcta 360
ctgtctatgg cctttgaccg ctttgtggct atctgccacc ccttgacta tgtttccatt 420
ctcaccaaca cagtcattgg caggattggc ctggctcttc tgggtcgtag tgtagcactc 480
atttttccat taccttttat gctcaaaaga ttccctatt gtggctcccc agttctctca 540
cattcttatt gtctccacca agaagtgatg aaattggcct gtgccgacat gaaggccaac 600
agcatctacg gcatgtttgt categtctct acagtgggta tagactcact gctcatcctc 660
ttctcttatg ctctgatcct ggcacccgtg ctgtccatcg cctccagggc tgagagattc 720
aaggccctta acacctgtgt ttccacatc tgtgctgtgc tgcctctcta cactcccatg 780
attggcctct ctgtcatcca tcgctttgga aagcaggcac cccacctggg ccaggtgggc 840
atgggtttca tgtatcttct ctttctctct gtgatgaatc ccattgtcta cagtgtgaag 900
accaaacaga tccgggatcg agtgacgcac gccttttgtt ac 942

```

&lt;210&gt; 465

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g314 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 465

```

atgggactct tcagacaatc caaacatcca atggccaata tcacctggat ggccaaccac 60
actggatggg cggatttcat cctgttggga ctcttcagac aatccaaaca tccagcacta 120
ctttgtgtgg tcatttttgt ggttttctct atggcgttgt ctggaaatgc tgtcctgatc 180
cttctgatac actgtgacgc ccacctccac acccccatgt actttttcat cagtcaattg 240
tctctcatgg acatggcgta ctttctgtc actgtgcccc agatgtcctt ggaccaggtc 300
atgggtgtga ataagatctc agcccctgag tgtgggatgc agatgttctt ctacgtgaca 360
ctagcagggt cagaattttt cttctagacc accatggcct atgaccgcta cgtggccatc 420
tgccatcctc tccgttacct tgcctcatg aacctatagg tgtgtctctt cctgtcatca 480
ggctgctggg tcctgggctc agtggatggc ttacattca ctcccatcac catgaccttc 540
cccttccgtg gatcccgga gattcatcat ttcttctgtg aagtccctgc tgtattgaat 600
ctctcctgct cagacacctc actctatgag attttcatgt acttgtgctg tgtcctcatg 660
ctcctcatcc ctgtggtgat catttcaagc tctattttac tcactctctt caccatccac 720
gggatgaact cagcagaggg ccggaaaaag gcctttgcca cctgctcctc ccacctgact 780
gtggctatcc tcttctatgg ggctgccatc tacacctaca tgcctccag ctccatccac 840
acccttgaga aggacatgat ggtatctgtc ttctatacca tcctcactcc agtggatgaac 900

```

cctttaatct atagtcttag gaataaggat gtcattggggg ctctgaagaa aatgttaaca 960  
gtggaacctg cctttcaaaa agctatggag 990

<210> 466

<211> 591

<212> DNA

<213> Unknown (H38g315 nucleotide)

<220>

<223> Synthetic construct

<400> 466

gctgccatgg	cttaagaccg	gtacatagca	atctgtaacc	cgctgctcta	tacagtgatt	60
atgtccaaga	agggtttgtg	ccagcttgca	attggagcat	ttttgggggg	cactatgagc	120
tcaattatct	ataccacgaa	cactttccat	ctgtcattct	gtccagaga	tattaacct	180
ttcttttgtg	atatctcccc	actcttctct	ctgtcctgca	ctgacacata	catgcatgac	240
atcattctgg	tggctcttgc	cagttttgtg	gaagcaatct	gtcttctatc	agttctcctt	300
tccttatgtc	tcattatggc	agctattctt	agaacagggt	ctgtggaggg	aagaagaaga	360
gggttctcca	cttgtgcttc	ccacctgact	gtggctcacta	tgtatcatgg	taccttgatc	420
ttcatttatt	tgcgtcccg	cactggccat	tcactggata	ttgacaaagt	gacctctgtg	480
ttctataact	tgattatacc	tatgttgaac	cctctaattt	acagtctaag	gaacaaagat	540
gtcaaaaatg	cttttagaaa	agtgtattgc	cgaaaattac	ttccttaagg	t	591

<210> 467

<211> 938

<212> DNA

<213> Unknown (H38g316 nucleotide)

<220>

<223> Synthetic construct

<400> 467

atgatgactc	ttaagaactg	cactgtgttt	actgacttta	tattcttagg	actttcaggt	60
acacaggata	tacagcaggg	gctctttgtg	cttttcttcc	tgatttatgg	cataactgtg	120
attgtcaatc	tagggatgat	cctactgatc	aagatggatc	tcagacttca	cacacccgtg	180
tattatttcc	tgagcaattt	gtctttctgt	gatgtctgct	actcttccac	gtctctccca	240
aatgctagct	gatttcttat	cggaccaaaa	gtggattccg	tataatttat	gtgccattca	300
gatgtattta	tttggagtct	ttgcagatgt	ggaatgtctc	atgttggctg	tcattggccta	360
tgatcggtat	gttgccattt	gcaatccact	tctttatacg	atcactatgc	ccaggaggat	420
ctgcacccag	ctagtggctc	ttgcctatgt	tgtaggtttg	gtggattctg	caatccacac	480
ctgctgcaca	ttcagattgt	cattctgcaa	ttctaattgc	atcaatcact	ttttctgtga	540
catccacccc	ttgctagccc	tcaatccctac	tattaattgc	tattaatgag	atagtgatgt	600
tcacattcgt	tggctgtgtt	gcgggggtgca	gcattgtcac	tgtcttctc	tcctacagct	660
acatcataat	taccatcctt	aaaatgagct	cagctgaggg	cagacggaaa	gccttctcta	720
cctgcacctc	ccacttgatg	gccgtggctg	tatttcatgg	cacactcctg	ttcatgtatt	780
tcgcacccag	ttcaagttac	tcaatggaaa	cagacaaaat	ggcctctgtt	ttctacacag	840
ttgtcatacc	tatgttaaat	ccactgatct	acagcttaag	gaatagggat	gtgaaagggtg	900
ctctgaaaaa	agcaataagc	actaaattat	attctgta			938

<210> 468

<211> 969

<212> DNA

<213> Unknown (H38g317 nucleotide)

<220>

<223> Synthetic construct

<400> 468

atgtcaacat	taccaactca	gatagccccc	aatagcagca	cttcaatggc	ccccaccttc	60
ttgctgggtg	gcatgccagg	cctatcaggt	gcacctcct	ggtggacatt	gcccctcatt	120
gctgtctacc	ttctctctgc	actgggaaat	ggcaccatcc	tctggatcat	tgccctgcag	180

cccgccctgc	accgccaat	gcacttcttc	ctcttcttgc	ttagtggtgc	tgatattgga	240
ttgggtactg	ccctgatgcc	cacactgctg	ggcatcgccc	ttgctgggtgc	tcacactgtc	300
cctgcctcag	cctgccttct	acagatgggt	tttatccatg	tcttttctgt	catggagtcc	360
tctgtcttgc	tcgccatgtc	cattgatcgg	gcactggcca	tctgccgacc	tctccactac	420
ccagcgctcc	tcaccaatgg	tgtaattagc	aaaatcagcc	tggccatttc	ttttcgatgc	480
ctgggtctcc	atctgcccct	gccattcctg	ctggcctaca	tgccctactg	cctcccacag	540
gtcctaaccc	attcttattg	cttgcaccca	gatgtggctc	gtttggcctg	cccagaagct	600
tgggggtgcag	cctacagcct	atthgtgggt	ctttcagcca	tgggtttgga	ccccctgctt	660
atthtcttct	cctatggcct	gattggcaag	gtgttgcaag	gtgtggagtc	cagagaggat	720
cgctggaagg	ctggtcaaac	ctgtgctgcc	cacctctctg	cagtgtctct	cttctatata	780
cctatgatcc	tcttggcact	gattaacat	cctgagctgc	caatcactca	gcatacccat	840
actcttctat	cctatgtcca	tttcttctt	cctccattga	taaaccctat	tctctatagt	900
gtcaagatga	aggagattag	aaagagaata	ctcaacagg	tgcagcccag	gaagggtgggt	960
ggtgctcag						969

&lt;210&gt; 469

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g318 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 469

tctcgctcag	atacacaggt	caatgagtta	gtgttattca	ccgtctttgg	ttttattgaa	60
ctgagtacca	tttcaggagt	tttcatttct	tattgttata	tcacccctatc	agtcttggag	120
atacactctg	ctgaggggag	gttcaaaagt	ctctctacat	gcacttccca	cttatctgcg	180
gttgcaattt	tccagggaac	tctgtctctt	atgtatttcc	ggccaagtcc	ttcctattct	240
ctagatcaag	ataaaatgac	ctcattgttt	tacacccttg	tggttcccat	gttgaacccc	300
ctgattttata	gcctgaggaa	caaggatgtg	aaagaggccc	tgaaaaaact	gaaaaataaa	360
atthtatttt	aaggaaatag	taaa				384

&lt;210&gt; 470

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g319 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 470

atgtttctgc	tcaatacctc	agaagttgaa	gtctccacat	tcctattgat	tgggatacca	60
ggacttgagc	atgcacacat	ttggatctct	atccccatct	gccttatgta	cctcatggcc	120
atcctgggca	actgcacat	cctatttgtt	atcagaacag	agcattccct	gcaagagccc	180
atgtactatt	tcctctccat	gctggccctg	tccgacctgg	gcctgtcttt	ctcctcccta	240
cccacgatgc	tgagaatctt	cttgttcaac	aacatgggga	tttctgctga	tacatgcatt	300
gcccagggaat	tcttcatcca	tggattcaca	gacatggagt	cttcagttct	cctaatacatg	360
tcctttgatc	acttagtagc	catttgcaac	cccctaagat	atagctctat	tctcaccagc	420
ttcaggggtt	tgcaaattgg	actggctttt	gccattaaaa	gcattctcct	agtgtctacc	480
cttttacttt	aaagagactc	agatactgta	ataaacacct	tttatcccac	tcctactgcc	540
ttcaccagga	tgtaatgaag	ctggcctgct	ctgacaacag	ggttaacttt	tactatgggt	600
tgttcgttgc	actctgcatg	atgtcagaca	gtgtttttat	tgtattttcc	tatatgtgtt	660
catcctgaag	actgtgttgg	gtattgcac	ccatggggag	tgcctcgaag	ctcttgacac	720
ctgtgtgtct	catatctgtg	ctgtactcgt	cttctatgtg	cccatcatca	ccttggtctac	780
catgcgtcgc	tttgctaagc	ataaatcccc	tttagctatg	attctgatag	cagatgcatt	840
cttgcgtgga	ccacccttga	tgaatcccat	tgtgtattgt	gtaaaaactc	ggcagattag	900
agtaaaggtc	ctggaaaaat	tggctctgaa	gcctaaatga	tggggc		946

&lt;210&gt; 471

&lt;211&gt; 942

&lt;212&gt; DNA

<213> Unknown (H38g320 nucleotide)

<220>

<223> Synthetic construct

<400> 471

atgatggcat	ctgaaagaaa	tcaaagcagc	acacccactt	ttattctctt	gggtttttca	60
gaataccag	aatccagg	tccactcttt	ctggttttct	tgttcgtcta	cacagtcact	120
gtagtggga	acttgggcat	gataataatc	atcagactca	attcaaaact	ccatacaatc	180
atgtgctttt	tccttagtca	cttgtccttg	acagacttct	gtttttccac	tgtagttaca	240
cctaaactgt	tggagaactt	ggttgtggaa	tacagaacca	tctctttctc	tggttgcac	300
atgcaatttt	gttttgcttg	catttttggg	gtgacagaaa	ctttcatgtt	agcagcgatg	360
gcttatgacc	gttttgctgg	agtttgtaaa	cccttgctgt	ataccactat	tatgtctcag	420
aagctctgtg	ctcttctggt	ggctgggtcc	tatacatggg	ggatagtgtg	ctccctgata	480
ctcacatatt	ttcttcttga	cttatcggtt	tgtgaatcta	ccttcataaa	taattttatc	540
tgtgaccact	ctgtaattgt	ttctgcctcc	tactcagacc	cctatatcag	ccagaggcta	600
tgctttatta	ttgcatatt	caatgagggt	agcagcctaa	ttatcattct	gacatcatat	660
atgcttattt	tcactaccat	tatgaagatg	cgatctgcaa	gtgggcgcca	gaaaactttc	720
tccacctgtg	cctccacact	gacagccatc	actatcttcc	atggaactat	ccttttcctt	780
tactgtgttc	ctaactcctaa	aacttctagc	ctcatagtta	cagtggcttc	tgtgttttac	840
acagtggcga	ttccaatgct	gaacccattg	atctacagcc	ttaggaacaa	agatatcaat	900
aacatgtttg	aaaaattagt	gtcaccaaaa	ttgatttacc	ac		942

<210> 472

<211> 965

<212> DNA

<213> Unknown (H38g321 nucleotide)

<220>

<223> Synthetic construct

<400> 472

cacacagagc	cacggaatca	cacaggggtc	tgagaatttc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggg	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggc	120
acgggtgctg	ggaacctgct	cagcatcctg	gctgtccgct	ctgactcccc	cctccacaac	180
cccattgtact	tcttcctctc	caacctgtgc	tgggctgaca	tcgggtttcac	ctcggccacg	240
gttgccaaga	tgattgtgga	atgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgctttgta	gccatctgtc	gtcctctgca	ctacccagtc	atcgtgaatc	420
ctcacctctg	tgtcttcttc	gttttgggtg	cctttttcct	tagcctgttg	gattcccagc	480
tgcacagttc	gattgtgtta	caattcacca	tcatcaagaa	tgtggaaatc	tctcattttg	540
tctgtgaccc	ctctcatctt	ctcaaacttg	cctgttctga	cagcgtcatc	aatagcatat	600
tcatatattt	cgatagtact	atgtttgggt	ttcttcccat	ttcagggatc	ccttgggtctt	660
actataaaat	cgtccctctc	attctaagga	tttcatcatc	agatgggaag	tataaagcct	720
tgcacacctg	tggctctcac	ctagcagttg	tttctgatt	tgatggaaca	ggcattggta	780
tgtacctgac	ttcagctgtg	gcaccacccc	ctaggaatgg	agtgggtggc	tcagtgtatg	840
aggctgtggt	cacccccatg	ctgaaccttt	tcatctacag	cctgagaaac	agggacatac	900
aaagtgcctt	gcggaggctg	ctcagcagaa	cagtcgaatt	tcatgatctg	tttcattctt	960
tttct						965

<210> 473

<211> 990

<212> DNA

<213> Unknown (H38g322 nucleotide)

<220>

<223> Synthetic construct

<400> 473

atgtcgggtc	tcaataatac	cattgctgag	cctctgatct	tcctcctgat	gggcattcca	60
ggcctgaaag	ccaccagta	ctggatctcc	atcccttttt	gtctcctata	tggtgttgcc	120

gtctctggaa	atagcatgat	cctgtttgtg	gtcctctgtg	aacggagcct	ccataagcct	180
atgtactatt	tcctctctat	gctttcagcc	acagacctga	gcttgtccct	gtgtacactt	240
tctactaccc	ttgggtgtctt	ctgggttgaa	gcccagagaa	tcaacctaaa	tgctgcatt	300
gcccagatgt	tctttctaca	cggatttact	ttcatggagt	ctggggttct	actggccatg	360
gcctttgatc	gttttgtggc	catctgttac	ccactgagat	acactacat	ccttaccaat	420
gcccgaattg	ccaagattgg	gatgagcatg	ttgataagaa	atgttgccgt	catgttgcca	480
gtcatgctct	ttgtcaagag	gttgtccttc	tgcagttcta	tggtccttcc	acattcttac	540
tgctaccatg	ttgatctcat	ccaactctcc	tgcacagaca	ataggatcaa	cagcatcctt	600
ggtctgtttg	cgcttttgtc	cactacaggg	tttgactgcc	cttgcatcct	gctctcctat	660
atcctgatca	ttgatctgt	cctcagcatt	gcttcctcag	aagagaggcg	gaaagccttc	720
aacacctgca	catcccacat	cagtgtgtgt	tccacttctt	acctccctct	catcagtttg	780
tctcttgttc	atcgctatgg	ccattcagca	cctccatttg	tccacatcat	catggccaat	840
gtctttctgc	taatccctcc	tgtgtctaac	cctattattt	acagtgtaaa	gattaagcag	900
attcaaaagg	ccattatcaa	ggtcttaatt	cagaagcact	ccaaatctaa	tcatacagta	960
tttctgatta	gagataaagc	catttatgaa				990

&lt;210&gt; 474

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g323 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 474

atgatgatgg	ttttaaggaa	tctgagcatg	gagccacact	ttgccctttt	aggtttcaca	60
gattacccaa	agcttcagat	tcctctcttc	cttgtgtttc	tgctcatgta	tgttatcaca	120
gtggtaggaa	accttgggat	gatacataata	atcaagatta	accccaaatt	tcacactcct	180
atgtactttt	tccttagtca	cctctctttt	gttgattttt	gttactcttc	cattgtcact	240
cccaagctgc	ttgagaactt	ggtaatggca	gataaaagca	tcttctactt	tagctgcatg	300
atgcagtact	tcctgtcctg	cactgctgtg	gtgacagagt	ctttcttgct	ggcagtgatg	360
gcctatgacc	gctttgtggc	catctgcaat	cctctgcttt	atacagtggc	catgtcacag	420
aggctctgtg	ccctgctggg	ggctgggtca	tatctctggg	gcatgtttgg	ccccttggtta	480
ctcctttgtt	atgctctccg	gttaaaacttc	tctggaccta	atgtaatcaa	ccacttcttt	540
tgtgagtata	ctgctctcat	ctctgtgtct	ggctctgata	tactcatccc	ccacctgctg	600
cttttcagct	tcgccacctt	caatgagatg	tgtacactac	tgatcatcct	cacttcctat	660
gttttcattt	ttgtgactgt	actaaaaatc	cgttctgtta	gtgggcgcca	caaagccttc	720
tccacctggg	cctcccacct	gactgctatc	accatcttcc	atgggaccat	ccttttcctt	780
tactgtgtac	ccaactccaa	aaactctcgg	caaacagtca	aagtggcctc	tgtattttac	840
acagtgtgtc	accccatgct	gaaccctccg	atctacagcc	taaggaataa	agacgtgaag	900
gatgctttct	ggaagttaat	acatacacia	gttccatttc	ac		942

&lt;210&gt; 475

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g324 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 475

atgggtgctgg	cttcagggaa	cagctcttct	catcctgtgt	ccttcaccc	gcttggaatc	60
ccaggcctgg	agagttttcca	gttgtggatt	gcctttccgt	tctgtgccac	gtatgctgtg	120
gctgttgttg	gaaatatcac	tctcctccat	gtaatcagaa	ttgaccacac	cctgcatgag	180
cccatgtacc	tctttctggc	catgctggcc	atcactgacc	tggtcctctc	ctcctccact	240
caacctaa	tggttgccat	attctggttt	catgctcatg	agattcagta	ccatgcctgc	300
ctcatccagg	tgttcttcat	ccatgccttt	tcttctgtgg	agtctggggg	gctcatggct	360
atggccctgg	actgctacgt	ggctacctgc	ttcccactcc	gacactctag	catcctgacc	420
ccatcggctg	tgatcaaaact	ggggaccatc	gtgatgtga	gagggtgctg	gtgggtgagc	480
cccttctgct	tcattggtgc	taggatgccc	ttctgccaac	accaagccat	tcccagtc	540
tactgtgagc	acatggctgt	gctgaagttg	gtgtgtgctg	atacaagcat	aagtcgtggg	600



tatgggctct	ttgtggcctt	ctctgtggct	ggctttgata	tgattgtcat	tggtatgtca	660
tacgtgatga	ttttgagagc	tgtgcttcag	ttgccctcag	gtgaagcccc	cctcaaagct	720
tttagcacac	gtgcctccca	tatctgtgtc	atcttggctc	tttatatccc	agcccttttt	780
tctttcctca	cctaccgctt	tggccatgat	gtgccccgag	ttgtacacat	cctgtttgct	840
aatctctatc	tactgatacc	tcccatgctc	aaccccatca	tttatggagt	tagaaccaaa	900
cagatcgggg	acagggttat	ccaaggatgt	tgtggaaaca	tc		942

&lt;210&gt; 476

&lt;211&gt; 860

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g325 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 476

tatatattgt	tagacatata	tatatgtcta	aacaacactc	atgtctaatt	gtgtgtagag	60
tcactagagg	caatttaaaa	taagttttta	tttttctttt	tttctattgg	caataacatg	120
attttagtga	taaattttta	taattatgaa	aacataacag	tactttttta	aacataaaca	180
tttaaagaaa	aagttttcat	gattcttcta	tacatcttaa	catacatact	ctccctttta	240
agtaagtctt	ttgcattggt	taaatctttg	cagacaaagc	ttttcaagag	caagtcagtg	300
gaaactagta	gagcaggagt	tgagaaagcc	ctgtgcatta	tacactcacc	atgtcccaga	360
agttttgtct	catccatcca	gcaggatggt	agaccagggc	atataatcta	tccccgggtca	420
ctcattttct	cattgtattg	cctattgtgg	gcacaatgta	gttaatatat	tttaaaataa	480
atattctgtt	gccatttcag	attcgtgagt	tcactctggat	agcggatttt	tgtttgtttg	540
tttgttttgc	tttagtcaat	tttgattaat	taaggaaatc	cagagtcctc	actccttagc	600
tttcattttc	aacttgtcta	aaaggcactt	tctgccagtg	cacatcaacc	ttctccaccc	660
atttcccaca	tttccaccat	ccttcctcac	tctagtgcac	taactccaaa	aactcacagg	720
caactgtgaa	agcacactct	gtatgttatg	ccatgttaat	ccccatgctg	aactcacaga	780
cttgttagcat	gcggtacaaa	aatgtgaatg	aatctctgca	gaagctgatg	gacttcaaaa	840
tatttttagca	ttgaaagcaa					860

&lt;210&gt; 477

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g326 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 477

agtcacacag	agccatagaa	tctcacaagt	gtctcagaat	tccttctcca	gggactctca	60
gaggatccag	aactgcagcc	cgctcctcgt	gggctgtccc	tgcccatgta	cctgggtcacg	120
gtgctgagga	acctgtctcat	catcctggct	gtcagctctg	actccacact	ccacaccccc	180
atgtacttct	tcctctccaa	cctctcctgg	gctgacattg	gtttcacctc	ggccatgggt	240
cccaagatga	ttgtggacat	gcagtcgcat	agcagagtca	tctcttaagc	gggctgcctg	300
acacagatgt	ctttctttgt	cctttttgca	tgtatagaag	acatgtctct	gactgtgatg	360
gcctatgacc	aatttgtggc	catctgtcac	ccctgcacta	cccagtcata	atgaatcctc	420
acctctgtgt	cttcttagtt	ttggtttctt	ttttccttag	cctgtttggat	tcccagctgc	480
acagttggat	tgtgttacaa	ttcaccttct	tcaagaatgt	ggaaatctct	aattttttct	540
gtgatccatc	tcaacttctc	aaccttgcc	gttctgacgg	catcatcaat	agcatattta	600
tatatattga	tagtattctg	ttcagttttc	ttccatttcc	agggatcctt	ttgtcttact	660
ataaaaattgt	cccctccatt	ctaagaattt	catcgtcaga	tgggaagtat	aaagccttct	720
ccatctgtgg	ctctcacctg	gcagttgttt	gcttatttta	tggaaacagg	attggcgtgt	780
acctaacttc	agctgtgtca	ccacccccag	gaatgggtgtg	gtggcgctcag	tgatgtatgc	840
tgtgggcacc	cccagctgta	actcttttat	ctacagcctg	agaaacaggg	acattcaaa	900
cgccctgtgg	aggctgcgca	gcagaacagt	cgaatctcat	gatctgttcc	atccttattc	960
ttgtgt						966

&lt;210&gt; 478

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g327 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 478

atgcaacccat	ataccaaaaa	ctggacccag	gtaactgaat	ttgtcatgat	gggctttgct	60
ggcatccatg	aagcacacct	cctctttctt	atactcttcc	tcacccatgta	cctgttcacc	120
ttgggtggaga	atttggccat	catttttagtg	gtgggtttgg	accaccgact	acggagaccc	180
atgtatttct	tcctgacaca	cttgtcctgc	cttgaaatct	ggtacacttc	tggtacagtg	240
cccaagatgc	tggtctgggtt	tattgggggtg	gatgggtggca	agaatatctc	ttatgctggt	300
tgcctatccc	agctcttcat	cttcaccttt	cttggggcaa	ctgagtgttt	cctactggct	360
gccatggcct	atgatcggtta	tgtggccatt	tgtatgcctc	tccactatgg	ggcttttgtg	420
tcctggggca	cctgcatccg	tctggcagct	gcctgttggc	tggtagggtt	cctcacaccc	480
atcttgccaa	tctacctctt	gtctcagcta	acattttgtg	gccccaaatgt	cattgacccat	540
ttctcctgtg	atgcctcacc	cttgctagcc	ttgtcgtgct	cagatgtcac	ttggaaggag	600
actgtggatt	tcctgggtgc	tctggctgtg	ctactggcct	cctctatggt	cattgctgtg	660
tcctatggca	acatcgctcg	gacactgctg	cacatccgct	cagctgctga	gcgctggaag	720
gccttctcta	cctgtgcagc	tcacctgact	gtgggtgagcc	tcttctatgg	cactcttttc	780
tttatgtatg	tccagaccaa	ggtgacctcc	tccatcaact	tcaacaaggt	ggtatctgtc	840
ttctactctg	ttgtcacgcc	catgctcaat	cctctcatct	acagtcttag	gaacaaggaa	900
gtgaagggag	ctctgggtcg	agtcttttct	ctcaactttt	ggaagggaca	g	951

&lt;210&gt; 479

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g328 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 479

atggatggag	agaatcactc	agtggatatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcgt	tgggtggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagcccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcctttcat	ttctggctgt	tgcctggacc	cttgggtgtca	gtcactccct	gttccaactg	480
gcatttcttg	ttaatttacc	cttctgtggc	cctaattgtgt	tggacagctt	ctactgtgac	540
cttcctcagc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggtcact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaacttc	ctacatcttc	660
atcctgttta	ctgtttggaa	acattcctca	ggtgttctcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagcggg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacatgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatatt	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagaag	atctca			936

&lt;210&gt; 480

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g329 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 480

gtgaggcacc	ccctgcgatg	cggggaagtaa	gagccagccc	ctctcccacc	cctggctctt	60
aggaacccca	tcatgacctc	gtgtttctgt	ggctttctag	ttttgtcttt	tttttttttt	120

ttctcagtc	tttagacgcc	cagctgcaca	acttgattgc	cttacaaatg	acctgcttcc	180
aggatgcgga	aattcctagt	ttcttctgtg	acccttctca	actcccccat	cttgcatggt	240
gtgacacctt	caccaataac	ataatcatgt	atttgctgc	tgccatattt	ggttttcttc	300
ccatctcggg	gacccttttc	tcttactata	aaattgtttc	ctccattctg	aggggttcat	360
catcacgtgg	gaagtataag	gccttctcca	cctgtgggtc	tcacctgtca	gttggttgct	420
gattttacgg	aacaggcttt	ggagggtacc	tcagttcaga	tgtgtcatct	tccccgagaa	480
aggctgcagt	ggcctcagtg	atgtacacgg	tgatcacctc	catgctgaac	cccttcatct	540
acagcctgag	aaacagggat	attaaagggtg	tcctgcgcca	gccgcacggc	agcaccgtcc	600
aatttcagta	tcttcttata	tgttccattc	cttttgtagt	gtgggttaaa	aaaggcagca	660
aggtcaaa						668

&lt;210&gt; 481

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g330 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 481

atgtacctgg	tcacgggtgct	gaggaacctg	ctcatcatcc	tggtgtgcag	ctctgactcc	60
cacctccaca	cccccatgtg	cttcttcctc	tccaacctgt	gctgggctga	catcggtttc	120
acctcgggcca	tggttcccaa	gatgattgtg	gacatgcagt	cgcatagcag	agtcattctt	180
tatgcgggct	gcctgacaca	gatgtctttc	tttgtccttt	ttgcatgtat	agaagacatg	240
ctcctgacag	tgatggccta	tgaccgattt	gtggccatct	gtcacccctc	gcactaccac	300
gtcatcatga	atcctcacct	tggtgtcttc	ttagtttttg	tgctcctttt	cctcagcctg	360
ttggattccc	agctgcacag	ttggattgtg	ttacaattca	ccttcttcaa	gaatgtggaa	420
atctccaatt	ttgtctgtga	cccattctca	cttctcaacc	ttgcctgttc	tgacagtgtc	480
atcaatagca	tattcatata	tttagatagt	attatgtttg	gttttcttcc	catttcaggg	540
atccttttgt	cttacgctaa	caatgtcccc	tccattctaa	gaatttcac	atcagatagg	600
aagtctaaag	ccttctccac	ctgtggctct	cacctggcag	ttgtttgctt	attttatgga	660
acaggcattg	gcgtgtacct	gacttcagct	gtgtcaccac	ccccaggaa	tggtgtgggtg	720
gcatcagtg	tgtacgctgt	ggtcaccccc	atgctgaacc	ctttcatcta	cagcctgaga	780
aatagggaca	ttcaaagtgc	cctgtggagg	ctgcgcagca	gaacagtcga	atctcatgat	840

&lt;210&gt; 482

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g331 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 482

atggaaacac	agaacctcac	agtggtgaca	gaattcattc	ttcttgggtc	gacccagtct	60
caagatgctc	aacttctggg	ctttgtgcta	gtcttaattt	tctaccttat	catcctccct	120
ggaaatttcc	tcatcatttt	caccataaag	tcagacctg	ggctcacagc	ccccctctat	180
ttctttctgg	gcaacttgge	cttactggat	gcatcctact	ccttcattgt	ggttcccagg	240
atgtttgggtg	acttccctctc	tgagaagaag	gtaatctcct	atagaagctg	catcactcag	300
ctctttttct	tgcattttct	tggagcgggg	gagatgttcc	tcctcgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggccttta	cactattcaa	ccatcatgaa	ccctagagcc	420
tgctatgcat	tatcggtggg	tctgtggctt	gggggcttta	tccattccat	tgtacaagta	480
gcccttatcc	tgcaattgce	tttctgtggc	ccaaaccagc	tcgataaact	cttctgtgat	540
gttccacagg	tcataagct	ggcctgcacc	aatacctttg	tggtggagct	tctgatgggtc	600
tccaacagtg	gcctgctcag	cctcctgtgc	ttcctgggcc	ttctggcctc	ctatgcagtc	660
atcctctgtc	gtataaggga	gcaactcctc	gaaggaaaga	gcaaggctat	ttccacatgc	720
accacccata	ttatcattat	atttctcatg	tttggacctg	ctattttcat	ctacacttgc	780
cccttccagg	ctttcccgag	tgacaaggta	gtttctcttt	tccatactgt	catctttcct	840
ttgatgaacc	cgtttattta	tacgcttcgc	aaccaggagg	tgaaagcttc	catgaggaag	900
ttgttaagtc	aacatatggt	ttgc				924

<210> 483  
 <211> 457  
 <212> DNA  
 <213> Unknown (H38g332 nucleotide)

<220>  
 <223> Synthetic construct

<400> 483  
 gggatgagaa aggaacaagc tgtctgtggt agtcatccat gattgagatg atgtgtggac 60  
 cctgagtcag actacctggt tcaaatgcag gctctctact ttttaccat ttgatcttgg 120  
 cctgtggctc tctacttctt atccatttca tcttggactt gtggcctctc atacctcatc 180  
 ttcctttacag tctccatat gaaatcccc taaagtagga acaaagcttt ggccaactgc 240  
 tctctccatc tttccgtggt ctttacttag gaactgtgtg tttaataatac gtgacacagg 300  
 gtttctccca catccctgag cagaaacaag ctgtgtctgt attttgcact gtactcaccc 360  
 ccatgctaaa cccctcatc tacatcctga gaaacaagga tgtggtgggg ctcttcagaa 420  
 agttctggga acacatcaag tctctaaaca gaacaca 457

<210> 484  
 <211> 972  
 <212> DNA  
 <213> Unknown (H38g333 nucleotide)

<220>  
 <223> Synthetic construct

<400> 484  
 atgtctttct tctttgtaga cttaagaccc atgaacaggt cagcaacaca catcgtgaca 60  
 gagtttatte tcttgggatt ccctgggtgc tgggaagattc agattttcct cttctcattg 120  
 tttttggtga tttatgtctt gaccttgctg ggaatggag ccatcatcta tgcagtgaga 180  
 tgcaaccac tactacacac ccccatgtac tttctgctgg gaaattttgc cttccttgag 240  
 atctgggatg tgcctccac tattcctaac atgctagtca acattctctc caagaccaag 300  
 gccatctcat tttctgggtg cttcctccag ttctatttct tcttttact gggaacaact 360  
 gaatgtctct tttctggcagt aatggcttat gatcgatacc tggccatctg ccaccactg 420  
 cagtaccctg ccatcatgac tgtaagggtc tgtggtgaagc tgggtgtctt ctgttggctt 480  
 attggattcc ttggataccc aattcccatt ttctacatct cccaactccc cttctgtggt 540  
 cctaatatca ttgatcactt cctgtgtgac atggacccat tgatggctct atcctgtgac 600  
 ccagctccca taactgaatg tattttctat actcagagct cccttgtcct ctttttact 660  
 agtatgtaca ttcttcgatc ctatatacctg ttactaacag ctgtttttca ggtcccttct 720  
 gcagctggtc ggagaaaagc cttctctacc tgtggttctc atttggttgt ggtatctctt 780  
 ttctatggga cagtcatggt aatgtatgta agtcctacat atgggatccc aactttattg 840  
 cagaagatcc tcacactggt atattcagta acgactcctc tttttaatcc tctgatctat 900  
 actcttcgta ataaggacat gaaactcgct ctgagaaatg tctgttttgg aatgagaatt 960  
 cgtcaaaatt cg 972

<210> 485  
 <211> 945  
 <212> DNA  
 <213> Unknown (H38g334 nucleotide)

<220>  
 <223> Synthetic construct

<400> 485  
 atggccaaca tcaccaggat ggccaaccac actggaaagt tggatttcat cctcatggga 60  
 ctcttcagac gatccaaaca tccagctcta cttagtgtgg tcatctttgt ggttttccctg 120  
 aaggcgttgt ctggaaatgc tgctctgac cttctgatac actgtgacgc ccacctccac 180  
 agccccatgt actttttcat cagtcaattg tctctcatgg acatggcgta catttctgtc 240  
 actgtgcccc agatgctcct ggaccaggtc atgggtgtga ataaggctc agccccctgag 300  
 tgtgggatgc agatgttccct ctatctgaca ctaggaggt cggaattttt ctttctagcc 360  
 accatggcct atgaccgcta cgtggccatc tgccatcctc tccgttaccc tgtcctcatg 420

aaccataggg	tctgtctttt	cctggcatcg	ggctgctggt	tcctgggctc	agtggatggc	480
ttcatgctca	ctcccatcac	catgagcttc	ccctctctgca	gatcctggga	gattcatcat	540
ttcttctgtg	aagtcctctg	tgtaacgac	ctgtcctgct	cagacacctc	actctatgag	600
accctcatgt	acctatgctg	tgctcctcatg	ctcctcatcc	ctgtgacgat	catttcaagc	660
tcctatttac	tcctcctcct	caccgtccac	aggatgaact	cagcagaggg	ccggaaaaag	720
gcctttgcca	cctgtcctc	ccacctgact	gtgggtcatcc	tcttctatgg	ggctgccgtc	780
tacacctaca	tgctccccag	ctcctaccac	acccctgaga	aggacatgat	ggtatctgtc	840
ttctatacca	tcctcactcc	ggtgctgaac	cctttaatct	atagtccttag	gaataaggat	900
gtcatggggg	ctctgaagaa	aatgttaact	gtgagattcg	tcctt		945

&lt;210&gt; 486

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g335 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 486

agccacctct	ccgtcattga	cacattatac	atctccacca	ttgtgcccaa	gatgctggta	60
gattatctca	tgggcgaggg	gaccatctct	ttcatcgctt	gcactgctca	gtgctttctc	120
tacatgggct	ttatgggggc	tgaattcttc	ctgctggggc	tcattggccta	tgaccgctac	180
gtggccatct	gcaacccact	gcgtatcct	gtcctcatca	gctggcgggt	ctgctggatg	240
atcctggcca	gctcttggtt	cgggtggggc	ttggacagtt	ttctcctcac	ccccattacc	300
atgagtctcc	cgttctgtgc	ctctcaccaa	atcaatcact	ttttctgtga	ggcaccacc	360
atgctgaggg	tggcctgtgg	ggacaaaacc	acctatgaaa	cagtgatgta	tgtgtgctgc	420
gttgaatgc	tgctgatccc	cttctcggtg	gtgactgcat	cctacaccag	gattctcatc	480
acagtgcac	agatgacatc	ggctgaaggg	aggaagaagg	cctttgccac	ctgctcttca	540
cacatgatgg	tggtagacatt	gttctatggg	gctgccttgt	atacgtatac	gcttccccaa	600
tcttaccaca	ccccaatcaa	agataaggtc	ttctctgcct	tttataccat	cctcacaccc	660
ttattaaacc	ctctcatcta	cagtctgagg	aacagggatg	tgatgggtgc	cttgaagaga	720
gttgtggcaa	gatgttaggg	gacatgtggt	gtgatgagg			759

&lt;210&gt; 487

&lt;211&gt; 857

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g336 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 487

gtttttctccc	gcacccgggt	tcgcctcaat	tgcaaacgca	tattctggct	aacgccagtc	60
ttttttttgt	ccccctcatg	cccattctct	atcgagtggt	ctaagagtgc	agtcagcttc	120
gtgtcacaga	gcaggcgcat	tagattttttg	ggctgtgaca	ttcaaacggg	atgtgttcct	180
gggcccctgg	gggaactgaa	gcccttctct	ttgggtttat	gtcttatgat	cgctatgtag	240
ctatctgtca	ccctttacat	tatcctatgc	ttatgagcaa	gaagatctgc	tgccctcatgg	300
ttgcatgtgc	atgggccagt	ggttctatca	atgcttttcat	acatacattg	tatgtgtttc	360
agcttccatt	ctgtaggtct	cggctcatta	accacttttt	ctgtgaagtt	ccagctctac	420
tatcattgggt	gtgtcaggac	acctcccagt	atgagtatac	agtcctcctg	agtggaactta	480
ttatcttgct	actaccattc	ctagccattc	tggcttccta	tgctcgtgtg	cttattgtgg	540
tattccagat	gagctcagga	aaaggacagg	caaaagctgt	ttccacttgt	tcctcccacc	600
tgattgtggc	aagcctgttc	tatgcaacca	ctctctttac	ctacacaagg	ccacactcct	660
tgcggtcccc	ttcacgggat	aaggcgggtg	cagtatttta	caccattgtc	acacctctac	720
tgaacccatt	tatctacagc	ctgagaaata	aggaagtgc	gggggcagtg	aggagactgt	780
tgggatattg	gatatgctgt	agaaaatatg	acttcagatc	tctgtattga	ttgagcatta	840
acaacataaa	aagctgt					857

&lt;210&gt; 488

&lt;211&gt; 812

&lt;212&gt; DNA

<213> Unknown (H38g337 nucleotide)

<220>

<223> Synthetic construct

<400> 488

agaagggaca	ttttctattt	tgccttcatt	tgtagctatt	catgactgac	tctccgttct	60
tttgtctact	tgttcatccg	tccatccatc	catccatcca	tccactcagc	cattcttttg	120
ttcaacagtg	atttactgaa	ttccttacta	tgactcttct	atatttgaca	tgccacacga	180
tgttcagcaa	tgactttctac	tcaagagcta	gttttttagtt	tcacactgct	tttctcttgt	240
tctttatctt	ttgcttttgt	agctcagaac	agaaaaatct	atagaaaaga	tcttgctacc	300
aggctatggg	accctcttgt	ccatggcgat	atcttactgt	ctttgtgtct	ttgggctgag	360
caatcctgca	gcatgggtga	tgctcaataa	tgctcatgga	acaaaatggt	gtgggttcctc	420
ttccaggaag	tgctgccatc	tctcttttga	ttgagaatag	gtttacctag	gtgattacat	480
cactaacatt	gtattcctgt	gatttcttcc	tcatgatagg	acagatttta	ctaaaaagtc	540
aaaaattatt	tattacatta	tgccgttcct	cttacttttc	atgccagatt	aaattttctt	600
ggtccttcaa	tgcccacttc	taatatcaat	aaacaagtaa	cctttcccca	acctactgaa	660
gtcgccatgt	ggaattgggc	attctttctg	ttgattccat	atcatccctt	tcattcttct	720
gtctgcccgt	ttgtccatcc	atztatccat	ccacttagct	attcgttcgt	tcaacaatga	780
tttagtgaat	acctacttac	tgtgacccta	tt			812

<210> 489

<211> 931

<212> DNA

<213> Unknown (H38g338 nucleotide)

<220>

<223> Synthetic construct

<400> 489

atgtcattag	ctgaaggaaa	tcagagttct	ggagccgtat	ttaccctctt	gggctttctca	60
gaatatgcag	acctccaggt	tctctgttcc	ctggcttctc	tgaccatcta	cacaatcact	120
gtattgggaa	acctgggcat	gatcatgata	atcaggatca	accccaact	ccacaccgc	180
atgtactttt	tcctcagcca	cttgtccttt	gttgatttct	gttattccac	cacagttaca	240
cccaactgc	tggaagaact	ggttgtggaa	gacagaacca	tctccttcac	aggatgcac	300
atgcaattct	tcttggcggt	tatatgtgca	gtggcagaaa	cattcatgct	ggcagtgatg	360
gcctatgatt	gatacgtggc	ggtgtgtaac	cctttgtctc	acacagttgt	caggtcccag	420
aaactctgtg	catcattagt	ggcagggccc	tacacatggg	gtataatctc	ttctctgaca	480
ctcacctatt	tctctttgtc	attatccttc	tgtgggtcta	acatcatcaa	taattttgtc	540
tgtgagcact	ctgtcatcat	ctctgtctcc	tgctctgacc	cctacatcag	ccaaatgctt	600
tgttttgtca	ttgcaatatt	caatgaggtg	agcagcttgg	gagtcacctc	cactacctat	660
attttcatct	ttattgctgt	cataaaaatg	ccttctgtgt	ttgggcacca	aaaagctttc	720
tctacctgtg	cttcccacct	gactgccatc	actattttcc	acgggactgt	cctgttcctt	780
tattgtgtac	ccaactccaa	aaactcatgg	ctcatagtca	aagtaggttc	tgtgttttat	840
acagtcatca	tccccacgtt	gaacccttta	acctacagcc	tcaggaacaa	agacgtgaaa	900
gagagtgttc	gaaagttaat	gaatcactca	a			931

<210> 490

<211> 651

<212> DNA

<213> Unknown (H38g339 nucleotide)

<220>

<223> Synthetic construct

<400> 490

ttcttgggtcc	tttttgcatg	tatagaagac	atgttctctga	ctgtgatggc	ctatgactgc	60
tttatagcca	tctgtcatcc	tctgcactac	ccagtcctcg	tgaatcctca	cctctgtgtc	120
ttcttcatct	tggtgtcctt	tttccattagc	ctgttggatt	cccagctgca	tagctggatt	180
gtgttacaat	tcaccatcat	caagaatgtg	gaagtctcta	attttgtctg	tgacccctct	240
caactttctca	aacttgcttg	ttctgacagc	gtcatcaata	gcatattcat	atatttcgat	300

aatactatgt	ttgggttttct	tcccatttca	gggatccttt	ggtcttacta	taaaatcgct	360
ccctacattc	tcaggatttc	atcgtcagat	gggaagtata	aagccttcgc	cacctgtggc	420
tctcacctgg	cagttgcttg	ctgattttat	ggaacaggca	ttggcatgta	cctgacttca	480
gctgtgtcac	cacccccag	gaatggtgtg	gtggcatcag	tgatgtacgc	tgtggtcacc	540
cccatgtga	acctttttat	ctacagcctg	agaaacaggg	acatacaaag	tgccctgcgg	600
aggctgcgcc	ccagaacagt	cgaatctcat	gatctgttcc	atcctttttc	t	651

&lt;210&gt; 491

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g340 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 491

atgggcaagg	aaaactgcac	cactgtggct	gagttcattc	tccttggact	atcagatgtc	60
cctgagttga	gagtcctgct	cttcctgctg	ttcctttctca	tctatggagt	cacgttggtta	120
gccaatctgg	gcatgactgc	actgattcag	gtcagctctc	ggctccacac	ccccgtgtac	180
tttttctctca	gccacttgct	ctttgtagat	ttctgctact	cctcaataat	tgtgccaaaag	240
atggttggtta	atatctttta	caaggacaaa	gccatctcct	tcctagggtg	catggtgcaa	300
ttctacttgt	tttgacatg	tggagtcact	gaggtcttcc	tgctggccgt	gatggcctat	360
gaccgctttg	tggccatctg	taacccctcg	ctgtacatgg	tgaccatgtc	tcagaagctg	420
cgtgtggagc	tgacctcttg	ctgctacttc	tgtgggacgg	tgtgttctct	gattcactcg	480
tccttagctc	ttaggacct	cttctataga	tctaagtga	ttaaccactt	cttctgtgat	540
ctacccctc	tcctaagtct	tgctgtctct	gatgtcactg	tgaatgagac	actgctgttc	600
ctggtggcca	ctttgaatga	gagtggtacc	atcatgatca	tcctcacctc	ctacctgcta	660
attctcacca	ctatcctgaa	gatacactct	gcagagagca	ggcacaaaagc	tttctccacc	720
tgtgcctccc	acctcacagc	catcactgtc	tcccatggaa	caatccttta	catttattgc	780
agggcgagtt	caggcaacag	tggagatggt	gacaaagtgg	ccaccgtgtt	ctacacagtt	840
gtgattccca	tgctgaaccc	cctgatctac	agcctgagaa	ataaggatgt	gaacaaagct	900
ctcagaaaag	tgatgggctc	caaaattcac	tcc			933

&lt;210&gt; 492

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g341 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 492

atgtttctga	cagagagaaa	tacgacatct	gaggccacat	tcactctctt	gggcttctca	60
gattacctgg	aactgcaaat	tcccctcttc	tttgtatttc	tggcagtcta	cggcttcagt	120
gtggtagggg	atcttgggat	gatagtgatc	atcaaaatta	acccaaaatt	gcataccccc	180
atgtattttt	tcctcaacca	cctctccttt	gtggatttct	gctattcctc	catcattgct	240
cccatgatgc	tggtgaacct	ggttgtagaa	gatagaacca	tttcattctc	aggatgtttg	300
gtgcaattct	ttttcttttg	cacctttgta	gtgactgaat	taattctatt	tgcggtgatg	360
gcctatgacc	actttgtggc	catttgcaat	cctctgctct	acacagttgc	catctcccag	420
aaactctgtg	ccatgctggg	ggttgatttg	tatgcatggg	gagtcgcatg	ttccctgaca	480
ctcgcgtgct	ctgctttaaa	gttatctttt	catggtttca	acacaatcaa	tcatttcttc	540
tgtgagttat	cctccctgat	atcactctct	taccctgact	cttatctcag	ccagttgctt	600
cttttccactg	ttgccacttt	taatgagata	agcacactac	tcatcattct	gacatcttat	660
gcattcatca	ttgtcaccac	cttgaagatg	ccttcagcca	gtgggcaccg	caaagtcttc	720
tccacctgtg	cctcccacct	gactgccatc	accatcttcc	atggcaccat	cctcttcttc	780
tactgtgtga	ccaactccaa	aaactccagg	cacacagtca	aagtggcctc	tgtgttttac	840
accgtggtga	tccccttggt	gaatcccctg	atctacagtc	tgagaaataa	agatgttaag	900
gatgcaatcc	gaaaaataat	caatacaaaa	tattttcata	ttaaacaatag	gcattggtat	960
cca						963

&lt;210&gt; 493

<211> 303  
 <212> DNA  
 <213> Unknown (H38g342 nucleotide)

<220>

<223> Synthetic construct

<400> 493

tgttgcccac	tccaccacca	ttacctgcct	agacagtcac	tggatcagct	cacatactta	60
attgctttga	ttttcaattt	tctctttgtt	tttggcctcc	agagtccctt	tattttctta	120
aaggcatgac	agtgccttcc	aaaggatata	cactatattt	tcgttaaggc	gagaagggct	180
tcaggttatc	taacctacca	tattgctgga	aatagaagtt	aaaccgtttt	tttcctagtc	240
tgtaactgcc	actattatgg	tgatgatata	ggctaagtct	gaatatttta	tgtgaacata	300
tta						303

<210> 494

<211> 957

<212> DNA

<213> Unknown (H38g343 nucleotide)

<220>

<223> Synthetic construct

<400> 494

atgcctgtgg	ggaaacttgt	cttcaaccag	tctgagccca	ctgagtttgt	gttccgtgcg	60
ttcaccacag	ccactgaatt	ccaggttctt	ctcttccttc	tcttctcctt	cctctacttg	120
atgatcctct	gtggcaacac	agccatcatc	tgggtggtgt	gcacacacag	caccctccgc	180
accccgatgt	atttcttctt	gtccaacctg	tctttcctgg	aactctgcta	caccaccgtg	240
gtagtaccct	tgatgctttc	caacattttg	ggggcccaga	agcccatttc	gttggtcgga	300
tgtggggccc	aaatgttctt	ctttgtcacc	ctcggcagca	cggactgttt	cctcttggcg	360
atcatggcct	atgaccgcta	tgtggctatc	tgccaccgcg	tgcactacac	cctcatcatg	420
acccgcgagc	tggtcacgca	gatgctgggt	ggggccctgg	gcctggccct	cttcccctcc	480
ctgcagctca	cgcctttaat	cttcaccctg	cccttttgcg	gccaccacca	ggaaatcaac	540
cacttctctt	gcgatgtgcc	tcccgtctct	cgcctggcct	gcgctgacat	cgcgctgcac	600
caggctgtcc	tctatgtcgt	gagcatcctc	gtgctgacca	tccccttcct	gctcatctgc	660
gtctcctacg	tggtcatcac	ctgtgccatc	ctgagcatcc	gttctgccga	gggccgcgcg	720
cgggccttct	ccacctgctc	cttccacctc	accgtggctc	tgctgcagta	tggctgtctg	780
agcctcgtgt	acctgcgtcc	tcggctccagc	acctcagagg	atgaggacag	ccaaatcgcg	840
ttggtctaca	cctttgtcac	ccccttactc	aaccttttgc	tttacagcct	taggaacaag	900
gatgtcaaag	gtgctctgag	gagtgcatt	atccgtaaag	cagcctctga	cgccaac	957

<210> 495

<211> 624

<212> DNA

<213> Unknown (H38g344 nucleotide)

<220>

<223> Synthetic construct

<400> 495

atggagctgg	agaatggcac	tgtgaagact	gggttctttc	tcctgggatt	cagcgaccat	60
ctggaacttc	agagtctcct	ttttgcagaa	tttttttcca	tctactctgt	tactctgatg	120
gggaaccttg	gaatgatttt	attaatcaca	atcagttccc	acttgcacac	tcctatgtac	180
tttttctctt	gtgtgttgtc	cttcatagat	gcatgctact	cttctgtcat	tgctcccaaa	240
ttacttgtga	acttgggttc	tgaaaagaag	accatttctt	acaatggctg	tggtgcacag	300
ttatatttct	tctgctcttt	agttgacaca	gaatctttcc	tcttggctgc	catggcttaa	360
gaccggtaca	tagcaatctg	taaccgcgtg	ctctatacag	tgattatgtc	caagaaggtt	420
tgttgccagc	ttgcaattgg	agcatttttg	gggggacta	tgagctcaat	tattcatacc	480
acgaacactt	tcacatctgc	attctgctcc	agagatatta	accatttctt	ttgtgatata	540
tcccactctt	tctctctgtc	ctgcactgac	acatacatgc	atgacatcat	tctgggtggtc	600
tttgccagtt	ttgtggaagc	aatc				624



<210> 496  
 <211> 963  
 <212> DNA  
 <213> Unknown (H38g345 nucleotide)

<220>  
 <223> Synthetic construct

<400> 496  
 cacacagagc cacggaatct cacagggtgc tcagaattcc tcctcctggg actctcagag 60  
 gatccagaac tgcagcctgt cctccctggg ctgtccctgt ccatgtatct gctcacggtg 120  
 ctgaggaacc tgctcatcat cctggctgtc agctctgact cccacctcca caccctcatg 180  
 tacttcttcc tctccaaccc gtcattgggt gacatcgctt tcacctcggc cacagttccc 240  
 aagatgattg tggacatgca gtgcgcatagc agtcattctt tatgcaagct gcctgacaca 300  
 gatgtctttc tttgcccttt ttgcatgcat agaagatcat gctcctgatt gtgatggcct 360  
 atgaccgatt tgtagccgtc tgtcactccc cacactaccc agtcattcat aatcctcggc 420  
 tcggtgtctt cttegttttg gtgtcctttt tccttagcct gttggattcc cagctgcaca 480  
 gttggactgt gttacaattc accttcttca agaattgtga aatctctaatt tttgtctgtg 540  
 acccatctca acttctcaac cttgcctgtt ctgacagcgt catcgatagc atattcatat 600  
 atttagatag tactatgttt cgttttcttc cgatttcagg gatccttttg tcttactcta 660  
 acattgtccc ctccattcta agaatttcat catcagatgg gaagtctaaa gccttctcca 720  
 cctgtcgtc tcacctggca gttgtttgct tattttatgg aacaggcatt ggcgtgtacc 780  
 tgacttcagc tgtggcacca cccccaggag tgggtgtgtg gtgtcagtga tgtacactgt 840  
 ggtcaccccc atgctgaacc ctttcatcta ctgcctgaga aacagggaca ttcaaagcgc 900  
 cctgtggagg ctgcgcagca gaacagtcga atctcatgat ctgttccatc ctttttcttg 960  
 tgt 963

<210> 497  
 <211> 932  
 <212> DNA  
 <213> Unknown (H38g346 nucleotide)

<220>  
 <223> Synthetic construct

<400> 497  
 gaaaagaatc tcattcttat gaatgggttt atgaacttca ctgattaccc agagttggaa 60  
 atgcccttgt tcttagtgtt tctcagttgc ttccctggcca ttattttgag aaatatggaa 120  
 tgggtcattc tgaccaaggt gaatgtgcat ctcttcaccc tatatacttc ttcctaacia 180  
 atgtcaccct ttgggatacc tcagtcatca tgcctcagat cctggccatt ctggccacag 240  
 gcaagacaac catttccfat ggccgctaata aaaagcaatg aggtcctttt tcttcatttg 300  
 tgtaggaact tagtgtttcc tgccaacagc aatgaccata agcagccac tgccccacac 360  
 tacaagccat gaacttcaag acatgttggg gttttttttt ggtggggatt tgttgttga 420  
 catgctgggt tttgatgggt aacgtgggtga atgcctacac ctgaggacta tcaggagcca 480  
 ctttcaacac catctgcaca tttgcccgct tcttctgtga tgacaattag atcaaattct 540  
 gtcacatcct gccctgctg aagctcattt gaaatacttc aggaaacagc aagataatta 600  
 ttgtgatctt tgacagcttt tatgattata gctggcacta gggtcacct gatctcttac 660  
 ctgctaataca tcagggtttt gaggatgaaa tcatcgagtg gcaaagccaa taattttatc 720  
 catccacttg tgectccac ctaactgcta tgaccttctt ttgggatccc catcttcaga 780  
 catgtgaagt acctcagata aatcactgac agaagacaag ttggcatcat gacttgcacc 840  
 atctttattc ctatgctaga acttttgatc caaagtctaa agaaggatat acaagttgcc 900  
 ttcaaaaagg ccataggtaa cttctgggtt tt 932

<210> 498  
 <211> 1005  
 <212> DNA  
 <213> Unknown (H38g347 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 498

tctacagacc	cacagaatct	aacagatgtc	tctatatattcc	tcctccgaga	acctcagagg	60
atccagaatg	gcagctgggc	cttgctgggt	tggttctgtc	catgtgcctg	gtaacgggtgc	120
tggggaacct	gtcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acttcttcc	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acggtagcca	240
agatgattgt	ggacatccaa	tctcacagca	gagtcattct	ctatgcaggc	tgcttgactc	300
agatgtctcc	ctttgccatt	tttggagtca	tggaagagag	acacgctcct	gagtgtgatg	360
gcctctgacc	gctttgtagc	catctgtcac	cctctatatc	attcagccat	catgaacccg	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttt	tttctgtcct	ttagatgccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctgtga	cccttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaataaca	600
taatcatgta	tttccctgct	gccatatttg	gttttcttcc	catctcggtt	tcccttttct	660
cttactataa	aattgtttcc	tccattctga	gggtttcatc	atcaggtggg	aagtattagg	720
ccttctcttc	ctgttggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggcggtg	780
gaggtagctc	agttgagatg	tgcatcttcc	cccaggaag	gttgtagtgg	cctcagtgat	840
gtacatgggt	gtcaccctca	tgctgaaccc	ctttgtctac	agcctgagaa	acagggatat	900
taaaagtgtc	ctgcgggtgc	cgcacggcag	cacggtctaa	tctcaatata	ttcttatctg	960
ttccattcct	tttgtagtgt	aggttaaaaa	ggcagcaagg	tcaaaa		1005

&lt;210&gt; 499

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g348 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 499

atgaagactt	ttagttcctt	tcttcagatc	ggcagaaata	tgcatcaagg	aaaccaaacc	60
accatcactg	aattcattct	cctgggattt	ttcaagcagg	atgagcatca	aaacctcttc	120
tttgtgtctt	tcttggtgat	gtacctgggc	actgtgattg	ggaacgggct	catcattgtg	180
gctatcagct	tgatagcgta	ccttcatacc	cccatgtatc	tcttccttgc	caatctatcc	240
tttgctgata	tttccctccat	ttccaactca	gtccccaaaa	tgctggtgaa	tattcaaacc	300
aagagtcaat	ccatctctta	tgagagctgc	atcacacaga	tgtacttttc	tatttgtgtt	360
gtcgtcattg	acaatttgct	cttggggacc	atggcctatg	accactttgt	ggcgatctgc	420
cacctcttga	attatacaat	tctcatgcgg	cccaggttcg	gcattttgct	cacagtcac	480
tcattggttc	tcagtaatat	tattgctctg	acacacaccc	ttctgtctcat	ccaattgctc	540
ttctgtaacc	acaacactct	cccacacttc	ttctgtgact	tgccccctct	gctcaaactg	600
tctgtttcag	atacattgat	caatgagctt	gtgttggtta	ttgtgggttt	atcagttatc	660
atcttccctt	ttacactcag	cttcttttcc	tatgtctgca	tcacagagc	tgctctgaga	720
gtatcttcca	cacagggaaa	gtggaaagcc	ttctccactt	gtggctctca	cctgacagtt	780
gtattactgt	tctacggaac	cattgttaggc	gtgtactttt	ttccctcctc	cactcaccct	840
gaggacactg	ataagattgg	tgctgtccta	ttcactgtgg	tgacacccat	gataaaccct	900
ttcatctaca	gcttgaggaa	taaggatatg	aaagggtgcc	tgagaaagct	catcaataga	960
aaaatttctt	ccctt					975

&lt;210&gt; 500

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g349 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 500

atgtactttt	tcctcagtea	tctatccttt	ttggatactt	gttatttcaa	tgtattttaca	60
cccaaaactgt	tagagatttt	ggttggtgaa	gacagaacta	tctccttcaa	aggatgcatg	120
gtacaatttt	tctttggttg	tgcatgtgta	atcacagaaa	tggtcatgtt	agcggtgatg	180
gcttatgact	tgtttatggc	tgtttgtaac	cccctgctct	acacagtggc	tatgtctcct	240
aagctctgtg	ctctcctggg	agctggaact	tacacatggg	gtggactctg	ttccctgaca	300

ctcacttatt	ctcttttggg	gttatcctac	tgtggatcta	acatcataaa	tcactttggc	360
tgtgagtact	ctgccattct	ttctctatcc	tgtctctgac	cctacttcaa	ccagatggcg	420
tgttttagtca	tttctatatt	cagtgaagct	tgtagcctcc	tggccatcct	tgccttctat	480
gtcttcatag	ttgccactgt	catcaagatg	ctttctacgg	gtggacccca	aaaggccatc	540
tccacctgtg	cctccacact	gaccacgctc	tccattttcc	atgggggtcat	cctgctcctt	600
tactgtgtgc	ccaactccaa	aagctcatgg	ctcctgggtca	aagtgggtac	tgtacttttt	660
acagtcataa	tccctatgct	gaatcccctg	atctacagcc	ttaggaacaa	agatgtaaaa	720
gggaccgtca	ggaagttgat	aaactcccaa	tcaccttttc	actcaaaa		768

&lt;210&gt; 501

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g350 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 501

atggcagaga	gtggcaccac	ggtgacagaa	ttttttctga	gggggttccg	gttgaaggca	60
gagctgcaga	taggtctctt	ctttgtgttt	ctggtcattt	ttctcatcac	catggggggc	120
aacctgggca	tgattgtgct	aatttaattc	agactgaccc	tgggtccag	actcccatgt	180
acttcttct	cagtcattct	tccttcctgg	acatttgcta	ctcttctgtt	attggctctc	240
agttgcttga	gactttggga	ctgataagat	gatcatcacc	tatgagcgt	gtgccagcca	300
attcttcttt	ttcacactct	gtgctagcat	tgagtgtttc	cttttggtg	tgatggctta	360
tgaccggtag	gtggctgtgt	gtaacccct	cctctatgcc	atagtcatga	caccaaagac	420
ccgctggcg	ctgctggccg	gggcatattc	tggtgccata	gtcaattctg	tgatctgcac	480
tggtgcacc	ttctctatct	ccttctctaa	gtccaaccat	gtagacttct	ttttctgtga	540
cctccacccc	ctgctgaagc	ttgcctgtag	tgaaccagg	ccacgggaat	gggtaatcta	600
cctctcagct	tttctggtca	tcacaaccag	catttcagtg	attcttacat	cgtacttggt	660
catcattcag	tctgttctga	agattcgtac	agcaggtgga	aagccaagac	cttctccacc	720
tgtgttctc	acatgactgc	attgactctc	ttctttggaa	cactcatatt	catatacttg	780
aaaggcaaca	tgggcgaatc	ccttgaggaa	gacaagatcg	tgtcaatatt	ttacactgtg	840
gtcatcccca	tgctaaatcc	aatgatctac	agcctgagaa	acaaagacat	gaaagaggct	900
ctgaagaaa	gtttcaacag	gataagggtt	tcccaagcag	agtaactctt	g	951

&lt;210&gt; 502

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g351 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 502

atgctgctga	cagatagaaa	tacaagtggg	accacgttca	ccctcttggg	cttctcagat	60
taccagaac	tgcaagtccc	actcttctct	gtttttctgg	ccatctacaa	tgtcactgtg	120
ctaggaata	ttgggttgat	tgtgatcatc	aaaatcaacc	ccaaactgca	taccccatg	180
tactttttcc	tcagccaact	ctcctttgtg	gatttctgct	attcctccat	cattgctccc	240
aagatgttgg	tgaaccttgt	tgtcaaagac	agaaccattt	catttttagg	atgcgtagta	300
caattctttt	tcttctgtac	ctttgtggtc	actgaatcct	ttttattagc	tgtgatggcc	360
tatgaccgct	tcgtggccat	ttgcaaccct	ctgctctaca	cagttgacat	gtcccagaaa	420
ctctgcgtgc	tgctggttgt	gggatcctat	gcctggggag	tctcatgttc	cttgggaactg	480
acgtgctctg	ctttaaagtt	atgttttcat	ggtttcaaca	caatcaatca	cttcttctgt	540
gagttctcct	cactactctc	cctttcttgc	tctgatactt	acatcaacca	gtggctgcta	600
ttctttcttg	ccacctttta	tgaatcagc	acactactca	tcgttctcac	atcttatgcg	660
ttcattgttg	taaccatcct	caagatgcgt	tcagtcatgt	ggcgccgcaa	agccttctcc	720
acctgtgcct	cccacctgac	tgccatcacc	atcttccatg	gcaccatcct	cttcttttac	780
tgtgtgccca	actccaaaaa	ctccaggcac	acagtcaaag	tggcctctgt	gttttacacc	840
gtgggtatcc	ccatgttgaa	tcccctgata	tacagtctga	gaaataaaga	tgtcaaggat	900
acagtcaccg	agatactgga	caccaaagtc	ttctctttac			939

<210> 503  
 <211> 932  
 <212> DNA  
 <213> Unknown (H38g352 nucleotide)

<220>  
 <223> Synthetic construct

<400> 503  
 atggctgaaa ggaattacac cgtagtgacg gagttcttcc ttactgcatt tactgaacat 60  
 ctccagtgga ggggttcctct cttcctcata tttttgagtt tctatcttgc cactatgtta 120  
 gggaacacag gcatgatcct cctgatccgt ggcatcgtc ggctccacac cccgatgtac 180  
 ttcttctctca gccaccttct cttggtggac atctgctact cgtccgccat catccctcag 240  
 atgctggctg tgctgtggga gcacggcaca accatctccc aggtcgcgtg tgcagctcag 300  
 ttcttctctct tcaccttctt tgctccatc gactgctacc ttctggccat catgcctatg 360  
 accgctacac ggccgtgtgc agccctgct ttatgtcacc atcataaccg agaaggaccg 420  
 ctgggctag tcactggggc ttacgttgct ggttttttca gtgcctttgt tgcacggtca 480  
 cagccttcac tctctccttt tgtggaaaca atgagatcaa cttcatttct tgtgacctcc 540  
 ctctcttatt aaaactctcc tgtggggaca gctacactca ggaagtgggt attattgtgt 600  
 ttgctctttt cgtcatgcct gcctgtatct tgggtatctt ggtatcctac ctgtttatca 660  
 ttgtggccat cctgcagatc cactctgctg gaggccgggc caagaccttc tccacctgcg 720  
 cctccacact cactgccgtc gctcttttct ttggcaccct catcttcattg tacctgcgag 780  
 acaacacagg ccagtcctcc gagggagacc gagtggtgtc tgtgctctac acggtggtga 840  
 cccaatgct gaatcccctt atctatagcc tgagaaacaa ggaggtaaaa gaggccacta 900  
 ggaaagccct gagcaaatca aagcctgcta ga 932

<210> 504  
 <211> 762  
 <212> DNA  
 <213> Unknown (H38g353 nucleotide)

<220>  
 <223> Synthetic construct

<400> 504  
 atgtactatt tctctccat gctgtccgcc actgacctcg gcctgtccat atccactctg 60  
 gtcaccatgc tgagtatatt ctggttcaat gtgagggaaa tcagctttaa tgcctgcttg 120  
 tcccacatgt tctttattaa attcttcact gtcattggaat cctcagtgtg gttggccatg 180  
 gcttttgcac gttttgtggc cgtctctaatt ccccttaggt atgccatgat tttaactgac 240  
 tccagaatag ctcaaattgg agtggcaagt gtcacaggg ggctcctaatt gctgacacca 300  
 atggtagcac ttcttataag actttcttac tgccacagcc aagtactcca ccactcctac 360  
 tgctaccacc ctgatgtgat gaagctctca tgcacagaca ccagaatcaa cagtgcagtt 420  
 gggctgactg ccattgtctc tactgttggg ttagacttac ttctcatcct cctttcttat 480  
 gttttgatca ttaggactgt ccttagcgtt gcttcccag aagagaggaa ggaaaccttc 540  
 agtacatgtg tctccacat tgtggctttt gctatatatt acattccatt gatcagctg 600  
 tccattgttc acagatttgg gaaacaagcc ccagcctatg tacatactat gattgctaac 660  
 acctacctgc tgatctcccc tttgatgaac cctgtcatct acagtgtgaa aaccaaacag 720  
 atacgtagag ctgtgataaa aattctccat tccaaagaaa ca 762

<210> 505  
 <211> 565  
 <212> DNA  
 <213> Unknown (H38g354 nucleotide)

<220>  
 <223> Synthetic construct

<400> 505  
 atggactggg aaaattgctc ctcattaact gatttttttc tcttgggaat taccaataac 60  
 ccagagatga aagtgaccct atttgctgta ttcttggctg tttatatcat taatttctca 120  
 gcaaatcttg gaatgatagt tttaatcaga atggattacc aacttcacac accaatgtat 180

ttcttctca	gtcatctgtc	tttctgtgat	ctctgctatt	ctactgcaac	tgggccaag	240
atgctggtag	atctacttgc	caagaacaag	tcaataccct	tctatggctg	tgctctgcaa	300
ttcttgggtct	tctgtatctt	tgcagattct	gagtgtctac	tgctgtcagt	gatggccttt	360
gatcggtaca	aggccatcat	caacccccctg	ctctatacag	tcaacatgtc	tagcagagtg	420
tgctatctac	tcttgactgg	ggtttatctg	gtgggaatag	cagatgcttt	gatacatatg	480
acactggcct	tccgcctatg	cttctgtggg	tctaatagaga	ttaatcattt	cttctgtgat	540
atccccctct	ctcttattac	tctct				565

&lt;210&gt; 506

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g355 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 506

ctcaatttca	ttatcttctt	cagggtgaacc	agctatatattg	agcctatggc	caaaagaaat	60
ctcagcactg	tgacagagtt	cattctttgta	gtcttcacag	atcacccctga	actggcagtt	120
ccactcttcc	tagtgtttct	cagtttctat	cttgctcactt	ttctggggaa	tgggggggatg	180
atcattctaa	tccaagtgga	tgcccaactc	cacacccccg	tgtacttctt	cctgagccac	240
cttgctttcc	tggatgcctg	ctgtgcctca	gtaatcaccc	ctcagattct	ggccacactg	300
gccacagaca	agacagttat	ctcctatggc	tgccgtgctg	tgacagttctc	tttcttcacc	360
atatgtgcag	gcacagagtg	ttacctgctg	tcagtgtatg	cctatgaccg	ctttgttgcc	420
attagcaatc	cactgcactg	taacatgacc	atgactccag	gtacctgcag	ggtctttttg	480
gccagtgcct	tcactctgtg	ggtgtcaggg	gccattctgc	ataccacgtg	caccttcacc	540
ctctccttct	gttgtgacaa	tcagatcaac	ttcttcttct	gtgacctccc	acctctgctg	600
aagctcgctc	gcagcagcat	gacacaaact	gagattgtca	ttctcctttg	tgcaaaatgc	660
atgttcctag	ccaatgtcat	ggttatcctg	atctgctaca	tgctcattat	cagagccatt	720
ttgaggggtga	agtcggcagg	tgggtaagcc	aagaccttct	ccacctgcac	ctccccatctc	780
accactgttg	tcctcttctt	tgggacactt	gccttcatgt	accagagaag	taactccgcc	840
aaatcctcag	aggaagacaa	gatagtgtct	gtcttttaca	ctgtaatcat	ccctatgttg	900
aacctcttga	tctacagtct	gaggaacaaa	gatgtaaaa	ctgcatttgg	aaaactcggt	960
ggtaaattcc	aatttcca					978

&lt;210&gt; 507

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g356 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 507

atgtctccctt	cccagaccta	tgtcaacatc	tccttcttcc	aaccgcctgc	tcttctcatg	60
attggcatcc	cagggtctga	ggcggttcat	ggctggctcg	ccatccccctt	ctcctccatg	120
tacactgtgg	ccctccctgg	gaactgcctg	atcctcctgg	ctgtgaagag	gaaccccagc	180
ctgcaccagc	ccatgtgcta	cttctctgtc	atgtgtggcg	tcccaaaagc	gggcctcacc	240
ttgtccacac	tgcccatcac	cttggtctgtg	ctctgggttg	accaccggct	catgggcttc	300
aatgcctgcc	tggtccagat	gttcttctctg	cactcctctg	tggtggagtc	ctcagtgtctc	360
ctggccatat	cctttgacca	ctttgtggcc	atctccaacc	ccctgcacta	tgacagtgtc	420
ctcacaata	gtgtcatcat	caggattggg	ctggccattg	tggtctcaagt	tacctgtgtc	480
ctcttctctg	gccatttccg	gttaagagtc	taaatttctg	ccctgggtgat	aacatcccat	540
ccactcgtt	ctgtttccac	cctgatgtaa	tgaggcgggc	ctgtgcggac	atcacgatca	600
atatatgcta	tggggtctac	gtgggtgttt	ctacaggggg	cttagactcg	ctgctcatct	660
ttctgtccta	taccttcac	ctgcacacag	tcatgggtct	ggctgtctcc	agggagcgca	720
tctgggccct	caacacctgc	gtttcccaca	ttccggctgt	ctttgtcttc	tttattccag	780
gtatcacctg	gtccatgac	caccattttg	ggaggcacct	gccccacatt	gtacatgtctc	840
ttgttaccta	tgtgtacctg	gtgatgcctt	ctgtgtctca	ccccatcatt	tacagtatga	900
agtccaagcc	catcaggag	gccatcctca	ggatgctgat	ggggagaagc	caaggctgat	960
gaaattacaa	aatattatag	ggt				983

<210> 508  
 <211> 933  
 <212> DNA  
 <213> Unknown (H38g357 nucleotide)

<220>  
 <223> Synthetic construct

<400> 508  
 atgggcaagg aaaactgcac cactgtggct gagttcattc tccttggact atcagatgtc 60  
 cctgagttga gagtctgcct cttcctgctg ttccttctca tctatggagt cacgttgta 120  
 gccaacctgg gcatgattgc actgattcag gtcagctctc ggctccacac ccccatgtac 180  
 ttttctctca gccacttgct ctctgtagat ttctgctact cctcaataat tgtgccaaaa 240  
 atgttggcta atatctttaa caaggacaaa gccatctcct tcctaggggtg catgggtgcaa 300  
 ttctacttgt ttgcaacttg tgtggctact gaggtcttcc tgctggccgt gatggcctat 360  
 gaccgcttgg tggccatctg taacccttgg ctatacacag tcaccatgtc ttggaagggtg 420  
 cgtgtggagc tggcttcttg ctgctacttc tgtgggacgg tgtgttctct gattcatttg 480  
 tgcttagctc ttaggatccc cttctataga tctaagtga ttaaccactt tttctgtgat 540  
 ctacctctg tcttaagtct tgcttgcctc gatatcactg tgaatgagac actgctgttc 600  
 ctgggtggcca ctttgaatga gagtggtacc atcatgatca tcctcacctc ctacctgcta 660  
 attctcacca ccattctgaa gatgggctct gcagagggca ggcacaaagc cttctccacc 720  
 tgtgcttccc acctcacagc tatcactgtc ttccatggaa cagtccttct catttattgc 780  
 aggccagtt caggcaatag tggagatgct gacaaagtgg ccaccgtgtt ctacacagtc 840  
 gtgattccta tgctgaactc tgtgatctac agcctgagaa ataaagatgt gaaagaagct 900  
 ctcagaaaag tgatgggctc caaaattcac tcc 933

<210> 509  
 <211> 621  
 <212> DNA  
 <213> Unknown (H38g358 nucleotide)

<220>  
 <223> Synthetic construct

<400> 509  
 cccctctgc gatgggggtc ctaagagcca gcgagggaag aggggctggc tctcagttcc 60  
 cgcctttttt ttttttctca gtgttttaga cgcccagctg cacaacttga ttgccttaca 120  
 aatgacctgc ttccaggatg cggaaattcc taatttcttc tgtgacctt ctcaactccc 180  
 ccattctgca tgttgtaga ccttcaccaa taacataatc atgtatttcc ctgctgtcat 240  
 atttggtttt cttcccatct ctgggaccct tttctcttac tataaaattg tttcctccat 300  
 tctgagtgtt tcatcatcac gtgggcagta taaggccttc tccacctgtg ggtctcacct 360  
 gtcagttgtt tgctgatttt acggaacggg cgttggagga tacttcagtt cagatgtgtc 420  
 atcttccccg agaaaggctg cagtggcctc agtgatgtac acgggtgatca ccccatgctg 480  
 aacccttcca tctacagcct gagaaacagg catattaaaa gtgtcctgcg gcggccgcac 540  
 agcagaccg tccaatctcc gtgtcttctt aactgttcca ttccttttgt agtgtgggtt 600  
 aacaaaggca gcaaggtaaa a 621

<210> 510  
 <211> 633  
 <212> DNA  
 <213> Unknown (H38g359 nucleotide)

<220>  
 <223> Synthetic construct

<400> 510  
 atttgactga aattgatctt tggaaatcct agatagtaat agattttcag atgtgtctat 60  
 gattattttg tgggactgtc aacccttgc tttatgacacc atcacaaactc tcaagatgtc 120  
 tggcagaagc tgggtactgc atattgtaga gggtttgaca aatgtaatcc aatgtatata 180  
 cttcacctgc tcactctcct tttgtgcctt catctatagg tttcactctc tgtgacctcc 240

attgctgctg	accctgaatt	gggtgatagc	ttcctccagc	agctgctgat	ttttcacttt	300
gctctgtata	tgattctgac	cagactagtt	ttgatcctgt	tctctgactt	gttcatcagc	360
aaggccatct	aaacacctgc	aaatcaggte	tctaggcaaa	gattcctcaa	cctttttcta	420
cctttgcctc	atgcagaact	gcagttcggg	tgattgttga	gactacagct	ttgatctatg	480
tgtgcagcag	taggcaagtc	ccttacaggg	gagagggccg	tgaccatgtt	ttagactgta	540
gtgaacacca	ggctgaccat	tccaatttta	tagcctgagg	aaaaaaaggc	aaaggaggcc	600
ctgaggaaag	gtcttaataa	agccaagttg	ttc			633

&lt;210&gt; 511

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g360 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 511

atgagttcct	gcaacttcac	acatgccacc	tttgtgctta	ttgggtatccc	aggattagag	60
aaagccatt	tctgggttgg	cttccccctc	ctttccatgt	atgtagtggc	aatgtttgga	120
aactgcatcg	tggtcttcat	cgtaaggacg	gaacgcagcc	tgacgctcc	gatgtacctc	180
tttctctgca	tgcttgacgc	cattgacctg	gccttatcca	catccaccat	gcctaagatc	240
cttgcccttt	tctggtttga	ttcccagagag	attagctttg	aggectgtct	taccagatg	300
ttctttattc	atgccctctc	agccattgaa	tccaccatcc	tgctggccat	ggcctttgac	360
cgttatgtgg	ccatctgcca	cccactgcgc	catgtgcag	tgctcaacaa	tacagtaaca	420
gcccagattg	gcategtggc	tgtgggtccg	ggatccctct	ttttttccc	actgcctctg	480
ctgatcaagc	ggctggcctt	ctgccactcc	aatgtcctct	cgcactccta	ttgtgtccac	540
caggatgtaa	tgaagtggc	ctatgcagac	actttgccc	atgtggtata	tggtcttact	600
gccattctgc	tggtcatggg	cgtggacgta	atgttcatct	ccttgtccta	ttttctgata	660
atacgaacgg	ttctgcaact	gccttccaag	tcagagcggg	ccaaggcctt	tggaacctgt	720
gtgtcacaca	ttggtgtggg	actcgcttcc	tatgtgccac	ttattggcct	ctcagtggta	780
caccgctttg	gaaacagcct	tcattccatt	gtgcgtgttg	tcatgggtga	catctacctg	840
ctgctgcctc	ctgtcatcaa	tcccatcatc	tatgggtgcca	aaaccaaaca	gatcagaaca	900
cgggtgctgg	ctatgttcaa	gatcagctgt	gacaaggact	tgag		945

&lt;210&gt; 512

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g361 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 512

atgtatgcct	tgccaccct	gggtaacctg	accattgtcc	tcattcattcg	tgtggagagg	60
cgactgcatg	agcccatgta	cctcttcctg	gccatgcttt	ccactattga	cctagtccctc	120
tcctctatca	ccatgcccaa	gatggccagt	cttttcctga	tgggcatcca	ggagatcgag	180
ttcaacattt	gcctggccca	gatgttcctt	atccatgctc	tgtagccgt	ggagtcagct	240
gtcctgctgg	ccatggcttt	tgaccgcttt	gtggccattt	gccaccatt	gcgcatgct	300
tctgtgctga	caggtgtac	tgtggccaag	attggactat	ctgccctgac	cagggggttt	360
gtattcttct	tcccactgcc	cttcactctc	aagtggttgt	cctactgcca	aacacatact	420
gtcacacact	ccttctgtct	gcaccaagat	attatgaagc	tgtcctgtac	tgacaccagg	480
gtcaatgtgg	tttatggact	cttcactc	ctctcagtc	tggtgtgga	ctctctcttc	540
attggcttct	catatatcct	catcctgtgg	gctgttttgg	agctgtcctc	tcggagggca	600
gcactcaagg	ctttcaacac	ctgcactctc	cacctctgtg	ctgttctggg	cttctatgta	660
cccctcattg	ggctctcggt	ggtgcatagg	ctgggtgggc	ccacctccct	cctcatgtg	720
gttatggcta	atacctactt	gctgctacca	cctgtagtca	accccttgt	ctatggagcc	780
aagaccaaag	agatctgttc	aagggtcctc	tgtatgttct	cacaagggtg	caag	834

&lt;210&gt; 513

&lt;211&gt; 957

&lt;212&gt; DNA

<213> Unknown (H38g362 nucleotide)

<220>

<223> Synthetic construct

<400> 513

atgctggggtc	cagcttacaa	ccacacaatg	gaaacccctg	cctccttctt	ccttggtgggt	60
atcccaggac	tgcaatcttc	acatcttttg	ctggctatct	cactgagtgc	catgtacatc	120
acagccctgt	taggaaacac	cctcatcgtg	actgcaatct	ggatggattc	cactcggcat	180
gagcccatgt	attgctttct	gtgtgttctg	gctgctgtgg	acattgttat	ggcctcctcc	240
gtggtaccca	agatggtgag	catcttctgc	tcgggagaca	gctccatcag	ctttagtgtc	300
tgtttcactc	agatgttttt	tgtccactta	gccacagctg	tggagacggg	gctgctgctg	360
accatggctt	ttgaccgcta	tgtagccatc	tgcaagcctc	tacactacaa	gagaattctc	420
acgcctcaag	tgatgctggg	aatgagtatg	gccgtcacca	tcagagctgt	cacattcatg	480
actccactga	gttggtgat	gaatcatcta	cctttctgtg	gctccaatgt	ggttgtccac	540
tcctactgta	agcacatagc	tttgccagg	ttagcatgtg	ctgaccccg	gcccagcagt	600
ctctacagtc	tgattgggtc	ctctcttatg	gtgggctctg	atgtggcctt	cattgctgcc	660
tcctatatct	taattctcag	ggcagtat	gatctctcct	caaagactgc	tcagttgaaa	720
gcattaagca	catgtggctc	ccatgtgggg	gttatggctt	tgtactatct	acctgggatg	780
gcatacgctt	atgcggcctg	gttggggcag	gatatagtgc	ccttgccacac	ccaagtgtctg	840
ctagctgacc	tgtacgtgat	catcccagcc	actttaaatc	ccatcatcta	tggcatgagg	900
accaaacaat	tgctggaggg	aatatggagt	tatctgatgc	acttcctctt	tgaccac	957

<210> 514

<211> 966

<212> DNA

<213> Unknown (H38g363 nucleotide)

<220>

<223> Synthetic construct

<400> 514

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagtcca	60
aggagagctc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atztatagac	gtatgtgttg	cctcttctgc	taccctaaa	240
atgattgcag	actttctggg	tgagcacaag	actatttctt	ttgatcccca	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtg	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tggtgtgtgc	tcgtcctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcacgt	taatctgcca	ttttgtgggc	ctaataagg	agatagtttt	tttctgtgac	540
cttcctctag	cgacgaagtt	agcctgcata	gacacttatg	ttgtcagcct	actaatagtt	600
gcagatagtg	gctttctttc	tctgagttcc	tttctcctct	tggttgtctc	ctacactgta	660
atacttgta	cagttaggaa	tcgctcctct	gtaagcatgg	tgaaggccca	ctccacattg	720
actgtcaca	tcactgtggg	cactttatct	tttggatcgt	gtattttcat	ctatgtgtgg	780
cccttcagca	gttactcagt	tgacaaagtc	ccttgctgtat	tctacaccat	cttcacgtct	840
attttaaac	ctgtaatcta	catgctaaga	aacaaagaag	tgaaggcagc	tatgtcaaaa	900
ctgaagagtc	ggtatcagaa	gcttggtcag	gtttctgtag	tcataagaaa	cgttcttttc	960
ctagaa						966

<210> 515

<211> 966

<212> DNA

<213> Unknown (H38g364 nucleotide)

<220>

<223> Synthetic construct

<400> 515

atgctggggtc	cagcttataa	ccacacaatg	gaaacccctg	cctccttctt	ccttggtgggt	60
atcccaggac	tgcaatcttc	acatcttttg	ctggctatct	cactgagtgc	catgtacatc	120



atagccctgt	taggaaacac	catcatcgtg	actgcaatct	ggatggattc	cactcggcat	180
gagcccatgt	attgctttct	gtgtgttctg	gctgctgtgg	acattgttat	ggcctcctcg	240
gtggtacca	agatgggtgag	catcttctgc	tcaggagaca	gtcfaatcag	ctttagtgtc	300
tgtttcactc	agatgttttt	tgccactta	gccacagctg	tggagacggg	gctgctgctg	360
accatggctt	tgaccgcta	tgtagccatc	tgcaagcctc	tacactacaa	gagaattctc	420
acgcctcaag	tgatgctggg	aatgagtatg	gccatcacca	tcagagctat	catagccata	480
actccactga	gttggatggg	gagtcactta	cctttctgtg	gctccaatgt	ggttgtccac	540
tcctactgtg	agcacatagc	tttggccagg	ttagcatgtg	ctgaccccg	gccagcag	600
ctctacagtc	tgattgggtc	ctctcttatg	gtgggctctg	atgtggcctt	cattgctg	660
tcctatatct	taattctcaa	ggcagtat	ggtctctcct	caaagactgc	tcagttgaaa	720
gcattaagca	catgtggctc	ccatgtgggg	gttatggcct	tgtactatct	acctgggatg	780
gcacccatct	atgcccgtc	gttggggcag	gatgtagtgc	ccttgccac	ccaagtcctg	840
ctagctgacc	tgtagctgat	catcccagcc	accttaaatc	ccatcatcta	tggcatgagg	900
accaaacaac	tgccgggagag	aatatggagt	tatctgatgc	atgtcctctt	tgaccattcc	960
aacctg						966

&lt;210&gt; 516

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g365 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 516

atggagggt	tcaactat	cagagtat	gaattcat	tacttgga	tactgatt	60
cctgaactcc	agatattct	ttctgtgg	ttttctgt	tctattta	gaccatgt	120
ggcaactgcc	tgattttg	cactgtcc	tccacctc	accttcact	tcgcatgt	180
ttctgtctca	gcaacatg	tcattgac	gtgcctgt	tcctttgcca	caccaaag	240
gattatggac	ttttttgct	tgcgtaag	catctcttt	gaaggctg	tttctcag	300
ctttttttta	cacctctca	atgggact	gattgtgt	ttgatctcca	tgtcttttga	360
caggtatatt	gccatatg	aacctctcca	ctattcaaca	attatgagcc	aaagagtgtg	420
tggtgagctt	gtggcagttt	cttgttgg	agtgggct	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgt	cccaatgtt	tagacagttt	tttctgtgat	540
cttcttttgg	tcateccagt	agcttgtata	gatatttat	ttcttgggac	ctccatgatt	600
tcaaccagt	gtgtgattgc	tcttataagt	tttctgctt	tgctcacctc	ctacatcatt	660
gttcttaata	ttgtcaggg	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcgcatt	ttattgttgt	gttaatgttc	tttgggcct	gtattttcat	ttatgtgtgg	780
ccttcacaaa	acttctcgtg	agacaaaatt	ctctccgtt	tctataccat	cttactccc	840
tttctgaatc	cacttatcta	tactttgaga	aaccaggaag	tgaagacagc	aatgaagaag	900
aaactgaata	ttcagtattt	cagtcttggg	aaaactgctc	cg		942

&lt;210&gt; 517

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g366 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 517

atgctcactt	ttcataat	ctgctcag	cccagctcct	tctggctcac	tggcatccca	60
gggctggagt	ccctacac	ctggctctcc	atccccctt	gctccatgta	cctgggtggc	120
gtgggtggga	atgtgacc	cctggctgtg	gtaaaagat	aacgcagcct	gcaccagccc	180
atgtactttt	tcttgtgc	gttggctgcc	attgacctgg	ttctgtctac	ttccactata	240
cccaaacttc	tgggaatct	ctgggtccgt	gcttgtgaca	ttggcctgga	cgctgcttg	300
ggccaaatgt	tccttatcca	ctgctttgcc	actgttgagt	caggcatctt	ccttgccatg	360
gcttttgatc	gctacgtggc	ccatctgcaa	cccactacgt	catagcatgg	tgctcactta	420
tacagtgggtg	ggtcgtttgg	ggcttgttcc	tctctccggg	ggtgttctct	acattggacc	480
tctgcctctg	atgatccgcc	tgccgctgcc	cctttataaa	acccatgtta	tctccactc	540
ctactgtgag	cacatggctg	tagttgcctt	gacatgtggc	gacagcaggg	tcaataatgt	600

ctatgggctg agcatcggct ttctgggtgtt gatcctggac tcagtggcta ttgctgcattc	660
ctatgtgatg attttcaggg cctgatggg gtttagccact cctgaggcta ggcttaaaac	720
cctggggaca tgcgcttctc acctctgtgc catcctgatc ttttatgttc ccattgctgt	780
ttcttccttg attcaccgat ttggtcagtg tgtgcctcct ccagtcacaca ctctgctggc	840
caacttctat ctctcattc ctccaatcct caatcccatt gtctatgctg ttcgcaccaa	900
gcagatccga gagagccttc tccaaatacc aaggatagaa atgaagatta ga	952

&lt;210&gt; 518

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g367 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 518

cagatgctga cagattggtg gggacctaata aggaccacaa gttacgtgaa ctcaccattc	60
aattccttgt ctctctgtag ttatgtgcca ctatataatt tctacaatta ttttataaatt	120
atatgccatc ctttgtaata tttgttaata atgaacctat atctcctcct taatcttact	180
ttaatacttg agggataatt cattcatttt tggcatcatg tatactctca tcctaaaaat	240
tccaaggatg aaaaaaaaaa accttcagat aattcccctc attggttgcg gccttgctga	300
a	301

&lt;210&gt; 519

&lt;211&gt; 506

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g368 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 519

aatagtgtg ccaagcattt cttactctta aaattgtgtt caatgtttgc agtcactttc	60
ctatccctga tattatcagg aaagggcctg caatttcctt tctacttctc tgagtcaact	120
gcaaagtctc agatgttttc acagtgtgaga caagagaaca agaagcacca atgaaaacca	180
cggggttcta tggaggcatc atggtgtggt gagtagaagc atgtactctt agctgtatct	240
cactgggttc aaatcctgac tatacggcat atggtgcatt aacagcccgc tgaccacaag	300
aatttctatg ctggtaaaaat aggtttataa taatgccagt caatctaaag atgctttaag	360
tgaagactat ttggtgtttt tcaaggactc aataatcatt aactgtgatc acgatctttc	420
ccttacctac tttcaataag taaataaatt acattttatta aacaaaagaa atttaattct	480
gcttttctga aacaacacaa ttctat	506

&lt;210&gt; 520

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g369 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 520

ctccctccc tgtttttttag agtttttgta attttggttt gtttactac tctttgttaa	60
gctatgcatt ctctttctaa ttattctact tgtaaattt ttattaaaaa caaaaatagc	120
aatgacatat ttacatatt tatctaatta taagctcaaa gcatgaaata gtattgactt	180
ccacatacat atgttttgtt acgtgtatat tatgaataaa ttagttcatc tcaaatatga	240
aactttaaca tctttaccat ttttttgga tagtctagga ttttagacac ttcttaattt	300
tgttttacct tttatgtcac atattcttca ttaatagtta ttaatatgtt gtattttcta	360
gctgttcttg caaaaagtag ttttatttta tgtttcaaca gtctcagcgt caactgtgac	420
actttctgtg tttggctttc ttgttttgga attgtttata ttgatgtgca tcccattgca	480
cattgttatg tttctcaaaa gattatttaa atgttatgtg tttttatgat cactcgtttt	540
ttgcttcatg catgcattat tgccttaaac attaaaaaat acttggtttg atgtgctttt	600

tatctttata	tgtgaaaaat	ctttgctggc	taatatgtct	tttgtcacia	ttgtttcctc	660
cttaattctc	ttaacgaatt	aagagattat	ttcattttct	tctgtcattt	tatgtggtac	720
aatacatctg	aatctgtcct	catttttctt	acatagggtt	ttcattttct	ttttctgctt	780
gaaattgccca	acatatatct	aaatgttgac	ctacttagta	ttatactgac	tttggtta	837

&lt;210&gt; 521

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g370 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 521

tgcacatgt	gtgtttggct	cttagcttga	gacaggcaaa	tccacataca	ctcacattcc	60
aacaagccaa	agcaagtcac	ccacccatt	gcttctggga	caaggatgta	cattcctcct	120
ggcgctgggg	gtgcgggtac	cgcaaggga	ataaattttt	cctgagctac	gatacactct	180
cccacaaaa	gtcatacacc	catttagata	acaacttttc	ttgagtagtt	cagatatcat	240
caatgatcca	catattgata	aacatgactc	gacactaata	acactgtgag	cattttacac	300
tattttctat	aaactccact	atgctccatt	tattctcaga	aattctctct	atgatatact	360
tcatgggcac	aaagaagaat	gagtgaagc	cacgcaaaaa	ggactgtgaa	agccactaaa	420
aagggctgga	ataaatggga	caaatcatca	tactcttcta	t		461

&lt;210&gt; 522

&lt;211&gt; 554

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g371 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 522

cctgtcacc	cccgttcccc	ccaccacct	ctctttcccc	cttacatcta	cccaaaaact	60
ttttccccac	catctttccg	caaaaccttc	tctcctcct	gttcaccacc	gtttttcccc	120
ctccacctac	cccacacatt	ttttccccac	cgtcttttcc	tcactgtcct	ttttgcaaca	180
ccttctcctg	ctcgccatcc	tcttttcccc	ttggcactaa	ccacctctct	tactcctcca	240
tctaccccaa	aactattttc	cccttccctac	cgctccagcc	acactgcagt	ctccgtcgct	300
gccaccaacc	gcagcgaggc	gagctgtggt	gccgcagcca	cagcctccag	catgcagcgg	360
tggttagccc	ttgtcctggt	cctctaagcc	gggaacggag	cagccccgcg	cgagacacg	420
catgagccta	gaacggcctg	acacctcttc	agcaccattt	atatactgag	gttatgcata	480
tgaggttctt	ggactacatg	ttccaggatt	gggtaagaga	aaacgcagag	gcctactctg	540
attggacttt	gtta					554

&lt;210&gt; 523

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g372 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 523

tatatagaaa	tggaacaacta	ttttetaaca	taactataac	gatattttact	atttttccat	60
tttataatct	ctactcaata	ttttggtatt	aaaaaattca	tcctaacttc	tttgttggtc	120
tattgttttt	gatgttcagc	attactaaat	ttttgactta	tggtttgaaa	tggtctgtca	180
ttcctgattg	ctgacccctg	tatcaacatg	cctgatattaa	cccttaacaa	attctattct	240
tacaaaatag	ctgaagtggg	ttggagggtt	atttttacca	tttcttttat	ttgctgtccc	300
ttttgataaa	attatttttc	ttagttaaaa	aatgtattta	aataagtaaa	taatatctgt	360
gctagtgggt	actcgggtgga	catttcagag	gtgtgtccat	actttatgta	ttttatcact	420
ggtt						424

<210> 524  
 <211> 246  
 <212> DNA  
 <213> Unknown (H38g373 nucleotide)

<220>  
 <223> Synthetic construct

<400> 524	
aatgtattta ggtaatttct tgactttctgc agggactctg atatacacag agcgtacctg	60
tgtatactgt ccagtttagct cagattctca gttttgggca ttttctaagg gagggcaatg	120
aacatcctga taggtttaac taaggtttta aaatgtccaa ttttatgtgt ggtttttaac	180
cacacctgca tcctaattac gaccttggtt gttatagctt ataggtttag gcaatctgga	240
tatagt	246

<210> 525  
 <211> 619  
 <212> DNA  
 <213> Unknown (H38g374 nucleotide)

<220>  
 <223> Synthetic construct

<400> 525	
gaaattatat tgattgggat ttctctcaaa ctaatctagt tgtattcacc attattaaaa	60
ttaagtgaca ctcaattgga ctaagtagca ataaaaatat gagacttcct agtgattttt	120
ttttatccca agccatttac tactgatggg ccttgatgtg tgtgcttgaa aacaaaacat	180
atgcaagtgt tagactgggt tgaagatttg ggtggtgaaa gttagctaata tagatgtcag	240
tgctctatct agaagccaat cttggaaata tgtgataatg ccctttttaa atagctgaaa	300
agaaattatt ttgtgtttgt ttccacttca ttcttgtttg gttgtatagc atttaagtga	360
aaggagattt ttatccctta tactagtatt tgcatttacc atcttttaata gatggagaga	420
aaagttagtt gtcttacttt gatatgtttg gcataggacc tatgacactt ttgatgtttt	480
tggtcacagt tctgtcacta gaatgctagc aattagatat atgcaatgag taacctactt	540
taatacaatg gtttgaagta ccacaggcag taactcctaa acaccaaata acagtgtttt	600
aatttgtaac atgttaaag	619

<210> 526  
 <211> 939  
 <212> DNA  
 <213> Unknown (H38g375 nucleotide)

<220>  
 <223> Synthetic construct

<400> 526	
atgagaaatt tgagtggagg ccatgtcgag gagtttgtct tgggtgggttt ccctaccacg	60
cctccccctc agctgtcctt ctttgtcctt ttttttgcaa ttaccttct gacattgttg	120
gagaatgcac ttattgtctt cacaatatgg cttgtctcaa gccttcacg tcccatgtac	180
tttttccctg gccatctctc ttccctggag ctatggtaca tcaatgtcac cattcctcgg	240
ctcttggcag cctttcttac ccaggatggt agagtctcct acgtagggtg catgacccaa	300
ctgtacttct ttattgcctt agcctgtact gaatgtgtgc tgggtggcagt tatggcctat	360
gatcgctacc tggccatctg tggacccctc ctttacccta gtctcatgcc ttccagtctg	420
gccactcgcc ttgctgtctc ctcttggggc agtggcttct tcagctccat gatgaagctt	480
cttttttattt cccaattgtc ctactgtgga cccaacatta tcaaccactt tttctgtgat	540
atttccccac tactcaacct cacctgtctt gacaaggagc aagcagagct agtagacttc	600
cttctggccc tgggtgatgat tctactccct ctattggctg tggtttcatc atacactgcc	660
atcattgcag ccacccctgag gatccctacg tccaggggac gccacaaagc cttttccact	720
tgtgcccgtc atctggcagt ggttggttat tactactcct ccactctctt cacctatgca	780
cggccccggg ccatgtacac cttcaaccac aacaagatta tctctgtgct ctacactatc	840
attgtaccat tcttcaacct agccatctac tgccctgagga acaaggaggt gaaggaggcc	900
ttcaggaaga cagtgatggg cagatgtcac tatcctagg	939

<210> 527  
 <211> 965  
 <212> DNA  
 <213> Unknown (H38g376 nucleotide)

<220>  
 <223> Synthetic construct

<400> 527  
 cacacagagc cactgaatct cacagggtgtc tgagaattcc tcctcctggg actctcagag 60  
 gatccagaac tgcagccggc cctcgctttg ctctccctgt ccctgtccat gtatctgggc 120  
 acgggtgctga ggaacctgct cagcatcctg gctgtcagct ctgactccca cctccacacc 180  
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcgggttacac ctcgggccacg 240  
 gttcccaaga tgattgtgga cagcagtcg catggcagag tcatctctca tgctggctgc 300  
 ctgacacaga tgcctttctt ggtccttttt gcatgtatag aagacatgct cctgactgtg 360  
 atggcctatg actgctttgt agccatctgt tgcctctgc actaccagc catcgtgaat 420  
 cctcacctct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt ggattcccag 480  
 ctgcacagtt ggattgtgtt acaattcacc atcatcaaga atgtggaaat ctctaatttt 540  
 gtctgtgacc cctctcaact tctcaaaact gcctgttctg acagcgtcat caatagcata 600  
 ttcatatatt ttgatagtag tatgtttggt tttcttccca tttcagggat ccttttgtct 660  
 tactctaaaa ttgtccctc cgttctaagg atgtcatcgt cagaaggga gtataaagcc 720  
 ttctccacct gtggctctca cctagcagtt gtttgctgat ttgatggaac aggcattggc 780  
 atgtacctga cttcagctgt ggcaccaccc cccaggaatg gtgtcgtgga gtcagggatg 840  
 tacgctgtgg tcaccccat gctgaacctt ttcactaca gcctgagaaa caggcacaca 900  
 caaagtgcgc tgcggaggct gcgcacagaa cagttgaatc tcatgatctc ttgcatcctt 960  
 tttct 965

<210> 528  
 <211> 557  
 <212> DNA  
 <213> Unknown (H38g377 nucleotide)

<220>  
 <223> Synthetic construct

<400> 528  
 ccagtacccc agcatctgtt cttcttctctg aaagtgactg gccaccattg acctaaatca 60  
 gaaacctatg atttgtccca gatttttctt ttcccttgc tcttcataac tatcagtgat 120  
 actaattcta aactaacctt aacgaactgc atctgtgcc ctctctcatc tctcctcct 180  
 cactttcagt gcattgactg aggtacacc atgtgaatta ttaccatggc atgctaacag 240  
 aattattgct tccaatggta ccatgccata atcactcct catatgggtg ccaataaatt 300  
 tttaaaatat ttatttgtat ctgctacttc tcagggttaa agcttcccag catgttgaag 360  
 atggaatgca aacagctctg catgcatgcc ctttgtctat gcagctccta ttgtccatcc 420  
 cccactctta cccactcttg ctggataatt cctttttatt ctttaagact catccaagaa 480  
 gcaagctctc atatttcctt catatacttc tgcataagcc ctttacatat gttaatcatc 540  
 tgttaccttt tctcttg 557

<210> 529  
 <211> 1007  
 <212> DNA  
 <213> Unknown (H38g378 nucleotide)

<220>  
 <223> Synthetic construct

<400> 529  
 tctagagacc cacagaatct aacagatgtc tctatatctc tcctcctaga agctcagagg 60  
 atccagaacg gcagccggc ctcactgggc tgttcctgtc cagtgccctg gtcattggcg 120  
 tggggaaact gctcatcctc ctggccatca gccctgactc ccacctccac acccccatgt 180  
 actttctctt ctccaacctg tcttgccctg acatcagttt cacctccacc acagtcccca 240

agatgactgt	ggacatccaa	tctcacagca	gagtcacctc	ctatgcaggc	tgccctgactc	300
agatgtctct	ctttgccatt	tttgaggcca	tggaagacag	acatactcct	gagtgtgatg	360
gcctatgacc	agttttagc	caaagtgtcac	cctctatatac	attcagccat	catgaacccg	420
tgtttctgtg	gctttctact	tttggtgtct	tttttttttc	cctcagtcct	ttagatgccc	480
agctgtacaa	tttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctgtga	cccttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	aacaataaca	600
taatcctgta	tttccctgat	gccatatttg	gttttcttcc	catctcgggg	acacttttct	660
cttacgataa	aattgtttcc	tccattctga	gggtttcatc	atcagggtggg	aagtataaag	720
ccttctccac	ctatgggtct	cacctgtcag	atgtttcctg	attttatgga	acaggcggtg	780
gaggggtacct	cagttcagat	gtgtcatctt	ccccgagaaa	gactgcagtg	gcctcagtgga	840
tgtacgcagt	ggtcaccccc	atgatgaacc	ccttcatcta	cagtcgcaga	aacagggata	900
tgaaaagtgt	cctgcggcgg	ccgcacggca	gcacgttcta	atctcaatac	cttcttatct	960
gttccattcc	ttttgcagtg	tgggtcgaaa	aaggctgcat	gatgaaa		1007

&lt;210&gt; 530

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g379 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 530

tttttaaaaa	tgagattaaa	ggaattaatg	taagatagaa	ccataatgga	ttattggagg	60
gaaggtaggc	acatttaggg	gatgttcttg	gcctttccgt	ttggctgacc	tatcccaaaa	120
cttttccctc	gggtctctat	cagagacatg	gcagtaacct	ggatggacca	taggcacgag	180
tccctgtagc	cattccctcc	gaagctgcag	cctttttcat	cctgccatgt	atctgagtta	240
tgacagtgcc	ttgacacctt	cactaaatca	tatataactt	gaatccgggg	actcaagggg	300
ttcaaccatc	tttgttttct	tctccattac	tgctactgtg	ctagagccca	agtctcctga	360
aatgcgcctc	ggagccttgc	tcaaagatgt	caacccaaca	tgctgatcag	gtagctattt	420
tgtctgaagc	tggtagtcca	tgacaggctc	tgacatgtgc	tgagcttgct	c	471

&lt;210&gt; 531

&lt;211&gt; 974

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g380 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 531

atgaagatca	accagacaat	cctgaaggaa	ttcattcttg	ttggcttttc	tgtgtaccca	60
catgtacaga	catttctttt	tgtgggtctc	ttttgtctct	accttctcac	ccttgcaggt	120
aatctgacca	tcatgggtct	aacttgagtg	gacaggctcc	tccacacccc	tatgtatctc	180
ttccttagtg	cactctcctt	ctctgagacc	tgctatacac	tgaccatcgt	ccccagatg	240
ctggaagatc	tactggccaa	ggacagaagc	atttcagtca	caggttgtag	cttacagatg	300
tgtcttctct	tgggacttgg	tggcacaaac	tgtatcattc	tcactttgat	gggatatgac	360
cgcttctctg	ccatttgtaa	ccctctaaga	tatccactgc	ttatgaccaa	cattgtatgt	420
ggacaacttg	tggcctctgc	ttgcactgca	ggcttcttta	tctctcttac	agagactgca	480
ctgatattca	gggactcttt	ctgcagaccc	aaccttgcca	aacacttctt	ctgccatatt	540
ctggcagtta	ttaggctgtc	ttgtatagac	agtaaccaca	cagaattcat	tataacactg	600
atctcagtg	ctgggttggc	gggtaccctt	ctgctcatca	tcttgactga	tgtcttctatt	660
atttctactg	tcttcaggat	cccttcagct	gagggcaagc	agaaggcctt	caccacctgt	720
gcctcccacc	tcaccgtggt	tataatccac	tttgggtttg	catctattgt	ttatttgaag	780
ccagaagcct	caggagatga	cacactcata	gcagtcctct	atactgtcat	taccccttct	840
ctcagcccca	tcatattcag	cctgaggaat	aaggacatga	aaaatgcttt	tagaagaatg	900
atgggaaaca	cagttgcctt	gaaaaaataa	tcttgggttg	ttgctgcttg	tttgaagaag	960
ggctcaatgt	cccc					974

&lt;210&gt; 532

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g381 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 532

atggggcaga	ccaacgtaac	ctcctggagg	gattttgtct	tcctgggctt	ctccagttct	60
ggggagttgc	agtcctctct	ctttgecttg	ttcctctctc	tgtatctagt	cactctgacc	120
agcaatgtct	tcattatcat	agccatcagg	ctggatagcc	atctgcacac	ccccatgtac	180
ctcttccttt	ccttcctatc	cttctctgag	acctgctaca	ctttgggcat	catccctaga	240
atgctctctg	gcctggctgg	gggggaccag	gctatctcct	atgtgggctg	tgctgcccag	300
atgttctttt	tgccctcatg	ggcctgtact	aactgcttcc	ttctggctgc	catgggcttt	360
gacagatatg	tggccatctg	tgctccactc	cactatgcca	gccacatgaa	tcctaccctc	420
tgtgcccagc	tggtcattac	ttccttcctg	actggatacc	tctttggact	gggaatgaca	480
ctagttattt	tcacactctc	attctgcagc	tcctatgaaa	tcagcactt	tttttgtgac	540
acgccacctg	tgctgagcct	agcctgtgga	gatacaggcc	cgagtgagct	gaggatcttt	600
atcctcagtc	ttttggctct	cttggctctc	ttcttcttca	tcaccatctc	ctacgcctac	660
atcttggcag	caatactgag	gatccctctc	gctgaggggc	agaagaaggc	cttctccact	720
tgtgcctcgc	accttacagt	ggtcattatt	cattatggct	gtgcttcctt	cgtgtacctg	780
aggcccaaag	ccagctactc	tcttgagaga	gatcagctta	ttgccatgac	ctatactgta	840
gtgaccccc	tccttaatcc	cattgtttat	agtctaagga	ctagggctat	acagacagct	900
ctgaggaatg	ctttcagagg	gagattgctg	ggtaaagga			939

&lt;210&gt; 533

&lt;211&gt; 866

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g382 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 533

cttttgtttt	ttatccttct	gctcctcatt	tacctattca	ccatcattgg	tagtcttatg	60
gtgttctttg	ccatcaaact	ggatttctgc	ctgcacagct	ccttgatatt	cttcatcagt	120
gtcctctcct	tcctagagat	ctgggtatacc	accatcacca	tccccaagat	gttcttcaac	180
ctagccagtg	agcagaagac	cacctccctg	gatggttgcc	tattgcagat	gtatttcttt	240
tactccctcg	gcatactga	ggtttgcttg	ctcaccacca	gggctatgga	cagataacctg	300
gccatctgta	atcacctttg	ctaccccaca	gtcacgacac	cttagctcta	cactcagggtg	360
attctaggtt	gttgcatctg	tggcttcttc	acgctgctcc	ctgagattgc	ttggatatcc	420
acactgccat	tttgtggtcc	aaatcaaate	cacaacattt	tctgtgacct	tgatectatc	480
ctgaatctag	catgtgtaga	cactggccca	gttgttttaa	tcaagggtgt	ggacattgta	540
catgctgtgg	agatcatcac	agctataatg	cttgtgactt	tggcttacgt	ccaaattatt	600
gcagtgatcc	taagaaactg	ctctgctgat	ggatgccaaa	aggcattttc	tacctatgct	660
ttccaccttg	ctattttctt	aatctttttt	ggaagtgtag	ccctgatgta	cctgctcttc	720
tctgccaagt	actccttttt	ctggggacaca	accatcagcc	taatgtttgc	agtgtgtgca	780
ccgacacaat	catctgtagt	ctgaggaata	aagagataaa	ggaagcaata	aaaaagcaca	840
tgtgccaatc	aatgatatgc	acacat				866

&lt;210&gt; 534

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g383 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 534

atggagagcc	ccaatcgaac	caccattcag	gagtttatct	tctccgcttt	cccttattcc	60
tgggttaagt	ctgttgtctg	ctttgttcca	ctgctcttca	tctatgcttt	cattgttgtt	120
ggaaacctgg	tcatcatcac	agtgtgccag	ttgaatactc	acctccacac	tcccatgtat	180

```

acttttatca gtgctctttc tttcctggag atttggata ccacagccac aatcccaaag      240
atgctgtcta gcctgcttag tgagaggagc atttccttca atggttgtct cctgcagatg      300
tatttcttcc attccaccgg catctgtgag gtgtgtctct tgacagttaa ggcctttgac      360
cactacctgg ccatatgcag cctcttcat tatccctcta tcatgacccc caagctatgt      420
acccaactga ctttaagtgt ctgtgtttgt ggctttatca cacccttcc tgagattgcc      480
tggatctcta cactgccatt ttgtggttcg aatcaccttg aacatatctt ctgtgacttc      540
ctcccagtgc tgcgtctggc ctgcacagac acacgagcca tcgtcatgat tcaggtagtg      600
gatgtcattc atgcagtgga gattattaca gctgtgatgc tcattctcat gtcctacgat      660
gggtattgtg ctgtaattct acgtattcat tcagctggag gccgcccgcac agcattttcc      720
acgtgtgtct ctcacttcat tgtcttttcg ctctcttttg gcagtgtgac tctcatgtac      780
ctacgcttct ctgccaccta ctctttgttc tgggatatag ccattgtctt ggcctttgca      840
gttttgtctc cttcttcaa cccattatc tatagcctga ggaataaaga aataaaagaa      900
gctataaaaa agcacatagg tcaagctaag atattttttt ccgtaagacc aggg          954

```

&lt;210&gt; 535

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g384 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 535

```

ctactgaaac tctcctgctc agacacacac ctcaatgagg tcataatcct tagtgagggg      60
gccctgggtca tgatcacccc atttctttgc atcctggctt cttatatgca catcacctgc      120
actgtcctga aggtcccatc cacaagggga aggtggaaag ccttctccac ctgtggttct      180
cacctggctg tggttctcct cttctacagc accatcattg ctgtgtattt taaccctctg      240
tcctcccact cagctgagaa agacactatg gctactgtgt tgtatacagt agtgactccc      300
atgctaaacc ctttatctac agcctgagga acaggtactt gaaaggggct ctgaaaaaag      360
tagttggcag ggtgggtgtt tctgtc

```

&lt;210&gt; 536

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g385 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 536

```

ctgtctcatca tcccagccat tgccactgac acccggctct ctgtgctcgt gcgctttttc      60
cttgccaacc tggccttcgt ggtcacttgc ttcacctcca ccaccatccc caagatgctg      120
gacgtgcaaa gagatccctt gtgtcatgtc aggatgcaaa gggattcctt atgctgggtg      180
cctgaccagc atgtcttctt tcatctgtta ggcaccaca gcttctgct gactgcaatg      240
gccaatgaac actgtgtggc catctgtcac tctctgaact ccacagggtc tgtgacacca      300
tagctctgtg gccctcctgt ggtggcctcc tggaccttcg cattcaggaa tgccctgacc      360
caccagtggt tactgaccgc cctctcactc tgcacctacg agtgggtcag ccatgtcttc      420
tgcaacctca gccagctgct gaagttggcc tgctcagacg ccactctcaa caatgtgacg      480
gtgcaa

```

&lt;210&gt; 537

&lt;211&gt; 980

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g386 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 537

```

atgttaaccc ctaataatgc ctgtccgtg cctacctctt tccggctcac tggcatccct      60
ggcctggaat cctgcacat ctggctctcc atccccttg gctccatgta cctggtagct      120

```



gtgctgggga	acataacccat	cctggcagtg	gtaaggatgg	agtacagcct	gcatcagccc	180
atgtacttct	tcctgtgcat	gttggtgtgc	attgacttgg	tcctgtcaac	ctctaccatg	240
cccaaaactac	tggccatctt	ctggtttggt	gcccaaca	ttggtgttaa	tgccctgttg	300
gcccagatgt	tcttcattca	ttgctttgcc	actgttgagt	caggcatctt	ccttgccatg	360
gcttttgatc	actatgtggc	catctgtgac	ccactgcac	ataccttggt	gctcacccat	420
gctgtgggtg	gtcgtttggg	gctgggtgcc	ctcctccggg	gggtaattcta	cattggacct	480
ctgcccctag	tgatttgtct	gaggttgccc	ctttaccaca	cccaaactcat	tgcccattcg	540
tactgtgagc	acatggctgt	ggtcaccttg	gcatgtgggt	tgacacaagg	gtcaacaact	600
tatatggaat	ggggattggc	tttctgggtat	taatcctgga	ttcattggcc	atcactgcct	660
cctatgtgat	gatttttcagg	gctgtaatgg	gcttggccac	ctctgaagcc	aggcttaaaa	720
ccttagggac	atgtggctct	cacatctgtg	ccatcctcgt	cttctacatc	cccatgtctg	780
tttctctct	cacacaccgc	tttggccatc	gtgtgcctcc	ccatatccat	atccatatcc	840
atatccatat	ccatatccat	atccttttgg	ccaacattta	cctcctcacc	ccacctatcc	900
tcaacccaat	agtctatgct	gtccgcacaa	agcagatccg	agaggctctt	ctccatatta	960
aggcaaggac	tcaaaccagg					980

&lt;210&gt; 538

&lt;211&gt; 967

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g387 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 538

gtagcctgct	acctccctga	gctgtagtgg	gatgtccagg	gggtaaagag	aatgagacag	60
gagttggcga	gttctctctg	ctcagcatca	ccagtgaact	agagaagcag	caggccctct	120
tctggctctt	cctgtgtatg	cacttagtca	ctgaggctgg	aaacacaccc	atcatcctgg	180
gcatcggtc	caaccctcgc	ctgcacaccc	ccacgtactt	cttcacccat	ctctcctttg	240
tcaacatctg	cttcacaccc	aaacctgatc	ccaagctcct	ggccaacct	gtggcaggaa	300
cagggtgat	cagcatctct	tctccccagt	gctgactca	gatgtacttc	ctcatctcct	360
ttgccaacgt	ggacaccttt	ctgctggcca	tcatggcact	ggaccactat	gtggccatct	420
gcagcgccct	gcggtactgc	tccatcatca	cccccggtc	tgtcaggggc	tgcccggtgt	480
agcgtgagca	ggctccagcc	tcatctccct	ggccacacg	gtcatcatga	gcagactggc	540
cttctgctcc	tccgcccaga	tttcacactt	ctactgtgac	gcctacctgc	tcatgaagat	600
tgccctgctca	catacatgtc	aatcagcatg	tgttccctgg	ggccgtggtc	ctgttccctg	660
ctccctgtgc	gtcctatctg	gtctcctaca	tccgcattgc	tgacagccatc	ctccggatct	720
cctctectac	aagaaggcgc	aaggcatgtt	ccatagttag	ctcccacctg	tctctgggtca	780
ccctgttcta	tggaactgtc	ctggggatct	gcatatgacc	cccagactcc	ttctcagccc	840
aggacacccat	agcaaccatc	atgtacactg	tggtgacctc	tatgctaaac	cccttcatct	900
acagtctgat	gaacaaggag	gtccaggagg	ccgtgagaag	gctcttcagt	agggggtcac	960
actcatc						967

&lt;210&gt; 539

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g388 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 539

cttcattttt	gtgggataga	tgtgacctca	taccaggctt	gacagatatt	ggcatagcaa	60
cccctacgac	actacataat	gtgggcaacg	cattgtcgca	ttatgtgtgc	gcatgggaat	120
tgtcttctcc	attcgttgag	ccagttggcc	tttgccgtgc	acttaccctt	ctgtgggtccc	180
aatgagttcg	atagttttta	ttgtgacctt	cctagggtta	tcaaacttgc	ctgtacagat	240
acctacaggc	tagatattat	ggtcattgct	aacagtgggt	tgctcactgt	gtgttctttt	300
gttcttctaa	tactctcata	cactatcatc	ctaattgacca	tccagcatcg	ccctttagat	360
aagtcgtcca	aagctctgtc	cactttgact	gtcacatta	cagtagttct	ttgttctttt	420
ggaccatgtg	tctttattta	tgccctggcca	ttcccatca	agtcattaga	taaatctctt	480
gctgtatttt	attctgtgat	caccctctc	ttgaacccaa	ttatatacac	actgagggaac	540

aaagacatga agacggcaat aagacagctg agaaaatggg atgcacattc tagtgtaaag 600  
 ttt 603

<210> 540

<211> 935

<212> DNA

<213> Unknown (H38g389 nucleotide)

<220>

<223> Synthetic construct

<400> 540

atgctcactt	ttcataatgt	ctgctcagta	cccagctcct	tctggctcac	tggcatccca	60
gggctggagt	ccctacacgt	ctggctctcc	atcccctttg	gtcccatgta	cctgggtggct	120
gtgggtggga	atgtgaccat	cctggctgtg	gtaaagatag	aacgcagcct	gcaccagccc	180
atgtactttt	tcttgtgcat	gttggctgcc	attgacctgg	ttctgtctac	ttccactata	240
cccaaacttc	tgggaatcct	ctgggtcggg	gcttgtgaca	ttggcctgga	cgccctgcttg	300
ggccaaatgt	tccttatcca	ctgctttgcc	actgttgagt	caggcatcct	ccttgccatg	360
gcttttgcac	gctacgtggc	catctgcaac	ccactacgtc	atagcatggg	gctcacttat	420
acagtgggtg	gtcgtttggg	gcttgtttct	ctcctccggg	gtgttctcta	cattggacct	480
ctgcctctga	tgatccgcct	gcggctgccc	ctttataaaa	cccatgttat	ctcccactcc	540
tactgtgagc	acatggctgt	agttgccttg	acatgtggcg	acagcaaggt	caataatgtc	600
tatgggatga	gcatcggcct	tctggtgttg	atcatggaat	cagtggatag	tgatgcatca	660
taggtgagga	gtatcagggc	cgtgatgggg	ttagccaatc	atgaggatag	gattagagac	720
catggggaca	ggcgaatata	acatatgtgc	catcatgata	ttataggatc	ccagtgatgt	780
atattccatg	agatcaccga	gatggtcagt	gtgtgcatca	tccagtccac	aatatgatgg	840
ccaggatata	tatcatcagt	catccaagca	tcaagcccag	tgtataggat	gatcgcacca	900
agcagagccg	agagagctat	atccaaagag	caaga			935

<210> 541

<211> 945

<212> DNA

<213> Unknown (H38g390 nucleotide)

<220>

<223> Synthetic construct

<400> 541

atggagacgt	gggtgaacca	gtcctacaca	gatggcttct	tcctcttagg	catcttctcc	60
cacagtactg	ctgaccttgt	cctcttctcc	gtggttatgg	cggtcttcac	agtggccctc	120
tgtgggaatg	tcctcctcat	cttcctcatc	tacatggacc	ctcaccttca	caccccatg	180
tacttcttcc	tcagccagct	ctccctcatg	gacctcatgt	tggctctgtac	caatgtgcca	240
aagatggcag	ccaacttcct	gtctggcagg	aagtccatct	cctttgtggg	ctgtggcata	300
caaattggcc	tctttgtctg	tcttgtggga	tctgaggggc	tcttgtctgg	actcatggct	360
tatgaccgct	atgtggccat	tagccaccca	cttcactatc	ccatcctcat	gaatcagagg	420
gtctgtctcc	agattactgg	gagctcctgg	gcctttggga	taatcgatgg	cttgatccag	480
atggtggtag	taatgaattt	cccctactgt	ggcttgagga	aggtgaacca	tttcttctgt	540
gagatgctat	ccttgttgaa	gctggcctgt	gtagacacat	ccctgtttga	gaagggtgata	600
tttgcttgct	gtgtcttcat	gcttctcttc	ccattctcca	tcacgtggc	ctcctatgct	660
cacattctag	ggactgtgct	gcaaatgcac	tctgctcagg	cctggaaaaa	ggccctggcc	720
acctgctcct	cccacctgac	agctgtcacc	ctcttctatg	gggcagccat	gttcatctac	780
ctgaggccta	ggcactaccg	ggccccagc	catgacaagg	tggcctctat	cttctacacg	840
gtccttactc	ccatgctcaa	ccccctcatt	tacagcttga	ggaacaggga	ggtgatgggg	900
gcactgagga	aggggctgga	ccgctgcagg	atcggcagcc	agcac		945

<210> 542

<211> 975

<212> DNA

<213> Unknown (H38g391 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 542

atgggaagat	gggtgaacca	gtcctacaca	gatggcttct	tcctcttggg	catcttttcc	60
cacagccaga	ctgaccttgt	cctcttctct	gcagttatgg	tggtcttcac	agtggccctc	120
tgtgggaatg	tcctcctcat	cttctctatc	tacctggacg	ctggacttca	cacccccatg	180
tactttctcc	tcagccagct	ctccctcatg	gacctcatgt	tggtctgtaa	cattgtgccca	240
aagatgcagc	caacttcctg	tctggcagaa	gtccatctcc	tttgtgggct	gtggcataca	300
aattggcttt	tttgtctctc	ttgtgggatc	tgaggggctc	ttgctgggac	tcattggctta	360
tgaccgctac	gtggccgtta	gccaccact	tcactatccc	atcctcatga	atcagagggt	420
ctgtctccag	attactggga	gctcctgggc	ctttgggata	atagatggag	tgattcagat	480
ggtaggcacc	atgggcttac	cttactgtgg	ctcaaggagc	gtggatcact	ttttctgtga	540
ggtacaagct	ttattgaagc	tggtctgtgc	agacacttcc	ctttttgaca	ccctcctctt	600
tgctgtctgt	gtcttcatgc	ttctccttcc	cttctccatc	atcatggcct	cctatgcttg	660
catcctaggg	gctgtgctcc	gaatacgtc	tgctcaggcc	tggaataaag	ccctggccac	720
ctgtcctccc	acctaacagc	tgtcacccct	ttctatgggg	cagccatgtt	catgtacctg	780
aggcctaggc	gctaccgggc	ccctagccat	gacaagggtg	cctctatctt	ctacacagtc	840
cttactccca	tgctgaacct	cctcatttac	agcttgagga	atggggagggt	gatgggggca	900
ctgaggaagg	ggctggaccg	ctgcaggatt	ggcagccagc	actgaacccc	agagtcgggt	960
gcctgtctgtg	cccc					975

&lt;210&gt; 543

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g392 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 543

atgggggatg	tgaatcagtc	ggtaggcctca	gacttcattc	tggtgggcct	cttcagtcac	60
tcaggatcac	gccagctcct	cttctccctg	gtggctgtca	tgtttgtcat	aggccttctg	120
ggcaacaccg	ttcttctctt	cttgatccgt	gtggactccc	ggctccacac	acccatgtac	180
ttctgtctca	gccagctctc	cctgtttgac	attggctgtc	ccatggtcac	catccccaag	240
atggcatcag	actttctgcg	gggagaagg	gccacctcct	atggagggtg	tgacagtcac	300
atattcttcc	tcacactgat	gggtgtggct	gagggcgctc	tggtggctct	catgtcttat	360
gaccgttatg	ttgctgtgtg	ccagccctctg	cagtatcctg	tacttatgag	acgccaggta	420
tgtctgtgta	tgatgggctc	ctcctgggtg	gtagggtgtc	tcaacgcctc	catccagacc	480
ttcatcacc	tgcattttcc	ctactgtgcc	tcccgatttg	tggtatcact	cttctgtgag	540
gtgccagccc	tactgaagct	ctcctgtgca	gatacctgtg	cctacgagat	ggcgctgtcc	600
acctcagggg	tgctgaccc	aatgtccct	cttccctca	tcgccacctc	ctacggccac	660
gtgttgacag	ctgttctaag	catgcgtcca	gaggaggcca	gacacaaggc	tgacaccacc	720
tgctcctcgc	acatcacgg	agtggggctc	ttttatgggt	ccgccgtgtt	catgtacatg	780
gtgccttgcg	cctaccacag	tccacagcag	gataacgtgg	tttccctctt	ctatagcctt	840
gtcaccccta	cactcaaccc	ccttatctac	agcttgagga	atccggagggt	gtggatggct	900
ttggtcaaa	tgcttagcag	agctggactc	aggcaaatgt	gc		942

&lt;210&gt; 544

&lt;211&gt; 350

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g393 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 544

aatattaagg	gcattgctgg	tgccccatgtt	tattgaagtg	ttggatctat	tctttatcat	60
cctattctat	atctttatcc	cttcaggcag	ttctacaact	ctcctctcag	aggccccgta	120
caaagcattt	gggacatgtg	tctctcacat	agggtccatc	ttagccttct	acacaccttc	180
agtcattctc	tcagtcattg	accgtgtggc	ccgctgtgct	gcgccacacg	tccacattct	240
cctcgccaat	ttctatctgc	tcttcccacc	catgggtcaat	cccatcatct	acggcggtta	300

gaccaagcag atccgtgaca gtcttgggag tattccccgag aaaggatgtg

350

<210> 545

<211> 948

<212> DNA

<213> Unknown (H38g394 nucleotide)

<220>

<223> Synthetic construct

<400> 545

atgcctagtc	agaactatag	catcatatct	gaatttaacc	tctttggctt	ctcagccttc	60
ccccagcacc	tcctgcccac	cttgttcctg	ctgtacctcc	tgatgttcct	gttcacattg	120
ctgggcaacc	ttctcatcat	ggccacaatc	tggattgaac	acagactcca	cacacccatg	180
tacctcttct	tgtgcaccct	ctccgtctct	gagattctgt	tcactgttgc	catcacccct	240
cgcagtctgg	ctgatctgct	ttccacccat	cattccatca	cctttgtggc	ttgtgccaac	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcct	ggtcatgggc	360
tatgatcgct	atgtggccat	ctgccaccca	ctgcgttaca	atgtgctcat	gagcccccg	420
gactgtgccc	atcttgtggc	ctgtacctgg	gctgggtgct	cagtcatggg	gatgatgggtg	480
acaacgatag	ttttccacct	cactttctgt	gggtctaata	tgatccacca	ttttttctgt	540
catgtgcttt	ccctcttgaa	gttggcctgt	gaaaacaaga	catcatctgt	catcatgggt	600
gtgatgctgg	tgtgtgtcac	agccctgata	ggctgtttat	tcctcatcat	cctctcctat	660
gtcttcattg	tggctgccat	cttgaggatt	ccctctgccg	aaggccggca	caagacattt	720
tctacgtgtg	tatccacact	cactgtgggt	gtcacgcact	atagttttgc	ctcctttatc	780
tacctcaagc	ccaagggcct	ccattctatg	tacagtgaag	ccttgatggc	caccacctat	840
actgtcttca	cccccttctc	tagcccaatc	attttcagcc	taagggaaca	ggagctgaag	900
aatgccataa	ataaaaaact	ttacagaaaa	ttctgtcctc	caagtccc		948

<210> 546

<211> 990

<212> DNA

<213> Unknown (H38g395 nucleotide)

<220>

<223> Synthetic construct

<400> 546

atgtgttctt	ttttcttgtg	ccaaacaggt	aaacaggcaa	aaatatcaat	gggagaagaa	60
aaccaaacct	ttgtgtccaa	gtttatcttc	ctgggtcttt	cacaggactt	gcagacccag	120
atcctgctat	ttatcctttt	cctcatcatt	tatctgtctg	ccgtgcttgg	aaaccagctc	180
atcatcatte	tcactcttct	ggattctcgc	cttcacactc	ccatgtattt	ttttcttaga	240
aatctctcct	ttgcagatct	ctgtttctct	actagcattg	tcctcaagt	gttggttcac	300
ttcttggtaa	agaggaaaac	catttctttt	tatgggtgta	tgacacagat	aattgtcttt	360
cttctgggtg	ggtgtacaga	gtgtgcgctg	ctggcagtga	tgtcctatga	ccggtatgtg	420
gctgtctgca	agcccctgta	ctactctacc	atcatgacac	aacgggtgtg	tctctggctg	480
tccttcaggt	cctgggccag	tggggcacta	gtgtctttag	tagataccag	ctttactttc	540
catcttccct	actgggggaca	gaatataatc	aatcactact	tttgtgaacc	tcctgccctc	600
ctgaagctgg	cttccataga	cacttacagc	acagaaatgg	ccatcttttc	aatgggcgtg	660
gtaatcctcc	tggccctgt	ctccctgatt	cttgggtctt	attggaatat	tatctccact	720
gttatccaga	tgcatctctg	ggaagggaga	ctcaaggctt	tttccacctg	tggctcccat	780
cttattgttg	ttgtcctctt	ctatgggtca	ggaatattca	cctacatgag	accaaactcc	840
aagactacaa	aagaactgga	taaaatgata	tctgtgttct	atacagcggt	gactccaatg	900
ttgaacccca	taatttatag	cttgagggaac	aaagatgtca	aaggggctct	caggaaacta	960
gttggggagaa	agtgtctctc	tcataggcag				990

<210> 547

<211> 676

<212> DNA

<213> Unknown (H38g396 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 547

ggaaaggaaa	gagagacacg	ggtctggagg	ccgagagcgc	aagaccgggg	ggtgagcacc	60
cggcacgctg	cgagggtaac	aagctatcag	gaatgcgggg	tccgtggcgg	gggagtgttg	120
tgggcgcggg	taggccgagt	ccttttagacg	cccagctgca	caacgtgatt	gcctacagaa	180
ggacctgctt	caaggatgtg	gaaattccga	atttcgctgt	gacctttctc	aattccccgt	240
cttgcatgtg	tggcaccttc	accaataaca	taatcatgta	ttccctgct	gccatatttg	300
gttttcttcc	catctcgggg	acccttttct	cttacgataa	aattgttttc	tccattctga	360
gggtttcatc	atcagggtggg	aagcataagg	ccttctccac	caggggggtct	cacctgtcag	420
ttgtttgctg	attttatgga	acaggcattg	gaggctacct	cagttcagat	gtgtcatctt	480
ccccgagaaa	ggctgcagtg	gcctcagtga	tgtacacggg	ggccatcccc	atgctgaacc	540
ccttcaccta	cagcctgaga	aacagggata	ttaaaagtgt	cctgcccac	cgcacggcag	600
cacggtctca	tctcaatata	ttcttatctg	ttccattcct	tttgtagtgt	gggttaaaaa	660
aggcagcaag	gtcaaa					676

&lt;210&gt; 548

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g397 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 548

atgaaaatct	tcaacacccc	cagcaactcc	agcaccttca	ctggcttcat	cctcctgggc	60
ttcccttgcc	ccaggggagg	acagatcctc	ctcgttgtgc	tcttactgt	tgtttacctc	120
ctgacctca	tgggcaatgg	ttccatcaac	tgtgctgtgc	actgggtcag	agactccatg	180
cccccatgta	catcctgctc	gccaacttct	ccttccctga	gatctgttat	gtcacctcta	240
cagtccccaa	cgtgctggcc	aacttcctct	ctgacacaag	atcatctcgt	tctctggctg	300
cttccctcaa	ttctactttt	ttttctcctt	gggctctaca	gaatgctttt	tcctgggagc	360
tatggcattt	gacctatacc	ttgccatctg	ccggcctcta	cgctatccaa	ccattatgac	420
cagacgtctc	tgcaacattc	ttgtgggcag	ctgctgggta	cttggtttct	tgtggttctt	480
gattcctatc	agtgtcattt	ctcaaatgac	ctgtggatct	aggattattg	accacttccc	540
atgtgaccca	ggtcctctgt	tagccctcac	ctgtgccaga	gccctctac	tagagttgac	600
tagctccacc	ttaagttctc	tacttctatt	tattcccttt	ctcttcatcg	tggggtgcta	660
tgtcttggtc	ctgagagctg	tgttgagggt	tccttcagca	tctggaagaa	gaaaggcttt	720
ctctacctgt	ggctcccacc	tggctgtagt	ttcactgttt	atggctcaat	gatgatcacg	780
tatgtgagcc	caacatctgg	gcatgaattc	ggaatgcaga	agactgtgac	tctgttctat	840
tctgtgggtc	ctccccttat	taatcctgtc	atatacagtc	tgaggaacaa	ggaaatgaaa	900
catgcaatga	ggaactacac	tgtaatgttt	tattttctag	aattcatagg	gctacaagag	960
atgtcaaaga	tgtattctat	ctctttaatt	tt			992

&lt;210&gt; 549

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g398 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 549

ttctcaagta	tatatgcttg	tatatatcag	atctctatct	caactatcta	tctaatactc	60
tatctatatt	taaattagta	gactggatta	tcaattgtta	tttgtattat	attttacagc	120
ctactcactt	tattctagca	gttcatttac	acttgtgaaa	tgaatcaatt	taaatagtaa	180
caaaatagga	acaatctgac	aacttttttag	ggatacttct	actcaggaat	atgtggcagg	240
agaaactgta	caatgtgatt	gataacaatc	ttcattttga	aatattgcta	gcatggcttc	300
atcacaaatt	actctgtcat	ggacagtggg	cagcacttgg	ccatctgcca	cccactgcac	360
taccttatcc	tcatgactga	tgaaaataga	gacgaatgt	ttatggggccc	gctgacagcc	420
tttccttaca	ccgatgccac	atctcagaac	atgcactatg	taaattttct	tattatcatt	480
ctcagtatct	tgtacatccc	tggaccatat	acgttgatcc	taagagctat	gcttcagctg	540

ctttcagcag	ctagccatca	aaatgccttt	tctatccgtg	ggctctcactt	aatagtgggtg	600
tctctgttct	gtgaaacat	atgatgatgt	gtgtgaatct	catatctgac	catttagtat	660
aaatgaagat	gacaaatcac	aatatcataa	tgatatcctc	cataaagact	ctagttttta	720
actttgtcaa	ttacacctta	ctcaatatga	acttaaaacc	tatcttcagt	ttttttttta	780
tggaatgagt	attagccaaa	gctca				805

&lt;210&gt; 550

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g399 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 550

atgaaaatct	tcaacagccc	cagcaactcc	agcaccttca	ctggettcac	cctcctgggc	60
ttcccttgcc	ccaggaggag	gcagatcctc	ctctttgtgc	tcttcactgt	tgtttacctc	120
ctgacctca	tgggcaatgg	ttccatcatc	tgtgctgtgc	actgggatca	gagactccac	180
gcccccatgt	acatcctgct	cgccaacttc	tccttcttgg	agatatgtta	tgtcacctcc	240
acagtcccca	gcattgctgg	caacttcctc	tctgacacca	agatcatctc	gttctctggc	300
tgttctctcc	agttctactt	tttcttctcc	ttgggtctca	cagaatgctt	tttctctggc	360
gttatggcat	ttgatcgata	ccttgccatc	tgtcggcctc	tacgctatcc	aaccattatg	420
accagacgtc	tctgtaccaa	tcttgtgggc	aattgtctgg	tacttggttt	catctgggtc	480
ttgattccta	tcgtcaacat	ctcccaaatg	tccttctgtg	gatctaggat	tattgaccac	540
ttcctatgtg	acccagctcc	tcttctaact	ctcacttgca	aaaaaggccc	tgtgatagag	600
cttgtctttt	ctgtcttaag	tcctctgcct	gtctttatgc	tctttctctt	cattgtgggg	660
tcctatgctc	tggtcgtgag	agctgtgttg	agggtccctt	cagcagctgg	gagaagaaag	720
gctttctcca	cctgtgggtc	tcacctgggt	gtggtttcac	tggtctacgg	ctcagtactg	780
gtcatgtatg	ggagcccacc	atctaagaat	gaagctggaa	agcagaagac	tgtgactctg	840
ttttattctg	ttgttaccac	actgcttaac	cctgtgatat	atagtcttag	gaacaaagat	900
atgagaaaag	ctctgaagaa	atgttgggga	aca			933

&lt;210&gt; 551

&lt;211&gt; 977

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g400 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 551

acagccctgg	aattcacaaa	caattcagag	acaagcacta	tgacggaatt	tgttctcctt	60
ggctttctctg	gttgtcagga	gatgcaaagt	ttcctcttct	ccctgttctt	tgtgatctat	120
gtattttacca	taataggaaa	tgggaccatt	gtctgtgtctg	tgagattgga	caaacggctt	180
cataccceaa	tgtatattct	cctagggaac	tttgctttcc	ttgaaatccg	gtaagtact	240
tccactgtac	ccaacatgct	agtcaacttc	ctctcagaga	caaaaaccat	ctcttttggt	300
ggctgtttcc	tccagttcta	cttttttact	tccttggta	caatagaagc	atacttctc	360
tgcacatgag	catatgatcg	gtaccttgct	atctgcgcgc	cattgcacta	cccaaccatc	420
atgacccac	aactctgcta	catattgatg	tctttttgct	gggtgtttgg	attcctcagt	480
tactctgtct	ccactgtgca	actgtctcaa	ctgcctttct	gtgggcccac	catcatcaat	540
cactttttgt	gtgacatgga	cccactgatg	gctctgtcct	gtgcctcagc	tcctatcact	600
gagattatct	tctatatect	gagctccctc	attatcattc	tcactcttct	gtacatctgt	660
ggctcctata	tgctttactg	atagctgtat	taaaagtcce	ttcagcagct	ggccagcaga	720
aggccttttc	cacctgtgga	tctcatctga	cagtgtgtgtg	tttattcttt	ggggccctac	780
tggcaatgta	tgtgagcccc	acaactgata	acccagctgc	aatttagaag	attataactt	840
tgttctatct	tgtggtgacc	cccttcttaa	acccctgat	ttacagctta	cgaacaaaag	900
agatgaaggc	tgctgtgaag	aaagtcctga	ggatagaatg	agaataaagt	catctacatg	960
agaccaagca	aaccatt					977

&lt;210&gt; 552

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g401 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 552

atggagagcg	gaaaccaatc	aacagtgact	gaatttatct	tactggatt	ccctcagctt	60
caggatggta	gtctcctgta	cttctttcct	ttacttttca	tctatacttt	tattatcatt	120
gataacttat	taatcttctc	tgctgtaagg	ctggacaccc	atctccacaa	ccccatgtat	180
aattttatca	gtatattttc	ctttctggag	atctggtaca	ccacagccac	cattcccaag	240
atgctctcca	acctcatcag	tgaaaagaag	gccatctcaa	tgactggctg	catcttgcaag	300
atgtattttc	tccactcact	tgaaaactca	gaggggatct	tgctgaccac	catggccatt	360
gacagatacg	ttgccatctg	caaccctctt	cgctatcaaa	tgatcatgac	cccccggtc	420
tgtgctcaac	tctctgcagg	ttcctgcctc	ttcggtttcc	ttatcctgct	tcccgagatt	480
gtgatgattt	ccacactgcc	tttctgtggg	cccaacccaa	tccatcagat	cttctgtgac	540
ttgggtccctg	tgctaagcct	ggcctgtaca	gacacgtcca	tgattctgat	tgaggatgtg	600
attcatgctg	tgaccatcat	cattaccttc	ctaactattg	ccctgtccta	tgtaagaatt	660
gtcactgtga	tattgaggat	tccctcttct	gaagggaggc	aaaaggcttt	ttctacctgt	720
gcaggccacc	tcatggtctt	cctgatattc	tttggcagtg	tatcactcat	gtacttgctg	780
ttcagcgaca	cttatccacc	agttttggac	acagccattg	caactgatgt	tactgtactt	840
gtccattctt	tcaatcccat	catttatagc	ctgagaaaca	aggacatgaa	caatgcgatt	900
aaaaaactgt	tctgtcttca	aaaagtgttg	aacaagcctg	gaggt		945

&lt;210&gt; 553

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g402 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 553

atgcattttg	tgactgagtt	tgctctcctg	ggtttccatg	gtcaaaggga	gatgcagagc	60
tgcttcttct	cattcatcct	ggttctctat	ctcctgacac	tgctagggaa	tgagagctatt	120
gtctgtgcag	tgaaattgga	caggcggtc	cacacacca	tgatcatcct	tctgggaaac	180
tttgcccttc	tagagatctg	gtacatttcc	tccactgtcc	caaacatgct	agtcaatatc	240
ctctctgaga	ttaaaacccat	ctccttctct	ggttgcttcc	tgcaattcta	tttctttttt	300
tcactgggta	caacagagtg	tttcttttta	tcagttatgg	cttatgatcg	gtacctggcc	360
atctgtcgtc	cattacacta	cccctccatc	atgactggga	agttctgtat	aattctgggtc	420
tgtgtatgct	gggtaggcgg	atttctctgc	tatccagtcc	ctattgttct	tatctcccaa	480
cttcccttct	gtgggcccac	catcattgac	cacttggtgt	gtgaccagc	cccattgttt	540
gcactggcct	gcattctctg	tccctccact	gagcttatct	gttacacctt	caactcgatg	600
attatctttg	ggcccttctc	ctccatcttg	ggatcttaca	ctctgggtcat	cagagctgtg	660
ctttgtatc	cctctggtgc	tggtcgaact	aaagctttct	ccacatgtgg	gtcccaccta	720
atggtggtgt	ctctattcta	tggaaccctt	atggtgatgt	atgtgagccc	aacatcaggg	780
aaccagcag	gaatgcagaa	gatcatcact	ctgggtatca	cagcaatgac	tccattctta	840
aatcccttta	tctatagtct	tcgaaacaaa	gacatgaaag	atgctctaaa	gagagtctctg	900
gggttaacag	ttagccaaaa	c				921

&lt;210&gt; 554

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g403 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 554

atgtataatt	ttatcagcat	tttctcattt	ctggagatct	ggtacacaac	tgccacaatt	60
cccaagatgc	tctccatcct	catcagcagg	cagaggacca	tctccatggt	tggtgcctc	120

ttgcagatgt	acttcttcca	ttcactggga	aattcagagg	ggattttgtt	gaccaccatg	180
gccattgata	ggtagcttgc	catctgtaac	cctctccgct	acccaaccat	catgaccccc	240
gggctctgtg	ttcagctctc	tgtgggggtcc	tgcattcttg	gctttcttgt	gttgctccca	300
gagattgcat	ggatttccac	actgcccttc	tgtggacca	accaaattcca	ccagatcttc	360
tgtgattttg	aacctgtgct	gcgcttggcc	tgtacagaca	cgtccatgat	tctgattgag	420
gatgtgatcc	atgctgtggc	cattgtattc	tctgtcctga	ttattgccct	ttcttatatc	480
agaatcatca	ctgtaatcct	gaggattccc	tctgttgaag	gccgccagaa	ggccttttct	540
acctgtgccg	cccattcttag	tgtctttctg	atgttctatg	gcagtgtatc	cctcatgtac	600
ctgcgtttct	ctgccacttt	cccaccgatt	ttggacacag	ctgttgcaact	gatgtttgca	660
gttcttgctc	cctttttcaa	ccctatcatc	tatagcttta	gaaataagga	catgaagatt	720
gcaattaaaa	agcttttctg	ccctcagaag	atggttaatt	tatctgta		768

&lt;210&gt; 555

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g404 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 555

agtctgggaa	gcatgaataa	ctcacagata	tctactgtga	cgcagtttgt	gttggtgggg	60
tttctgggtc	cctggaaaat	tcagatcatc	tttttctcaa	tgattttgtt	gggtctacatc	120
ttcactctga	ctgggaatat	ggccatcatc	tgtgcagtga	gggtgggacca	tcgactccat	180
acccctatgt	acgtgctcct	agccaacttc	tccttcctag	agatctggta	tgtgacctgc	240
acagtcacca	acatgctggt	aaattttttc	tccaaaacta	agaccatata	attctctgga	300
tgtttcaactc	agttccactt	cttcttttcc	ctgggcacaa	ctgaatgctt	cttcctctgt	360
gtcatggctt	atgatcggtg	cctggccatc	tgccaccac	tgcactatcc	ctccattatg	420
actggccagc	tctgtggcat	cttgggtgtc	ctttgttggc	tcattggttt	ccttggacat	480
tcaatttcca	ttttcttcat	ttttcaacta	cctttctgtg	gtcccaacat	cattgatcat	540
tttctgtgtg	atgtagacct	actgatggca	ttgtcctctg	cccctactca	catcataggg	600
catgtgttcc	attctgtgag	ctctcttttc	atcaacctca	ccatgggtga	catccttggg	660
tcctatacct	tgggtctcag	aactgtgctt	taggttcctt	cttcagctgg	atggcaaaag	720
gccatctcta	cctgtgggtc	acacttgggt	gttgtgtctc	tgttctatgg	agccataatg	780
ctgatgtatg	tgagtccac	acctggcaac	tcagttgcta	tgcataagct	catcacactg	840
atatattctg	tggtaacacc	tgtcttaaac	cccctcatct	acagcctacg	caacaaggac	900
atgaaatatg	ccctccatca	tgtcttctgt	ggaatgagaa	ttatccagag	atcatgaata	960

&lt;210&gt; 556

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g405 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 556

atggatccag	agaatcagac	aatggtgact	gagttttatt	tctctgattt	tcctcaatct	60
aagaatggca	gcctcttatt	cttcattcct	atgctcttta	tttatatatt	cattcttgtt	120
ggaaatttca	tgattttctt	tgtcttccaa	ccggaccccc	atctccataa	tcctatgtac	180
agttttatca	gtgtcttctc	cttcctggag	atttgggtaca	ccaccgtgac	tatccccaa	240
atgctctcca	accttctcag	tgaacagaaa	accatctctt	tcataggttg	cctcctgcag	300
atgtacttct	tccactcact	cggggtcaca	gaagccctag	tcctcacagt	gatggccatt	360
gacaggtgtg	tagccatctg	caacccccct	cgtatgcaa	tcactatgtc	cccttgactg	420
tgcattccagc	tctccactgg	ctcttgcaat	tttggcttcc	tcattgttact	gccagagatt	480
gtgtgcattt	ccactcttcc	attctgtggc	gccaaacaaa	ttcatcaact	cttttgtgac	540
tttgaacctg	tgtctgcagt	agcctgcaca	gatacgtaca	taattctggg	tgaagatgtg	600
atccgtgcta	tttccattct	gacctctgtc	tctgtcatca	cccttttcta	tttaagaatc	660
atcacgtgta	tcctgaggat	tcctctgtgt	gagagtgcgc	agaaggcttt	cttcacatgt	720
gcagcccaca	ttgtcttttt	cttgcgtgtt	tttggcagtg	tgtcactcat	gtatctgcgc	780
ttctctgtca	cattcccacc	attactggac	aaggccattg	cactgatgtt	tgctgtcctt	840



gccctacttt tcaacccagt aatctatagt ctgaggaaca aagatatgaa aaacgccacc 900  
aagaaaaatcc tctgttctca aaagatgttc aatgcctctg ggagctaata gagttca 957

<210> 557  
<211> 951  
<212> DNA  
<213> Unknown (H38g406 nucleotide)

<220>  
<223> Synthetic construct

<400> 557  
atgacacagt tgacggccag tgggaatcag acaatgggtga ctgagttcct cttctctatg 60  
ttcccgcatg cgcacagagg tggcctctta ttctttatc ccttgcttct catctacgga 120  
tttatcctaa ctggaaacct aataatgttc attgtcatcc aggtgggcat ggccctgcac 180  
acccctttgt atttctttat cagtgtcctc tccttcctgg agatctgcta taccacaacc 240  
accatcccca agatgctgtc ctgcctaate agtgagcaga agagcatttc cgtggctggc 300  
tgcctcctgc agatgtactt ttccactca cttggatca cagaaagctg tgtcctgaca 360  
gcaatggcca ttgacaggta catagctatc tgcaatccac tccgttacct aaccatcatg 420  
attcccaaac ttgtatcca gctgacagtt ggatcctgct tttgtggctt cctccttggtg 480  
cttctgaga ttgcatggat ttccaccttg cctttctgtg gctccaacca gatccaccag 540  
atattctgtg atttcacacc tgtgctgagc ttggcctgca cagatacatt cctagtgggtc 600  
attgtggatg ccattccatgc agcggaaatt gtacccctct tcctgggtcat tgctctatcc 660  
tacatccgga ttattatagt gattctggga atgcactcag ctgaagggtca tcacaaggcc 720  
ttttccacct gtgctgctca ccttgctgtg ttcttgctat tttttggcag tgtggctgtc 780  
atgtatttga gattctcagc cacctactca gtgttttggg acacagcaat tgctgtcact 840  
tttgttatcc ttgctccctt tttcaacccc atcatctata gcctgaaaaa caaggacatg 900  
aaagaggcta ttggaaggct tttccactat cagaagaggg ctggttgggc t 951

<210> 558  
<211> 831  
<212> DNA  
<213> Unknown (H38g407 nucleotide)

<220>  
<223> Synthetic construct

<400> 558  
atggctctaa ttggaaacct atccatgatt cttctcatct tcttggacac ccattctccac 60  
acacccatgt atttcctact tagtcagctc tccctcattg acctaaatta catctccacc 120  
attgttctta agatggcatc tgattttctg tctggtaaca agtctatctc cttcactggg 180  
tgtgggattc agagtttctt cttctcggca ttagggaggtg cagaagcact acttttggca 240  
tctatggcct atgatcgta cattgtctatt tgctttcctc ttactatcc catccgcatg 300  
agcaaaagaa tgtgtgtgct gatgataaca ggtcttggga tcataggctc gatcaatgct 360  
tgtgtcaca ctgtatatgt actccatatt ccttattgcc aatccagggc catcaatcat 420  
ttcttctgtg atgtcccagc aatggtgact ctggcctgca tggacacctg ggtctatgag 480  
ggcacagtgt ttttgagcac caccatcttt ctcgtgtttc ccttcattgc tatttcatgt 540  
tcctatggcc gggttctcct tgctgtctac cacatgaaat ctgcagaagg gaggaagaaa 600  
gcctacctga cctgcagcac ccacctcact gtagtaactt tctactatgc accttttgtc 660  
tacacttata tacgtccaag atccctgcga tctccaacag aggacaagg tctggctgtc 720  
ttctacacca tcctcaccac aatgctcaac ccatcatct atagcctgag gaacaaggag 780  
gtgatggggg ccctgacacg agtgagtcag agaactctgt ctgtgaaaat g 831

<210> 559  
<211> 725  
<212> DNA  
<213> Unknown (H38g408 nucleotide)

<220>  
<223> Synthetic construct

<400> 559  
 atggatagag taaataattc tgcggtatct aaatttgtat tgattggact ttcaagctct 60  
 tgggagatgc atctttttct tttttgggtc ttctctgtgt tctacatggg aattatcctg 120  
 gaaaatctct tcatttgtgt cacagtaatt attgactctc atttaaattc cccagggtact 180  
 gcctactggc caacatttat cttcttgatc tgggtcttct cctacagttc tgactttttc 240  
 actaactgca gcatcatttc ttttccaaga tgcattgatac agatattttt catttgtgtc 300  
 atgcgtaaaa attgagatgg tgctgctcat aaccatggca tagagcaggt acactgccaa 360  
 tctgtaagcc tccccattac ctgaccacaa tgaaccccaa aatgtgtgtt tcctttgttg 420  
 gaggcacccg ggatagtcag gataatccat gctgtatctc agtttgtttt tgccataaac 480  
 ttgccttttt gtggccctaa tagagtaggt agttttcact gtgattttcc ttatgtcatg 540  
 aaacttgctt gtgtagatac ttacaaacta gaggtttagt tcaactgctaa cagtgggctt 600  
 atatccatag ctacctgttt cttattaata ataccctata ttttcatttc ggtaaccgtc 660  
 tagaatcctt cttcaggaga cttatctaaa gcatttgtgt catgttagat cacatcacag 720  
 taggg 725

<210> 560

<211> 936

<212> DNA

<213> Unknown (H38g409 nucleotide)

<220>

<223> Synthetic construct

<400> 560  
 atggacacag ggaactggag ccaggtagca gaattcatca tcttgggctt ccccatctc 60  
 cagggtgtcc agatttatct cttcctcttg ttgcttctca ttacatcat gactgtgttg 120  
 ggaaacctgc tgatattcct ggtggtctgc ctggactccc ggcttcacac acccatgtac 180  
 cactttgtca gcattctctc cttctcagag cttggctata cagctgccac catccctaag 240  
 atgctggcaa acttggtcag tgagaaaaag accatttcat tctctgggtg tctcctgcag 300  
 atctatttct ttcactccct tggagcgact gagtgctatc tctgacagc tatggcctac 360  
 gataggtatt tagccatctg ccggccctc cactacccaa cctcatgac cccaacactt 420  
 tgtgcagaga ttgccattgg ctgttggttg ggaggcttgg ctgggccagt agttgaaatt 480  
 tccttgattt cagccctccc attctgtggc cccaatcgca ttcagcacgt cttttgtgac 540  
 ttccctcctg tgctgagttt ggcttgcaat gatacgtcta caaatgtcct agtagatttt 600  
 gttataaatt cctgcaagat cctagccacc ttctgtctga tctctgtctc ctatgtgcag 660  
 atcatctgca cagtgtctag aattccctca gctgccggca agaggaaggc catctccacg 720  
 tgtgcctccc acctcactgt ggttctcatc ttctatggga gcaccccttc catgtatgtg 780  
 cggctgaaga agagctactc actggactat gaccaggccc tggcagtggt ctactcagtg 840  
 ctacacacct tctcaaccc cttcatctac agcttgcaca acaaggagat caaggaggct 900  
 gtgaggaggc agctaaagag aattgggata ttggca 936

<210> 561

<211> 635

<212> DNA

<213> Unknown (H38g410 nucleotide)

<220>

<223> Synthetic construct

<400> 561  
 gaattccttt ttataatta caatcaaaca tcaactgatt tcatcttatt ggggctgttc 60  
 ccacaatcaa gaattggcct ttctgtatct accctcattt ttctcatttt cctaattggct 120  
 ctaattggaa atctatccat gattcttctc atcttttttg acatccatct ccacacacct 180  
 atgtatttcc tacttagtca gctctccctc attgacctaa attacatctc caccattgtt 240  
 ccaaagatgg tttatgattt tctgtatgga aacaagtcta tctccttcac tggatgtggg 300  
 attcagagtt tcttcttctt gacttttagca gttgcagaag ggctgtcctt gacatcaatg 360  
 gcctatgata gttatgtggc catttgcttt cctctccact atcccatccg tataagcaaa 420  
 agagtgtgtg tgatgatgat aacaggatct tggatgataa gctctatcaa ctcttgtgct 480  
 cacacagtat atgcactctg tatcccatat tgcaagtcca gagccatcaa tcattttttc 540  
 tgtgagggat cctctgagag gtacctggga gctgcaagc ttggcgctgg gccgcggtgg 600  
 aaacggcgtg actggtaaaa ccctgggctg gccca 635

<210> 562  
 <211> 789  
 <212> DNA  
 <213> Unknown (H38g411 nucleotide)

<220>  
 <223> Synthetic construct

<400> 562  
 atgttgggga attactctag cgccactgaa ttttttctct taggcttccc tggctcccaa 60  
 gaagtatgcc gtatcctatt tgcgacctt ttcctcttgt atgcagtgc agtgatggga 120  
 aacgtgggca tcatcatcac tgtctgtgt gataaatgtc tgcagtcccc catttatatt 180  
 ttcttgggcc acctctgtgt cctggagatc ctgatcacat ccaccgctgt cccttttatg 240  
 ctctgggggt tgcctgttcc aagcaccag atcatgtctt tgacagcctg tgcctgcacag 300  
 ctatatttat acctttcttt gggtagcttg gagttggcat taatgggagt gatggctgtg 360  
 gaccgttatg tggctgtgtg taaccctttg aggtacaaca tcattatgaa cagcagcacc 420  
 ttcatattggg tgataattgt gtcattgggt ttggggtttc tttctgaaat ctggccagtt 480  
 tatggcactt ttcagcttac tttctgcaaa tcaagtgtgt tagatcattt ttattgtgac 540  
 cgaggacaat tgcctcaagt atcctgtgag gacactctt tcagagagtt tattcttttt 600  
 ctaatggctg ttttcattat cattggttct ttgatcccta cgattgtctc ctacacctac 660  
 atcatctcca ccaacctcaa gattccgtca gcctctggct ggaggaaatc cttttccacc 720  
 tgtgcctccc acttcaccta tgttgtgatt ggctatggca gctgcttgtt tctctacgtg 780  
 aaaccaag 789

<210> 563  
 <211> 951  
 <212> DNA  
 <213> Unknown (H38g412 nucleotide)

<220>  
 <223> Synthetic construct

<400> 563  
 atggatcaat acaaccattc aagcctggct gaatttgtgt tccttggctt tgccagtgtg 60  
 ggctatgtca ggggctggct ttttgtcctg ctgctattgg catacctgtt caccatctgt 120  
 ggtaacatgc tcatcttctc agtcatccga ctggatgcag ctctgcacac acctatgtac 180  
 cactttgtca gtgttcttcc ctctctggag ttgtggtata cagctaccac tatccctaag 240  
 atgttgtcta atattctcag tgagaagaaa accatttctt ttgcaggatg cctccttcag 300  
 acctacttct tccactcctt gggagcgtct gaatgctacc ttcttacagc catggcctat 360  
 gatagatacc tggccatttg tcggcccttc cactacccta taattatgac caccacactc 420  
 tgtgccaaga tggctgctgc ttgttggact tgtggcttcc tgtgtcccat ttctgaggtc 480  
 atccttgctt cccagctccc attttgtgct tacaatgaaa tccaacacat tttctgtgac 540  
 tttccacctt tgcctgagctt ggcttgcaag gacacatctg ctaacattct ggtggacttt 600  
 gccattaatg ctttcataat tcttatcact ttcttcttta tcatgatttc ttatgcaagg 660  
 atcattgggg ctgtgctgaa gataaaaaca gcatcaggaa gaaagaaggc cttttctacc 720  
 tgtgcctcac atcttgctgt ggctctcatc ttctttggga gcatcatctt catgtatgtg 780  
 cggctaaaga agagctatcc cctgacctt gaccgaacac ttgctatagt ttactccgta 840  
 ctaacaccaa tgggtcaatcc aattatctac agtcttcgta acaaggaaat cattaaagct 900  
 atcaaggaga ccatcttcca gaaggagat aaagctagtc ttgctcatct t 951

<210> 564  
 <211> 945  
 <212> DNA  
 <213> Unknown (H38g413 nucleotide)

<220>  
 <223> Synthetic construct

<400> 564  
 atgcaggggc taaaccacac ctccgtgtct gaattcatcc tcgttggctt ctctgccttc 60

ccccacctcc	agctgatgct	cttcctgctg	ttcctgctga	tgtacctgtt	cacgctgctg	120
ggcaacctgc	tcatcatggc	cactgtcttg	agcgagcgca	gcctccacat	gcccattgtac	180
ctcttctctg	gtgccctctc	catcacccag	atcctctaca	ccgtggccat	catcccgcgc	240
atgctggccg	acctgctgtc	cacccagcgc	tccatcgctt	tcctggcctg	tgccagtcag	300
atgttcttct	ccttcagctt	cggcttcacc	cactccttcc	tgtcactgt	catgggttac	360
gaccgctacg	tggccatctg	ccacccctg	cgttacaacg	tgtcatgag	cctgcggggc	420
tgcacctgcc	gggtgggctg	ctcctgggct	gggtggcttg	tcatggggat	gggtggtgacc	480
tcggccattt	tccacctcgc	cttctgtgga	cacaaggaga	tccaccattt	cttctgccac	540
gtgccacctc	tgttgaagtt	ggcctgtgga	gatgatgtgc	tggtgggtgc	caaaggcgtg	600
ggcttgggtg	gtatcacggc	cctgctgggc	tgttttctcc	tcatcctcct	ctcctatgcc	660
ttcatcgtgg	ccgccatctt	gaagatccct	tctgctgaag	gtcggaacaa	ggccttctcc	720
acctgtgcct	ctcacctcac	tgtgggtggtc	gtgcactatg	gctttgcctc	cgtcatttac	780
ctgaagccca	aaggctccca	gtctccggaa	ggagacacct	tgatgggcat	cacctacag	840
gtcctcacac	ccttctctag	ccccatcatc	ttcagcctca	ggaacaagga	gctgaaggtc	900
gccatgaaga	agacttgctt	caccaaactc	tttccacaga	actgc		945

&lt;210&gt; 565

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g414 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 565

cacacagagc	cacggcatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcctgt	cctcgctggg	ctgtcccat	ccatgtatct	ggtcacagt	120
ctgaggaacc	tgtcgtcat	cctggctgtc	agctctgact	cccacctcca	caccccatg	180
tacttcttcc	tctccaaccc	gtgctgggct	gacatcggtt	tcacttcggc	cacggttccc	240
aagatgactg	tggacatgca	gtcacatata	agagtcattt	cttatgagag	ctgcctgaca	300
cggatgtctt	tcttggtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
taggactgct	ttgtagccat	ctgtcgccct	ctgcactacg	cagtcactgt	gaatcctcac	420
ctctgtgtct	tcttagtttt	gggtgtcctt	ttccttagcc	tggtggattc	ccagctgcac	480
agttagattg	ttacaattca	ccttcttcaa	gaatgtggaa	atctctcatt	ttgtctgtga	540
gccatctcaa	cttctcaacc	ttgcctgttc	tgacagcgtc	atcaatagca	tattcatgta	600
tttcaatagt	actatgtttg	gttttcttcc	catttcaggg	atccttttgt	cttactataa	660
aattgttccc	tccattctaa	ggatttcatc	gtcagatggg	aagtataaag	ccttctccac	720
ctgtggctct	cacctggcag	ttgtttgctt	attttatgga	acaggcattg	gcatgtacct	780
gacttcagct	gtggcaccac	ccccaggaa	tggtgtgggtg	gcgtcagtga	tgtacgctgt	840
ggtcaccccc	atgctgaacc	ctttcatcta	cagcctgaga	aacagggaca	ttcaaagcgc	900
cctgtggagg	ctgcgcagca	gaacagtcga	atctcatgat	ctgttccatc	ctttttct	958

&lt;210&gt; 566

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g415 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 566

gtctccccac	tgtgggaatg	tgtgtcatga	cagcggcttc	cccacttctt	atgctctgga	60
gactcagttt	tctgtctggg	tcacagtgtg	ggctgctgca	cactacttct	ttcacagagt	120
ttgcggcttc	tttcagtttt	cctgtttaagt	tcctgtgctg	cttcttggaa	aaaagtccac	180
agcatgaatc	tctacacacc	attttgtctt	tctaagtggg	agaatcacgt	taacaatgcc	240
ttcaacctgc	catcatggaa	aaaaagttaa	agtgtggtca	ccatgttcta	agggcccgcc	300
atgatcacgt	acttgaggtc	tgactcctag	tataacctac	agtgggaaaa	cagttgggtgc	360
tgttctacag	cattgtctct	gccttcataa	aaccatcat	ctccagcctc	aggaacaagg	420
atgtaaaagg	ggcttcttgg	aaagtactta	gagtcaaagg	gacagctcaa		470

&lt;210&gt; 567

<211> 862  
 <212> DNA  
 <213> Unknown (H38g416 nucleotide)

<220>  
 <223> Synthetic construct

<400> 567  
 atggaaaatt acaatcaaac atcaactgat ttcattcttat tggggctgtt tccaccatca 60  
 agaattgacc ttttcttctt cattctcttt gttctcattt tcctgatggc tctaattgga 120  
 aacctatcca tgattcttct catcttcttg gacaccatc tccacacacc catgtatttc 180  
 ctgcttagtc agctctccct cattgacctt aattacatct ctacgattgt tcctaagatg 240  
 gcttctgatt ttctgtatgg aaacaagtct atctccttca ttgggtgtgg gattcagagt 300  
 ttcttcttca tgacttttgc aggtgcagaa gcgctgtctc tgacatcaat ggcctatgat 360  
 cgttatgtgg ccatttgctt tcctctccac tatcccatcc gtatgagcaa aagaatgtat 420  
 gtgctgatga taacaggatc ttggatgata ggctccatca actcttgtgc tcacacagta 480  
 tatgcattcc gtatcccata ttgcaagtcc agagccatca atcatttttt ctgtgatgtt 540  
 ccagctatgt tgacattagc ctgtacagac acctgggtct atgagtacac agtggtttttg 600  
 agcagcacca tctttcttgt gtttcccttc actggcattg cgtgttccta tggctgggtt 660  
 ctcttctgtg tctaccgcat gcaactctga gaaggaggaa aaaggcctat tcgacctgca 720  
 gacccacct cactgtagta actttctact atgcaccctt acgttatacc tatctatgtc 780  
 caagatccct gtttatttct gacagaggac aaggttgggg gggggggggg acaccatcct 840  
 cacctcaatg ctcaacccca tc 862

<210> 568  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g417 nucleotide)

<220>  
 <223> Synthetic construct

<400> 568  
 atggataaag aaaacagctc aatgggtgact gagtttatct tcatgggcat caccaggagc 60  
 cctcagatgg agatcatctt cttcgtggtc ttcctcatag tttacctggg taatgtagtg 120  
 gggaatatgt gtatgattat cctgattaca acagacatc agcttcacac acccatgtat 180  
 tttttcctct gcaacctctc ctttgttgac ctgggctact cctcagccat tgccccagg 240  
 atgctggctg acttcctaac aaatcacaaa gttatctcct tctccagctg tgccaccag 300  
 ttgctttttt ttgtaggttt tgtggatgct gagtgctatg tcctggcagc catggcctat 360  
 ggtcgttttg tggccatttg tcgacctc cactatagca ccttcatgtc caagcaggtc 420  
 tgcttggtgc tcatgctggg ctcttacctg gctgggtctag tgagtttagt agcccacact 480  
 accctcacct tcagcctgag ttactgtggt tccaatatca tcaatcattt cttctgcgaa 540  
 atcccaccac tcttgccctt ctcttgctca gacacctaca tcagttagat cttgctcttc 600  
 agtctgtgtg gcttcattga attcagcacc atcctcatca tcttcatctc ctataccttt 660  
 atccttggtg caatcatcag aatgcgttca gctgaaggcc gccttaaggc tttctccacc 720  
 tgcgggtctc accttactgg catcaccctc ttctatggca cagtcattgt tatgtacctg 780  
 aggccaacat ccagctactc cctggaccaa gacaagtggt cctctgtgtt ctacacggtt 840  
 atcatcccca tgttaaatcc cttgatctac agtttgcgga acaaggatgt gaaagctgct 900  
 ttcaaaaagc taattggaaa aaaatctcaa 930

<210> 569  
 <211> 1005  
 <212> DNA  
 <213> Unknown (H38g418 nucleotide)

<220>  
 <223> Synthetic construct

<400> 569  
 tctacagacc cacagaatct aatagatgtc tctatatctc tcctcctaga acctcagagg 60  
 atccagaacg gcagctgggc cttgctgggc tgttctgtgc catgtgcctg gtcacgggtg 120

tggggaacct	gctcatcatc	ctggccgtca	gtcctgactc	ccacctccac	acccccatgt	180
acttcttcc	ctccaaacct	tccttgctg	acatcggttt	cacctccacc	acgggtcccca	240
agatgattgt	ggacatccga	tctcacagca	gagtcattct	ctatgcaggc	tgcttgactc	300
agacgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgctcct	gagtgtgatg	360
gcctatgacc	agtttgtagc	catctgtcac	cctctatatc	attcagccgt	catgaacct	420
tgtttctgtg	gctttctagt	tttgttgact	tttttttttc	tcagtctttt	agacgcccag	480
ctgcacaact	tgattgcctt	acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	540
ttctgtgacc	cttctccact	cccccatctt	gcatgttggt	acaccttcac	caataacata	600
atcatgtatt	tccctgctgc	catatttggt	tttcttccca	tctcggggac	ccttttctct	660
tactataaaa	ttgtttcctc	cattctgagg	gtttcatcat	caggtgggaa	gtataaggcc	720
ttctccacct	gtgggtctca	cctgtcggtt	gtttgctgat	tttatggaac	aggcattgga	780
gggtacctca	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcgggtggc	ctcagtgatg	840
tacacgggtg	tcaccccat	gctgaacccc	ttcatctaca	gcctgagaaa	cagggatatt	900
aaaagtgtcc	tgcggtgggt	gcacggcagc	tctgtcta	ctcaacatct	tcttatctgt	960
tgcattcctt	ttgtagtgtg	ggttaaaaaa	ggcagcaggg	tcaaa		1005

&lt;210&gt; 570

&lt;211&gt; 907

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g419 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 570

atggatcacg	tcagtcataa	ctggactcag	agttttatcc	ttgctgggtt	caccaccact	60
gggaccctac	aacctcttgc	cttcttgggg	accctatgca	tctatctcct	cacacttgca	120
gggaacattc	tcattcattgt	cctggtacag	ttagattctg	gactgttcac	gcccattgtac	180
ttatttatca	gtgtcctctc	ctttgtagag	gtgtggtatg	tcagcaccac	agtgtcccatg	240
ctgctgcaca	ccttgctcca	agggtgttca	cccgtctcat	cagctgtatg	ctttattcag	300
ctatgtcttt	cattccttag	ggatgactga	gtgctacctg	ctgggtgtca	tggtactgga	360
tagctacctt	atcatctgcc	accactcca	ctaccacgca	ctcatgagca	gacaggta	420
gttacgacta	gctggggcca	gttgggtggc	tggcttctca	gctgcacttg	tgccagccac	480
cctcactgcc	actctgccct	tctgcttgaa	agaggtggcc	cattactttt	gtgacttggc	540
accactaatg	cgggtggcat	gtgtggacac	aagctggcat	gctagggccc	atggcacagt	600
gattggtgtg	gccactgggt	gcaactttgt	gctcattttg	ggactctatg	gaggtatcct	660
gaatgctgtg	ctgaagctac	cctcagctgc	cagtagtgcc	aaggccctct	ctacctgttc	720
ctcccacgta	actgtggtgg	cactattcta	tgcttctgcc	ttcacagtat	atgtgggctc	780
acctgggagt	cgacctgaga	gcacagacaa	gcttgttgcc	ttgggtttatg	cccttattac	840
cccttctctc	aatcctatca	tctatagcct	tcgcaacaag	gaggtgaaga	aggctttaag	900
gagagtc						907

&lt;210&gt; 571

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g420 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 571

ccaacgaaga	gagagaacca	cacagtgata	agggagtgtg	ttttccaggg	tttctccagc	60
tttcatgaac	acaagcttac	cctctttgtg	gtatttctta	ccttggtgtc	tttaacctg	120
gctggcaatg	tcataattgt	gacaattatc	agcattgata	gtcaccttca	cacccccatg	180
tacttctttg	ttagtatgct	ttccacttca	gagactgtct	acacattagt	cattgtacca	240
cggatgctct	ccagtctctt	aagtctaagc	caacctatct	ctttgggtgg	ctgtgccacc	300
cagatgtttt	ttttattacc	ttggccatca	acaactgctt	tctgtcaca	gcaatggggt	360
atgatcgcta	tgtggccatc	tgtaaccctt	tgaggtagat	gatcatcatg	aacaagaaag	420
tgtgtgtcca	gctggtagtg	gggtcctgca	gtgttgggct	gcttgtggcc	atagttcaga	480
tttcatctgt	gttcaggctg	cctttttgtg	ataaacagg	ggccatttat	ttctgtgata	540
tccacccagt	tatgaaactt	tctgtgtgtg	ataccactct	acatgaccta	attaattttg	600

ttgttagttc	cctgggttatt	gtgggtgccgc	tgggttttgg	cttcatctcc	tacatcctca	660
tcctctctac	catcctcaag	gtcacctctc	ctgagggccg	gaaaaaggct	tttgcaactt	720
gtgcctccca	cctcactgtg	gttatcatcc	actatggctg	tgctccatt	gcctacctca	780
agcccaagtc	agagaacacc	agggatcagg	accagcta	ttcagtgaca	tacaccgtct	840
ttactccact	acttaatcct	gttgtgtaca	ctttgaggaa	caaggaggtc	aagaatgccc	900
ttcacgtgc	tattggcaaa	aaaccttttg	cctagaatct	tcctcagttt	gacatatagt	960
cagtcatagt	ctgggtattt	ttttaagctc	gagaaaattg	aatcct		1006

&lt;210&gt; 572

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g421 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 572

atgtccataa	ccaaagcctg	gaacagctca	tcagtgacca	tggtcatcct	cctgggattc	60
acagaccatc	cagaactcca	ggccctctc	tttgtgacct	tcctgggcat	ctatcttacc	120
accctggcct	ggaacctggc	cctcattttt	ctgatcagag	gtgacacca	tctgcacaca	180
cccattgact	tcttcttaag	caacttatct	ttcattgaca	tctgtactc	ttctgtgtgt	240
gtccccaata	tgctcactga	cttcttcttg	gagcagaaga	ccatatcatt	tggtggctgt	300
gctgctcagt	tttttttctt	tgctggcatg	ggtctgtctg	agtgcctcct	cctgactgct	360
atggcatacg	accgatatgc	agccatctcc	agcccccttc	tctacccac	tatcatgacc	420
cagggcctct	gtacacgc	ggtgggtggg	gcatatgttg	tggtcttctc	gagctccctg	480
atccaggcca	gtcccatatt	taggcttcac	ttttgcgac	ccaacatcat	caaccacttc	540
ttctgcgacc	tcccaccagt	cctggctctg	tcttgctctg	acaccttcct	cagtcaagtg	600
gtgaatttcc	tcgtgggtgt	cactgtcgga	ggaacatcgt	tcctccaact	ccttatctcc	660
tatggttaca	tagtgtctgc	ggtcctgaag	atcccttcag	cagagggccg	atggaaagcc	720
tgcaacacgt	gtgcctcgca	tctgatgggt	gtgactctgc	tggttgaggac	agcccttttc	780
gtgtacttgc	gacccagctc	cagctacttg	ctaggcaggg	acaaggtggt	gtctgttttc	840
tattcattgg	tgatcccat	gctgaaccct	ctcatttaca	gtttgaggaa	caaagagatc	900
aaggatgccc	tgtggaaggt	gttggaagg	aagaaagtgt	tttct		945

&lt;210&gt; 573

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g422 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 573

atgccttgaa	agatggagtc	aataaacaca	aacttcactg	tcactgaatt	tgtgttctctg	60
gggttgctct	ctgaacaaaa	gatacagctt	attcttttta	ttatgttctt	gttctattta	120
tcaacgggtg	ctggaaatgt	tataatcate	actattatct	agatggaacc	tctctccaa	180
accccatgt	acttcttctc	cactaattta	tcctttcttg	acatttgcta	cacatccacc	240
aatgtccccc	aaatgctgtc	caacatggcg	gggaaaaaga	acaccatctc	attctccagc	300
tgcgctactc	agatgtactt	ctccctctcc	tttggaatga	ttgtgtctctc	cttggtgtca	360
tggtttatga	cagatatgta	gccatttgct	atcctcttca	ttataccttc	attatggacc	420
aaaacacctg	cattcaactg	gcagttat	cttggtccag	tagcttctctg	agttccatgg	480
ttatcaatgt	tctcacgttg	agtttgccct	actgtgggcc	taatctctg	aatcactttt	540
tctgtgaggt	actttctgtc	ctgaggttgg	cttgaccaa	cacctcttc	acagagctgg	600
ttgtttttat	cttcagtatc	atcattgtct	tcctcccttt	cctctcatt	gttggttctc	660
atgtccggat	ccttcaatct	gttctcagga	tgcggtcagc	ctctgggcgg	tatcaggcat	720
tatccacctg	tacctccat	ttgacagtgg	taaccttatt	tatgggactg	ccatcttcat	780
ggacatgaga	ccacagtcga	ggtcctcctg	ggctggcgcc	aagatcattg	cggttttcta	840
cacgggtggc	acacccatgc	ttaacccctt	gatttacagc	ctgaggaacc	aagatgtgaa	900
aggagctcga	aggagagcta	ttgcaaagca	gaggatgtga	cagctgtta		949

&lt;210&gt; 574

<211> 1022  
 <212> DNA  
 <213> Unknown (H38g423 nucleotide)

<220>  
 <223> Synthetic construct

<400> 574  
 atgccaaagc taaattccac ttttgtgact gagttcctct ttgaagggtt ctccagcttc 60  
 aggcggcagc acaaacttgt cttctttgtt gtcttcctaa ctttgtacct gctgactctc 120  
 tctggcaatg tgattatcat gaccattatt cgcttgacc atcatcttca caccctcatg 180  
 tactttctcc tgtgcatgct atccatctct gagacctgct acactgtggc catcattccc 240  
 catatgcttt ctggtctctt gaatcctcat cagccattg ccacccaaag ctgtgccact 300  
 cagctcttct tctatctcac ctttggcatc aacaactgct tcctgctcac agtcatggga 360  
 tatgaccgct atgtggccat ctgcaacccc ctaaggattt cagtcacatc gggtaagagg 420  
 gcctgtatcc aactggcctc tggatcactg gggattggcc ttggcatggc cattgtccaa 480  
 gtaacatctg tgtttggcct gccattctgt gatgcctttg tcatctccca cttcttctgt 540  
 gatgtgagac acctgctgaa gctggcctgc acagacacca ctgtcaatga gataatcaac 600  
 tttgttgtca gcgtctgtgt ccttgttcta cctatgggcc tggctcttat ctctatgtc 660  
 ctcatcatct ccaccattct taagattgct cagctgaag gtcagaagaa ggcctttggc 720  
 acctgcgctt ccacctcac agtggctatc atccactatg gctgtgcctc catcatctac 780  
 ctgaagccta agtccagag ttccctggga caggacagac tcatctcagt gacctacact 840  
 catcactccc ctactgaacc ctgttgtgta cagcctgaag aacaaggagg tcaaagatgc 900  
 tctgcacaga gccgtggggc aaaaaactct gtctccttaa tgaagagagg ttgtgaaggc 960  
 ttttcctttg cgtttataaa tatgtactaa tttttaatgc tctttcaata atgcccttat 1020  
 gt 1022

<210> 575  
 <211> 938  
 <212> DNA  
 <213> Unknown (H38g424 nucleotide)

<220>  
 <223> Synthetic construct

<400> 575  
 atggatattg gcctgagtat agccaatagc tcagggtttc aactgtctga gttcattctg 60  
 atagggttcc caggcattca tgagtggcag cactggctct ccctgccctt agctcttggt 120  
 gccaatctcc tcatcataat caccattcaa catgagacca tgctacatga acccatgtac 180  
 catttgctgg gcatattagc agtgggtggc attggcctgg ccaccacat catgcccaag 240  
 atcctggcca tcttctggtt tgatgccaag gccatcagcc tccttgagtg ttttgctcag 300  
 atctatgcca tccactcttt catgtgcatg gagtcaggca tcttcctctg catggcagtg 360  
 gatagatata tggccatttg ttatcccctt cagtacactt ccatagttac tgaagctttt 420  
 gtcacaaag ccacactgtc agtagtgctc aggaatggcc tgttgaccat ccagtgcca 480  
 gtattggctg ccagcgaca ctactgtcc aggaatgaga ttgatcagtg cctctgctct 540  
 aacttggggg tcacaagtct ggctgtgat gacaccata ttaacagggt ttaccagctg 600  
 gccttggtct gggttgtggt tgggagtgc atgggtctgg tctttgcttc ctattctttg 660  
 attattcact cagtgtgaa gctgaactct gctaaagcaa catctaaggc cctgaatacc 720  
 tgcagctccc acctatcct cattctcttt ttctacacag ctattattgt agtatctgtc 780  
 accacctggc aggaagaagg gctcccgcga tccctgttct cctcaatgtg ctgcatattg 840  
 tcatcccctc agccctaac cccatagtat atgcccttag gacctaggag ctgagagcgg 900  
 gcttcagaa gctgcttggt ttgggcgagt atgtgtcc 938

<210> 576  
 <211> 945  
 <212> DNA  
 <213> Unknown (H38g425 nucleotide)

<220>  
 <223> Synthetic construct



&lt;400&gt; 576

atgtttctccc	caaaccacac	catagtgaca	gaattcattc	tcttgggact	gacagacgac	60
ccagtgtctag	agaagatcct	gtttggggta	ttccttgcca	tctacctaat	cacactggca	120
ggcaacctgt	gcatgatcct	gctgatcagg	accaattccc	acctgcaaac	acccatgtat	180
ttcttctctg	gccacctctc	ctttgtagac	atttgctatt	cttccaatgt	tactccaaat	240
atgtgtcaca	atttctctc	agaacagaag	accatctcct	acgctggatg	cttcacacag	300
tgtcttctct	tcategccct	ggtgatcact	gagttttaca	tccttgcttc	aatggcattg	360
gacgctatg	tagccatttg	cagccctttg	cattacagtt	ccaggatgtc	caagaacatc	420
tgtgtctgtc	tggtcactat	cccttacatg	tatgggtttc	ttagtgggtt	ctctcagtca	480
ctgctaacct	ttcactttatc	cttctgtggc	tcccttgaaa	tcaatcattt	ctactgcgct	540
gatectctc	ttatcatgct	ggcctgctct	gacaccctg	tcaaaaagat	ggcaatgttt	600
gtagttgcag	gctttaatct	ctcaagctct	ctcttcacga	ttcttctgtc	ctatcttttc	660
atttttgcag	cgatcttcag	gatccgttct	gctgaaggca	ggcacaaaag	cttttctacg	720
tgtgcttccc	acctgacaat	agtcactttg	ttttatggaa	ccctcttctg	catgtacgta	780
aggcctccat	cagagaagtc	tgtagaggag	tccaaaataa	ctgcagtctt	ttatactttt	840
ttgagcccaa	tgctgaaccc	attgatctat	agcctacgga	acacagatgt	aatccttgcc	900
atgcaacaaa	tgattagggg	aaaatccttt	cataaaattg	cagtt		945

&lt;210&gt; 577

&lt;211&gt; 771

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g426 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 577

atgtttctac	tggtggccat	cctggcagcc	acagacctgg	gcttagccac	atctatagcc	60
ccagggttgc	tggctgtgct	gtggcttggg	ccccgatctg	tgccatatgc	tgtgtgcctg	120
gtccagatgt	tctttgtaca	tgcactgact	gccatggaat	caggtgtgct	tttggccatg	180
gcctgtgatc	gtgctgcggc	aatagggcgt	ccactgcact	accctgtcct	ggtcacaaaa	240
gcctgtgtgg	gttatgcagc	cttggccctg	gcactgaaag	ctgtggctat	tgttgtacct	300
ttcccactgc	tggtyggcaaa	gtttgagcac	ttccaagcca	agaccatagg	ccataacctat	360
tgtgcacaca	tggcagtggg	agaactgggtg	gtgggttaaca	cacaggccac	caacttatat	420
ggctctggcac	tttactggc	catctcaggt	atggatatc	tgggtatcac	tggctcctat	480
ggactcattg	cccatgctgt	gctgcagcta	cctaccggg	aggcccatgc	caaggccttt	540
ggtacatgta	gttctcacat	ctgtgtcatt	ctggccttct	acataacctg	tctctctctc	600
tacctgcac	accgcttttg	tcatacact	gtcccaaaag	ctgtgcacat	ccttctctcc	660
aacatctact	tgtgtgtgcc	acctgcctc	aacccctca	tctatggggc	cgcaccaag	720
cagatcagag	accgactcct	ggaaaccttc	acattcagaa	aaagcccggt	g	771

&lt;210&gt; 578

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g427 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 578

gtgagcatga	gcttcttaat	aagaagtgat	tcaacactac	acactccaat	gtgcttgttc	60
ctcagtcate	tctcctttgt	agatctctat	tatgccacca	atgccactcc	tccgatgctg	120
gttaactttt	ttttccaag	agaaaaaccg	tttcctttat	tggttgcttt	atccaatttc	180
accttttcat	tgacttgggt	atcacagatt	atcatatgct	cacagtgatg	gtgtatgacc	240
actacatggc	catctgcaag	cctttgttat	atggaagcaa	aatgtccagg	tgtgtctgcc	300
tctgtctcac	tgctgtcccc	tatatattatg	gctctgcaaa	tggcttggtg	caggatcatcc	360
tgatgctttg	tctgttcttc	tgtgaaccca	atgagatcaa	ccactttttt	ttttttggag	420
aaaatgcatt	atatgcacat	ttaattccac	tataaatttt	tgaatggacg	gttggagagg	480
aagggagaaa	tacatattaa	cggagagaat	accacccaga	aagtatatac	aatgggagaa	540
aggaacctgt	tgatccaagt	ttccatattc	ttattatggc	atataagggtc	atgattattt	600
tctcagtatg	aagcatctcc	cagggtctgac	tctgatgtaa	aattggagat	caaccacttt	660

tattatgcag	aaccacccct	cttagtcctc	gcctgcttgg	atacttatgt	caaagaaact	720
gccatgttca	tgggtggctg	ttccaacctc	atctgccctc	tcactatcat	ctttattttc	780
tacactttca	tcttcacaga	cattctgcat	atctgcactg	ctgaggggaag	gtacaatgcc	840
ttctccacct	gcgggtccct	tgtgactgcc	gtcactgtct	ttcaaggaac	gctgtttcac	900
atgtgcctga	ggcccccttc	tgaggcatct	gtagaacagg	ggaaaattgt	agctgctttt	960
tatatctttg	tgagtcctac	gttaaaccce	ttgatctacc	gtctgaggaa	taaaaatgtt	1020
aaaagaacaa	taaggggaagt	tatccaaaag	aaactgtttg	ctaagtaagg	taga	1074

&lt;210&gt; 579

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g428 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 579

atgtttggtg	ctaattctcac	caccttccat	cccactctat	tcattctcct	tggcatccca	60
ggactggagc	aataccacat	ctggctttcc	attcctttct	accttatgta	catcactgca	120
gtcttgggaa	atggagccct	catectagtt	gtcctcagtg	aacacaccct	ccatgtcttc	180
ctatccatgc	tggctggcac	tgatatectg	ctatccacca	ccactgtgcc	taaggccttg	240
gcgatcttct	gggtccacgc	tggggagata	gcctttgatg	cctgcattac	tcagatgttt	300
ttcattcatg	ttgcctttgt	ggctgagtca	ggaatcctgc	tggccatggc	atttgacagt	360
tatgtagcca	tttgtactcc	cttgagatac	actaccatct	taacttctat	ggtaaatgga	420
aaaatgacct	tgacaatctg	gggacaaaag	attgggacaa	tttttcctgt	catattcctg	480
ctgaagaggc	tgccatactg	tcagaccaat	atcatcccc	actcatactg	tgagcacatt	540
ggggtggccc	aattggcctg	tgctgacata	actgtcaata	tctggtatgg	cttttcagtg	600
ccaatggcat	cggttttggt	agatgttgca	ttcattgggt	tttccctacac	tttgatcctc	660
caggctgtgt	ttagacttcc	ttcccaggag	tcccagcaca	aagctcttaa	cacctgtggg	720
tctacattgg	agttgttctc	ctcttcttca	tcccatcatt	ttttactttc	ctgacccacc	780
gctttggcaa	gaatatcccc	catcatgtcc	acatacttct	ggcaaatctc	tacttgcttg	840
ttcccccatg	cttaacccca	ttatctacgg	agagaagacc	aagcaaatca	gggacagtat	900
ggctcatatg	ttatctgtgg	tggggaagtc	ttgagac			937

&lt;210&gt; 580

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g429 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 580

atgaagatga	agatagatcc	caaatgcaat	ggcacggagg	taactgaatt	tattctgttg	60
ggactgacta	gccagccaga	gctgcagcct	atgctctttg	tggatttcct	cctgattttac	120
ctcatcacc	tgactgggaa	atttgggatg	attttcctaa	tcagattcac	tcctcagctc	180
caaaccaca	tgtatttttt	ccttactcat	ttagcatgtg	tggatatatt	ttactccact	240
aatgtctctc	cacagagcct	gttaatttct	tatctgagaa	gaagaccatt	tcctacgctg	300
gggtgtctgg	ccagtgtttt	gtctttgtga	ctctgctcct	tactgagtat	tacatgcttg	360
gtgccatggc	ctatgactgc	tacatggcaa	tctgcaatcc	cctacattac	agcagcaaaa	420
tgtccagagc	agtttgcac	tgccctggta	ctttcccta	cttctggggg	tctatgggtg	480
gcacgatgca	agtaatactg	acctctcggt	tgctcttttt	tggacccaac	accatcaacc	540
atttctactg	tactgaccca	cccctcttaa	tgttgacatc	ttctgacact	tacataaaaac	600
aaactgcctt	gtttgtgtca	gcagggatta	acctcacagt	ttccctgctc	atcattctca	660
tctcctacat	tttcattttc	atcaccatta	tgaggatccg	ttccagtga	gggcagctca	720
aagccttctc	cacctgtggc	tcccacctga	cagctgtcac	tatgttctat	gggtccctat	780
tctgcatgta	cctgagacca	acaaatgagc	tgtctgttga	gcaagggaaa	atgggagtgg	840
tgttttgtat	ttttgtgagt	cccatgctga	acctgtttat	ctaccgcctg	agaaacaagg	900
atgtgaaaca	ggccttgaaa	agagtgttta	tgagaaacct	t		941

&lt;210&gt; 581

<211> 958  
 <212> DNA  
 <213> Unknown (H38g430 nucleotide)

<220>  
 <223> Synthetic construct

<400> 581

atgagtccttc	tattctgaga	ctaagatatg	agaaacttta	caccactgtc	tggatttatt	60
atcctgggat	tcacggatca	cccagaatta	cagtgtcttc	tttttgtgtt	gtttcttctc	120
atctatatgt	tcaccgttgt	tggaatctt	ggcatgattc	tattaatcaa	gattgactca	180
catctccata	ctccaatgta	cttttctctc	agtaacttgt	gccttggtga	cttctgttat	240
tcttctgtca	ttgcccctaa	tatgctgata	aatttctggg	tggagaaccc	agtcatttca	300
tttaaatgaat	gtgccactca	attcttcttt	tttggctcct	ttgctggcat	tgagggtttt	360
ctgttggctg	tcattggccta	tgactgttat	gtggccatct	gcaagcctct	gctttataca	420
gtcctgatgt	cacccacact	cagtgccctc	ctgggtgttag	ccacatatct	tttgggcttt	480
gtaaatgctg	ccattcacac	tggtctcacc	ttccagctgt	cattctgccca	ctccaatctc	540
attaactatt	ttttttgtga	tattccaccc	ctcctgaaac	tcttggtctg	atacacacat	600
caatgagggt	gtcatttttg	cctttgccag	ttttaatgaa	ttgagctgtc	tcctactgat	660
tcttgtttcc	tgtctctaca	tccttgctgc	catcttgaag	atccactctg	cagaagggag	720
gcacaaggcc	ttctccacct	gtgcttccca	cttggcggtg	gtcactatct	tctttgggac	780
aatcctgttc	atgtatctct	gcgtcccagc	tccagctact	caatggatca	agacaaagtg	840
gtgtctgtct	tacacagtag	tcattcccat	gttgaatcct	ttcatctata	gtttgagaaa	900
caaggaagtc	aaagcttctt	taagtaaaat	gtttaaaaca	gtctcttata	tctctact	958

<210> 582  
 <211> 897  
 <212> DNA  
 <213> Unknown (H38g431 nucleotide)

<220>  
 <223> Synthetic construct

<400> 582

atgggattac	caggcattca	tgagtggcag	cactggctct	ccctgcccct	gactctgctc	60
tacctcttag	ctcttggtgc	caacctctc	atcataatca	ccattcaaca	tgagaccgtg	120
ctacatgaac	ccatgtacca	tttgctgggc	atattagcag	tggtggacat	tggcctggcc	180
accaccatca	tgcccaagat	cctggccatc	ttctggtttg	atgccaaagg	cattagcctc	240
cccattgtgt	ttgctcagat	ctatgccatc	cactgcttct	tctgcataga	gtcaggcatc	300
tttctctgca	tggcagtaga	cagatacata	gccatctgtc	gccctcttca	gtaccctctc	360
atagtcacta	aagcttttgt	cttcaaagcc	acagggttca	tcattgctcag	gaatggcctg	420
ttgaccatcc	cagtgcctat	actggctgcc	cagagacact	actgttccag	gaatgaaatc	480
gagcactgcc	tctgctctaa	cttgggggtt	atcagcctgg	cttgtgatga	catcactgtg	540
aacaaatttt	accaactgat	gctagcatgg	gtcttggttg	ggagtgatat	ggctctggta	600
ttttcttctc	atgctgtaat	ccttactct	gtgctgaggc	tgaactcagc	agaagcaatg	660
tccaaggctc	tgagcacttg	tagctccac	ctcatctcca	tcctcttcca	cacaggtatc	720
attgtgctgt	ctgtcacaca	ccttgagag	aaaaagattc	cccttatctc	tgtgttctct	780
aatgtgctgc	acaatgtcat	ccccctgca	ctcaaccccc	tggcctgtgc	actcaggatg	840
cacaaactca	gactgggctt	tcagagactg	cttggactgg	gtcaggacgt	gtccaag	897

<210> 583  
 <211> 951  
 <212> DNA  
 <213> Unknown (H38g432 nucleotide)

<220>  
 <223> Synthetic construct

<400> 583

atgatgagac	ttatgaaaga	ggttcgaggc	agaaatcaaa	cagaagtaac	agaatttctc	60
ctcttaggac	tttccgacaa	tccagatcta	caaggagtcc	tctttgcatt	gtttctgttg	120

atctatatgg	caaacatggt	gggcaatttg	gggatgattg	tattgattaa	gattgatctc	180
tgtctccaca	cccccatgta	tttctttctc	agtagcctct	cttttgtaga	tgctctttac	240
tcttcttccg	tactcccaa	gatgctggtg	aacctcatgg	ctgagaataa	ggccatttct	300
tttcatggat	gtgctgcccc	gttctacttc	tttggtcctc	tcctggggac	tgagtgtctc	360
ctggtggcca	tgatggcata	tgaccgctat	gcagccattt	ggaacccctc	gctctacca	420
gttctcggtg	ctgggagaat	ttgctttttg	ctaatagcta	cctccttctt	agcaggttgt	480
ggaaatgcag	ccatacatac	agggatgact	tttaggttgt	ccttttggtg	ttctaatagg	540
atcaaccatt	tctactgtga	caccccgcca	ctgctcaaac	tctcttgctc	tgataccac	600
ttcaatggca	ttgtgatcat	ggcattctca	agttttattg	tcatcagctg	tgttatgatt	660
gtcctcatct	cctacctgtg	tatcttcatt	gccgtcttga	agatgccttc	gttagagggc	720
aggcacaagg	ccttctccac	ctgtgcctct	tacctcatgg	ctgtcaccat	attcttttga	780
acaatcctct	tcatgtactt	gcgccctaca	tctagtact	caatggagca	agacaagggt	840
gtctctgtct	ttatacagt	aataatccct	gtgctaaatc	ccctcatcta	tagtttaaaa	900
aataaggatg	taaaaaaggc	cctaaagaag	atcttatgga	aacacatctt	g	951

&lt;210&gt; 584

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g433 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 584

atgagtcaca	ccaatgttac	catcttccat	cctgcagttt	ttgtccttcc	tggcacccct	60
gggttggagg	cttatcacat	ttggctgtca	atacctcttt	gcctcattta	catcactgca	120
gtcctgggaa	acagcatcct	gatagtggtt	attgtcatgg	aacgtaacct	tcatgtgccc	180
atgtattttct	tcctctcaat	gctggccgct	atggacatcc	tgctgtctac	caccactgtg	240
cccaaggccc	tagccatctt	ttggcttcaa	gcacataaca	ttgcttttga	tgctgtgtgc	300
accaaggcct	tctttgtcca	tatgatgttt	gtgggggagt	cagctatcct	gttagccatg	360
gcctttgatc	gctttgtggc	cattttgtgc	ccactgagat	atacaacagt	gctaacatgg	420
cctgtttgtg	ggaggattgc	tctggccgct	atcacccgaa	gcttctgcat	catcttccca	480
gtcatattct	tgctgaagcg	gctgcccttc	tgccaaacca	acattgttcc	tcactcctac	540
tgtgagcata	ttggagtggc	tcgttttagcc	tgtgtgaca	tcactgttaa	catttgggat	600
ggcttctcag	tgcccattgt	catggtcac	ttggatgtta	tcctcatcgc	tgtgtcttac	660
tcactgatcc	tccgagcagt	gtttcggttg	ccctcccagg	atgctcggca	caaggccctc	720
agcacttggt	gctccacact	ctgtgtcatc	cttatgtttt	atgttccatc	cttctttacc	780
ttattgacct	atcatttttg	gcgtaatat	cctcaacatg	tccatatctt	gctggccaat	840
ctttatgtgg	cagtgccacc	aatgctgaac	cccattgtct	atgggtgtgaa	gactaagcag	900
atacgtgagg	gtgtagccca	ccggttcttt	gacatcaaga	cttgggtgctg	t	951

&lt;210&gt; 585

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g434 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 585

atgcagagga	gcaatcatac	agtgactgag	tttatactgc	tgggcttcac	cacagaccca	60
ggaatgcagc	tgggcctctt	cgtgggtgttc	ctgggcgtgt	actctctcac	tgtggttagga	120
aatgacaccc	tcacgtgttt	gatctgtaat	gactcctgcc	tccacacacc	catgtatttt	180
gtcgcgtgaa	atctgtcggt	tctggatctc	tgggtattct	ctgtctacac	cccaaagatc	240
ctagtgcact	gcattctctga	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
ttcttctctg	cagggtctggc	ctatagttag	tgctacctgc	tggctgccgt	ggcttatgac	360
cgctacgtgg	ccatctccaa	gcccttgctt	tatgcccagg	ccatgtccat	aaagctgtgt	420
gcattgctgg	tagcagtcct	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
aaaacgtttt	cctttaactt	ctgccgtgaa	aacatcatgt	atgacttttt	ctgtgatttg	540
cttcccttgg	tggagctggc	ctgtggcgag	aagggcggtc	ataaaaattat	gatgtacttc	600
ctgctggcct	ccaatgtcat	ctgccccgca	gtgctcatcc	tggcctccta	cctctttatc	660

atcaccagt	g	tcttgaggat	ctcctcctcc	aagggctacc	tcaaagcctt	ctccacatgc	720
tctcccacc	g	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgctctc	780
cccagatcta	g	ctattctttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttccccatgt	t	gaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	t	ccca					915

&lt;210&gt; 586

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g435 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 586

atgcttccct	ctaatactac	ctcaacacat	ccagctgtct	ttttgttgg	aggaattcct	60
ggtttggaac	acctgcatgc	ctggatctcc	atccccctt	gctttgctta	tactctggcc	120
ctgctaggca	actgtaccct	tctcttcatt	atccgggctg	atgcagccct	ccatgaaccc	180
atgtacctct	ttctggccat	gttggcaacc	attgacttgg	ttctttcttc	tacaacgctg	240
cccaaaatgc	ttgccatatt	ctggttcagg	gatcaggaga	tcaacttctt	tgctgtctg	300
gtccagatgt	tcttccctca	ctccttctcc	atcatggagt	cagcagtgtc	gctggccatg	360
gcctttgacc	gctatgtggc	catctgcaag	ccattgcact	acacgacgg	cctgactggg	420
tcctcatca	ccaagattgg	catggctgct	gtggcccggg	ctgtgacact	aatgactcca	480
ctccccctcc	tgctcagacg	cttccactac	tgccgaggcc	cagtgtattg	ccattgtctac	540
tgtgaacaca	tggtgtgggt	aaggctggcg	tgtggggaca	ctagcttcaa	caatatctat	600
ggcattgctg	tgccatgtt	tagtgtgtg	tggacctgc	tctttgttat	cctgtcttat	660
gtcttcatcc	ttcaggcagt	tctccagctt	gcctctcagg	aggcccgtca	caaggcattt	720
gggacatgtg	tgtctcacat	aggtgccatc	ctgtccacct	acactccagt	agtcactctc	780
tcagtcatgc	accgtgtagc	ccgccatgct	gcccctcgtg	tccacatact	ccttgctatt	840
ttctatctcc	ttttcccacc	catggtcaat	cctatcata	atggagtcaa	gaccaagcag	900
attcgtgagt	atgtgctcag	tctattccag	agaaagaaca	tg		942

&lt;210&gt; 587

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g436 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 587

atgttaaaga	aaaaccatac	agccgtgact	gagtttgttc	tcttgggact	gacagatcgg	60
gctgagctgc	agtcctctct	ttttgtggta	tttctagtca	tctaccttat	cacagtaatc	120
ggcaatgtga	gcatgatctt	gttaatcaga	agtgactcga	cactacacac	tccaatgtac	180
ttcttctca	gtcacctctc	ctttgtagat	ctctgttata	ccaccaatgt	tactcctcag	240
atgctgggta	actttttatc	caagagaaaa	accatttcct	tcacgggctg	ctttatccaa	300
tttcaacttt	tcattgcact	gggtgattaca	gattattata	tgctcacagt	gatggcttat	360
gaccgctaca	tgcccatctg	caagcccttg	ttatatggaa	gcaaaatgac	caggtgtgtc	420
tgctctgtgc	tcgctgtctg	tccttatatt	tatggctttg	caaatggtct	aagcacagac	480
caccctgatg	cttcgtctgt	ccttctgtgg	acccaatgac	atcaaccact	tttactgtgc	540
ggacccaccc	ctcttagtcc	tcgctgtctc	agatacttat	gtcaaaagaga	ccgccatgtt	600
ggtggtggct	ggttccaacc	tcatttgctc	tctcaccgtc	atcctcattt	cctacacttt	660
catcttcaat	gccattctgc	gtatccacac	tgctgagggg	aggcgcaagg	ccttctccac	720
ctgcgggtct	catgtgaccg	ctgtcactgt	cttctatggg	acactgttct	gcatgtacct	780
gaggccccct	tctgagacat	ctatacaaca	ggggaaaatt	gtagctgttt	tttatatctt	840
tgtgagtcgg	atgttaaacc	cattgatcta	cagcctgagg	aataaagacg	ttaaaagaag	900
tataaggaaa	gttattcaaa	agaaactgtt	tgctaag			937

&lt;210&gt; 588

&lt;211&gt; 942

&lt;212&gt; DNA

<213> Unknown (H38g437 nucleotide)

<220>

<223> Synthetic construct

<400> 588

atgtcagcct ccaatatcac cttaacacat ccaactgcct tcttgttggt ggggattcca	60
ggcctggaac acctgcacat ctggatctcc atccctttct gettagcata tacactggcc	120
ctgcttggaa actgcactct ccttctcatc atccaggctg atgcagccct ccatgaaccc	180
atgtacctct ttctggccat gttggcagcc atcgacctgg tcctttcttc ctcagcactg	240
cccaaaatgc ttgccatatt ctggttcagg gatcgaggaga taaacttctt tgcctgtctg	300
gcccagatgt tcttccttca ctcccttctcc atcatggagt cagcagtgct gctggccatg	360
gcctttgacc gctatgtggc tatctgcaag ccactgcact acaccaaggt cctgactggg	420
tcctcatca ccaagattgg catggctgct gtggcccggg ctgtgacact aatgactcca	480
ctccccctcc tgctgagatg tttccactac tgccgaggcc cagtgatcgc tcaactgtac	540
tgtgaacaca tggctgtggt gaggctggcg tgtggggaca ctagtctcaa caatatctat	600
ggcatcgctg tggccatggt tattgtggtg ttggacctgc tccttggtat cctgtcttat	660
atctttatct ttcaggcagt tctactgctt gcctctcagg aggcccgcta caaggcattt	720
gggacatgtg tctctcatat aggtgccatc ttagccttct acacaactgt ggtcatctct	780
tcagtcatgc accgtgtagc ccgccatgct gcccctcatg tccacatcct ccttgccaat	840
ttctatctgc tcttcccacc catggtcaat cccataatct atggtgtcaa gaccaagcaa	900
atccgtgaga gcatcttggg agtattccca agaaaggata tg	942

<210> 589

<211> 936

<212> DNA

<213> Unknown (H38g438 nucleotide)

<220>

<223> Synthetic construct

<400> 589

atgtcagcct ccagtatcac ctcaacacat ccaacttcct tcttgttgat ggggattcca	60
ggcctggagc acctgcacat ctggatctcc atccctttct cagcatatac actggccctg	120
cttggaact gcacctcct tctcatcacc caggctgatg cagccctcca tgagcccata	180
tacctcttcc tggccatggt ggcagccatc gacctggtcc tttctctctc agcattgccc	240
aaaatgcttg ccatattctg gttcagggat cgggagatca acttttttgc ctgtctggtc	300
cagatgttct tccttctctc cttctccatc atggagtcag cagtgtctgct ggccatggcc	360
tttgaccgct atgtggccat ctgcaagcca ctgactaca ccacggtcct gactgggtcc	420
ctcatcacca agattggcat ggctgtctg gcccgggctg tgacactaat gactccactc	480
cccttctctg tgagatgttt ccactactgc cgaggcccag tgattgcccg ctgtactgt	540
gaacacatgg ctgtgtcag gctggctgtg ggaacactag cttcaacaat atctatggca	600
ttgctgtggc catgtttatt ggagtgttg atctattctt tatcatccta tcttatatct	660
ttatccttca ggcagttcta caactctcct ctcaggaggc ccgctacaaa gcatttggga	720
catgtgtctc tcacataggt gccatcttag ccttctacac accttcagtc atctcttcag	780
tcatgcaccg tgtggccgc tgtgtctgcg cacacgtcca cattctctc gccaatctct	840
atctgctctt cccaccatg gtcaatccca tcactacagg cgtaaagacc aagcagatcc	900
gtgacagtct tgggagtatt cccgagaaag gatgtg	936

<210> 590

<211> 955

<212> DNA

<213> Unknown (H38g439 nucleotide)

<220>

<223> Synthetic construct

<400> 590

atgacaaccc acaactccac tggtagcagc cactcactct tcattctgct gagcattcct	60
ggcttagaag accagcacac atggatgtct ctccctttct ttatttctta ccttgttgct	120
ttccttggga acagctcat catcttcac atcatcactg aatgcagcct ccacgaaccc	180

atgtacac	ttt	tcctctgcat	gctggctgtg	gctgac	ctta	tcctgtctac	taccactgtg	240
cccaaggccc	tagccatatt	ttggttctat	gctggagcaa	tatcccttgg	tggtgtgtt			300
acccaaatct	tctttatcca	tgtacac	ttc	atcgaggaat	caggaattct	gttggcgatg		360
gcacttgacc	gctatgtggc	catctgtgat	ccactgcact	ataccacagt	gctcagtcgt			420
gcaaaaatca	caaagattgg	cttggctgtg	gtcctgagaa	gcttctgtgt	gatcatgcca			480
gatgtgtttc	tggtaaagcg	gctgccttcc	tgccatagca	atctgctgcc	acatacctac			540
tgtgagcaca	tggtgtgtgc	caagtttgct	tgtgctgata	ttcatgtcaa	tggttggtat			600
ggcttgtctg	tccttctcta	tactgtagt	ctagatgcct	tgcttatctt	agtgtcctaa			660
agcttcatcc	tgtatacag	cttccac	ctc	ggagctcggc	aaaaggctct			720
gggcacatgt	ggctcccacc	tcagagtc	at	ttccatgttc	tacttgcc	gtatttttac		780
cataattacc	cagcggtttg	ggcaccatgt	tcctctccat	acacacattc	tgctgggtaa			840
tgtctgggtg	ttggctcctc	ccatgctgaa	ccccatcatt	tatgggatca	acaccaggca			900
gattcaagag	tgtgtgctca	gtcttttctc	ctcacagagg	aatgatgct	agatt			955

&lt;210&gt; 591

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g440 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 591

atgaattggg	taa	atgacag	catcatacag	gagtttattc	tgctgggttt	ctcagatcga	60
ccttggtg	agtttccact	ccttggtg	ttcttgattt	cttacactgt	gaccatcttt		120
ggcaatctga	ccattattct	agtgtcacgc	ctggacacca	aacttcatac	ccccatgtat		180
ttttttctta	ccaatctatc	actcctggat	ctttgttaca	ccacatgtac	agtcccacaa		240
atgctagtaa	atttatgcag	catcaggaaa	gtaatcagtt	atcgtggctg	tgtagccag		300
cttttcatat	ttctggcctt	gggggctact	gaatatcttc	tcctggccgt	catgtccttt		360
gataggtttg	tagctatttg	tcggcctctc	cattactcag	ttatcatgca	ccagagactc		420
tgccctcag	tggtcagctgc	atcctgggtt	actgggttta	gtaactcag	gtggttgtct		480
accctgactc	tcagctgcc	actctgtgac	ccctatgtga	tagatcactt	tctctgtgaa		540
gtccctgcac	tgctcaagtt	atcttgtgtt	gagacaacag	caa	atgaggc	tgaactattc	600
cttgtcagtg	agctcttcca	tctaataccc	ctgacactca	tccttatatc	atatgctttt		660
attgtccgag	cagtattgag	gatacagctc	gctgaaggtc	gacaaaaagc	atttgggaca		720
tgtggttccc	atctaattgt	ggtgtctctt	ttttatagta	cagccgtctc	tgtgtacctg		780
caaccacctt	cgcccagctc	caaggaccaa	ggaaagatgg	tttctctctt	ctatggaatc		840
attgcaccca	tgctgaatcc	ccttatatat	acacttagga	acaaggagg	aaaggaaggc		900
tttaaaaggt	tggttgcaag	agtcttctta	atcaagaaa				939

&lt;210&gt; 592

&lt;211&gt; 997

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g441 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 592

atggaaaaat	ccaatgtcag	ctcagtgat	ggttttatct	tggtgggttt	ctctgatcgt	60
cccaagctgg	agatgggtgct	ctttacagta	aattttattc	tgtattcag	ggctgtgctg	120
ggaaattcaa	ccataatcct	tgtgtgtata	ttagactctc	aacttcatac	cccaatgtac	180
ttctttcttg	caaatcttcc	ctttctagat	ctctgcttca	gtactagt	catcccacaa	240
atgctggtaa	acctctgggg	ccctgacaag	actattagct	gtgctggctg	tggtgtccag	300
cttttctctt	tcctttctgt	caggggaatt	gagtgcatcc	ttctggctgt	catggcctat	360
gacagctatg	ctgcagctcg	caaaccgttg	cgctatctgg	tcattatgca	cctccagctg	420
tgtctaggac	tgatggctgc	agcctggggg	agtggtactg	tcaatgccgt	tgctcatgca	480
ccactaacia	tgaccctctc	cagaagtggc	cgccgcccag	ttaaccattt	cctctgtgaa	540
agccagcact	gatcaagatg	gcttgttttg	atgttcgtgc	agtggaatg	ctggcttttg	600
cttttgccgt	tctcattgtc	ctactgcccc	tcactcttat	tcttgtctcc	tacggctaca	660
ttgctgcagc	tgtgctaagc	atcaagtcag	ctgccaggca	atggaaggcc	ttccatacct	720

gtagctctca	cctcacagt	gtctccctgt	tttatgggag	catcatctat	atgtatatgc	780
agccaggaaa	cagttcttcc	caagaccaag	gcaagtttct	cactctcttc	tacaacctgg	840
tgactcctat	gttgaatctg	ctcatctata	ctttaaggaa	taaggagggtg	aaaggagcac	900
tgaagaaggt	tttggggagg	caataatgaa	ctggagaaat	atgataagtt	gtgaagtctt	960
aggcaaaata	tctttttcaa	atacatttat	tttgtgc			997

&lt;210&gt; 593

&lt;211&gt; 950

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g442 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 593

caagtagttc	atacaggctt	ttctccctag	ctatacgtct	tcaccctgct	gggaaatggg	60
gcacccctggg	gctcatctgg	ctggactcca	gactgcacac	ccccatgtac	ttctttctct	120
cacacctggc	catcattgat	atttcgtatg	cttccaacaa	tgcccccaag	atgctgacaa	180
accttggcct	gaacaagaga	aaaacaatct	cctttgtccc	atgcacaatg	cagacctttt	240
tatacatggc	ttttgtcac	actgagtgtc	tcactcttgg	aatgatgtcc	tacgatcggt	300
acatggctgt	ctgccaccct	ctgcaatatt	ctgtcatcat	gagatgggga	gtgtgcacag	360
tcctggctgt	cacttcttgg	gcatgtggtt	ccttctggcc	ctgggtccatg	tggttctcat	420
cctgaggctg	cccttctgtg	ggccccatga	aatcaaccac	ttcttctgtg	aaatcctgtc	480
tgctctcaag	ttggcctgtg	ctgacacctg	gctcaaccag	gtgggtcatct	ttgcttcttc	540
agtgttcac	ctgggtgggg	cgctctgcct	ggtgctggtc	tcctactcgc	gcacccctggc	600
ggccatcttg	aggaatcagt	ctggggaggg	gcgcagaaag	ggcttctcca	cctgtctactc	660
ccacctttgc	atggtgggac	tcttctttgg	cagcgccatt	gtcacgtaca	tggcccccaa	720
gtcccgcct	cctgaggagc	agcagaaagt	tcttccctg	ttttacagcc	ttttcaatcc	780
aatgctgaac	ccccctgata	tatagcctaa	ggaatgcaga	ggtcaagggc	gccctgagga	840
gtgcactgag	gaaggagagg	ctgacgtgag	acatctcaaa	gggaaccatg	gggagggagc	900
cttgctccct	gcaaaatata	gaagttggct	tttttttttg	tcttctgcta		950

&lt;210&gt; 594

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g443 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 594

cagatgctga	cagattgggtg	gggacctaat	aggaccacaa	gttacgtgaa	ctcaccattc	60
aattccttgt	ctctctgtag	ttatgtgcca	ctatataatt	tctacaatta	ttttataatt	120
atatgccatc	ctttgttaata	tttggttaatc	atgaacctat	atctcctcct	taatcttact	180
ttaatacttg	agtataaatt	cattcatttt	tgatcatcatg	tatactctca	tcctaaaatt	240
cccaagggtat	gaaaaaaaaa	aaccttcagg	ataattccct	ccatgtgttg	ctagctatgc	300
tgaaaacagt	ttttctagat	gctacaattg	aagaaatgtc	tgtatttgtg	ttaatacaat	360
gtaaatgtcc	taatatgcct	tatcagtaat	tttacctgct	atggctacat	tgaggtgcac	420
taagaatgaa	tactagtaat	taaattagaa	gcaagctgag	aaatcagtat	catcatcatc	480
atcatagggtg	tcatttcatt	atagattcaa	tcttctatgg	aatcattgtg	taaagtctct	540
tgaagatgggt	aacaactcct	cccaagacca	agaaatgatt	ctttatcttg	ttttacacta	600
tactaactcc	aagtctcaaa	cttctagttt	atctgttaag	aataaagata	taaaggatat	660
ttcaaggaga	atactaagat	tggcagggaa	tcttcaaaaa	tgaaaggaaa	c	711

&lt;210&gt; 595

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g444 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 595

atgtatttcc	tactgagtca	gctctccctc	attgacctaa	attacatctc	caccattgtt	60
cctaagatgg	catctgattt	tctgcatgga	aacaagtcta	tctccttcac	tgggtgtggg	120
attcatagtt	tcttcttcac	gacttttagcc	gttgtagaag	cgctactcct	gatataaatg	180
gcctatgttc	gttgcatgac	tatttgcttt	cctctccact	atctcatgcg	catgagcaaa	240
agagtgtgtg	tgctgatgat	aacaggatct	tggatcatag	gctcgatcaa	tgcttgtgct	300
cacactgtat	atatactcca	tattccttat	tgcccatcta	gggttatcaa	tcatttcttc	360
tgtgatgtcc	cagcaatggg	gactctggcc	tgcatggaca	cctgggtcta	tgagggcaca	420
gtgcttttga	gcgccaccat	ctttctcggt	tttcccttca	ttgctatttc	atgttcctat	480
ggacgggttc	tccttgctgt	ctaccacatg	aaatctgcag	aagggaagaa	gaaggcctac	540
ctgacctgca	gcacccacct	cactgtagtg	actttctact	atgcaccctt	tgcttacacc	600
tatctacgcc	caagatccct	gcgatctccg	acagaggaca	aggttctggc	tgcttcttac	660
accatcctca	tcctaatgct	caaccccatc	atctacagcc	tgagaaacaa	ggaggtgatg	720
ggggccctga	cacgagtgat	tcagaaaatc	ttttcagtga	aaata		765

&lt;210&gt; 596

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g445 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 596

ctgtcatgac	caaccagagc	tgcccagaaa	cagttcatct	tactgggttt	ctcaggcaga	60
cccaggctgg	agcatgtcct	ctttgtgttt	gtccctcatct	tctaccttgt	gaccttagtg	120
ggcaacatca	tcattatctt	gatctccac	ctggaccctt	gcctccacat	gcccattgtac	180
ttcttccctca	ctaaactgtc	tttccctagat	ctctgcttca	ccaccagttc	tatccccccag	240
ctgcttttca	atctaggcag	cccaggcaag	actatcagcc	acacgggctg	tgccatccag	300
ctcttcatgt	tcctgggcct	gggtggcaag	agtgtattct	cttggcagcc	gtggcctatg	360
accgcttcat	tgcaatctgc	aagccccttc	actattctgt	cattatgcac	cctcagctgt	420
gctggaagtt	ggtgtctgtg	gcccgggggt	gttgactcc	tcagttctct	agttatgtct	480
cctgtgacta	tgaagctgcc	acgatgtgga	agatgtaagt	tgaaacattt	cctgtgtgag	540
atgccagctc	taataaaaaat	cacctgtgtg	gacacagtgg	ctatggagag	cactgttttc	600
accttatcgg	tagtaattgt	cctgatgcct	ttgtgtctta	tcctcatctc	ttatagctac	660
attgccctag	cagtgtctgag	aatcaagtca	gccgcaggaa	gaaggaaggc	cttcaatatg	720
tgccgggtccc	acctcaccgt	ggtctccttg	ttttatggga	atattatcta	tatgtatatg	780
caaccatgaa	ataattcttc	tcaggaccaa	gggaagttcc	ttaccctttt	ctacaactta	840
atgaccccca	tgtaaacc	tgcatcttat	acactgagaa	acaaggatgt	aaaagggtgca	900
ctgaagaggc	ttgtgtctag	aaaacacagt	gacagtgcct	gctcttgaga	ctgcttcttt	960

&lt;210&gt; 597

&lt;211&gt; 377

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g446 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 597

atggaaaatt	acaatcaaac	atcaactgct	ttcatcttgt	tgggattgtc	gccaccacca	60
aaaattggcc	atttcatctt	cattctcatt	aatttcgttt	tcctaattggc	tctaattgga	120
aacctatcca	tgattcttct	catcttcttg	gacatccatc	tcacacacac	catgtatttc	180
ctacttagtc	agctctccct	cattgacctc	aattatattt	ccaccattgt	tcctaagatg	240
gtttatgatt	tttcatgtat	ggaaacaagt	ctatctcctt	cactgggtgt	gggattcaga	300
gtttcttctt	cctgacttta	gcagggtgcag	aagcgctgct	cctgacatca	atggcctatg	360
atcggttatg	ggctatt					377

&lt;210&gt; 598

&lt;211&gt; 979

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g447 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 598

atggaaagag ctaacgacag caccttctct ggattcatcc tectgggctt ctccaacagg	60
cctcagctgg aaacagctct ctttgtggtc atcttgatca tctactttct gagctttctg	120
ggcaatggca ccattatact tttatccatt gtagatcctc gcctccatac ccctatgtat	180
ttcttctct ccaatctctc ttttatggat ctttgtttga ccacttgtag tgccctcag	240
acactgggca actttaaggg gaaggacaag accatcacct atgggtggctg cgtgaccag	300
ctattcattg ccttgggact cggggggagt ggagtgtgtc ttattgtctg ccattggccta	360
tgaccgctat gcagccgtct gccgccact ccactacatg gtgagcatgc atccccact	420
ttgcttgtag ttggttgtaa ccacttggct cacagggttt ggcaattctg tgatacagac	480
agcattgacc atgactctcc ccctctgtga taaaaaccaa gtggatcatt tcttctgtga	540
agttccagtg atgctgaaac tgcctgcac caacacctcc atcaacgagg ctgaaatctt	600
tgctgtcagt gtcttctctc tgggtgtgcc tctctcactc atcttagcat cctatgggta	660
cattactcat gcagtcctga agataaagtc agctcaaggg aggcagaagg cttttggaac	720
ctgtgggtct cacttcctgg tagtgatcat tttctttggg acactcatct ccattgtacct	780
ccagcctccc tccagttatt cacaggatgt gaacaaaagc attgcactct tctatactct	840
gggtgactct ctactgaatc ccctaattta cactctgagg aacaaggaag tcaaaggggc	900
aactaagaag actagtgggg aggaccatag atgcatgaga aagttaacgc aggggtttgca	960
gttccaaaca tttgtgcac	979

&lt;210&gt; 599

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g448 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 599

atggaaaatt acaatcaaac atcaactgat ttcattctat tggggctgtt tccaccatca	60
ataattgacc ttttctctt cattctcatt gttttcattt tcctgatggc tctaattgga	120
aacctgtcca tgattcttct catcttcttg gacaccatc tccacacacc catgtatttc	180
ctactgagtc agctctccct cattgacctt aattacatct ccaccattgt tcctaagatg	240
gcactgtgatt ttctgcatgg aaacaagtct atctccttca ctgggtgtgg gattcagagt	300
ttcttcttct tggcattagg aggtgcagaa gcactacttt tggcatctat ggcctatgat	360
cgttacattg ctatttgcct tcctctccac tatctcatcc gcatgagcaa aagagtgtgt	420
gtgctgatga taacaggggc ttggatcata ggctcgatca atgcttgtgc tcacactgta	480
tatgtactcc atattcctta ttgccgatcc agggccatca atcatttctt ctgtgatgtc	540
ccagcaatgg tgactctggc ctgcatggac acctgggtct atgagggcac agtgtttttg	600
agtgccacca tctttctcgt gtttcccttc attgggtattt catgttccta tggccagggt	660
ctctttgtct tctaccacat gaaatctgca gaaggagga agaaagccta tttgacctgc	720
agcaccaccc tcaactgtagt aactttctac tatgcacctt ttgtctacac ttatctacgt	780
ccaagatccc tgcgatctcc aacagaggac aagggttctgg ctgtcttcta caccatcttc	840
accccaatgc tcaaccccat catctatagc ctgaggaaca aggaggtgat gggggccctg	900
acacgagtga gtcagagaat ctgctctgtg aaaatg	936

&lt;210&gt; 600

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g449 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 600

atgcccaatt caaccaccgt gatggaattt ctctcatga ggttttctga tgtgtggaca	60
--	----

ctacagattt	tacattctgc	atccttcttt	atgttgatt	tggttaactct	aatgggaaac	120
atcctcattg	tgaccgtcac	cacctgtgac	agcagccttc	acatgcccac	gtacttcttc	180
ctcaggaaac	tgtctatctt	ggatgcctgc	tacatttctg	ttacagtccc	tacctcatgt	240
gtcaattccc	tactggacag	caccaccatt	tctaaggcgg	gatgtgtagc	tcaggctctc	300
ctcgtgggtt	tttttgata	tgtggagctt	ctgtttctca	ccattatggc	tcatgaccgc	360
tatgtggctg	tctgccagcc	acttcactac	cctgtgatcg	tgaactctcg	aatctgcac	420
cagatgacac	tggcctccct	actcagtggg	cttgtctatg	caggcatgca	cactggcagc	480
acattccagc	tgcccttctg	tcgggtccaac	gttattcatc	aattcttctg	tgacatcccc	540
tctctgctga	agctctcttg	ctctgacacc	ttcagcaatg	aggctcatgat	tggtgtctct	600
gctctggggg	taggtggcgg	ctgtttcatc	tttatcatca	ggtcttacat	tcacatcttt	660
tcgaccgtgc	tcgggtttcc	aagaggagca	gacagaacaa	aggccttttc	cacctgcac	720
cctcacatcc	tggtgggtgc	agtcttcttc	agttcatgct	cttctgtgta	cctcaggcca	780
cctgcgatac	ctgcagccac	ccaggatctg	atcctttctg	gtttttatcc	cataatgcct	840
ccctcttcta	accctattat	ttacagtctt	agaaataagc	aaataaagg	ggccatcaag	900
aaaatcatga	agagaatttt	ttattcagaa	aatgtg			936

&lt;210&gt; 601

&lt;211&gt; 931

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g450 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(931)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 601

aggaatgccc	cactggaaaa	atacaatcaa	acatcaactg	atttcatctt	attggggatc	60
ttcccaccat	ccagaattgg	ctttctcttc	ttcattctcc	ttgttctcat	tttgctattg	120
gctttaattg	gcaatcagtc	cgtgatccct	ctcatcttct	tggacactca	tctccacacg	180
cccatttatt	tcttacttag	tcggctctac	ctcattgacc	taaattacat	ctccactatt	240
gtcccagat	gttttctgat	tttctgtttg	gaaacaagtc	tatttccctc	attgggtgtg	300
gaattcagag	tttcttcttt	gtgactttag	cagggtgcaga	aatgctgcca	ctgacatcaa	360
tggcctgtga	tcattatgta	gctgtttgct	ttcctctcca	ctatcccatc	catatgagca	420
agatagtatg	tgctgatgat	aataggatct	tggataatgg	gctctatcga	cacttgtgct	480
cacatttcat	atatgcccc	tatccctggt	gctcagccag	ggctgtgatg	tcccagccat	540
ggtgactctg	gccttcgtgg	acacctgggt	ctatgagtgc	acagtgtttt	tgagcacaac	600
cctctttctc	atgtttacct	ttattgggat	tgcattgttc	tatgggtgag	ttctccttac	660
tgtctaccac	attaaatctg	cagaagggag	gaagaaggcc	tattcgacct	gtagcaccca	720
cctcactgta	gtaattntct	actatgcaat	gtttgcttat	acctatctat	atccaagata	780
cctgcaatct	ccaacagagg	acaagggtct	ggctgtgttc	tacaccatcc	tcacctcaat	840
gctcaacccc	atcatctaca	gcctgagaaa	cagggagggtg	atggggggccc	tgacacgagt	900
gagtcagaga	atcttccctg	tgaagatgaa	g			931

&lt;210&gt; 602

&lt;211&gt; 577

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g451 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 602

agacacacag	agccacggaa	tctcacaggt	gtctgagaat	tcctcctcct	gggactctca	60
gaggatccag	aactgcagcc	tgtcctcget	ttgctgtccc	tgtccctgtc	cctgtccttg	120
tatctgggtca	tggttctgag	gaacctgtct	agcatcctgg	ctgtcagctc	tgactccccc	180
ctccataccc	ccatgtactt	cttccctctc	aacctgtgct	gggctgacat	cgggttcaat	240
tcggccacgg	ttcccaagg	gactgtggac	atgcagtcgc	atagcagagt	catctctcat	300
gcgggctgcc	tgacacagat	gtctttcttg	gtcctttttt	gcatgtatag	aatgcatgct	360

cctgactgtg atggcctatg acggctttgt agccatctgt ctcctctgc actaccaggt	420
catcatgaat cctcacctct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt	480
ggattcccag ctgcacggtt ggattgtgtg acaattcacc atcatgaaga atgtggaaat	540
ctctcatttt gtaagtgacc cctctcaact tctcaac	577

&lt;210&gt; 603

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g452 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 603

atggacagaa gaaaccagac ctgcatctat gaatttcttc tcatgggctt ctctgaacac	60
caggagcagc aggcctctttt gtttgggctt ttctgggtca tgtacttggg cactgtgttg	120
gagaacctgc taatcatcct ggccattggc tctgacctgc acctccacac ccccatgta	180
cctcttcctg tccaacctgt cctttttgga tattggcttt atctctacaa taattcccaa	240
gatgctagat catattagct caggaattaa gctgatttct tatggggagt gtctgacaca	300
actctatttc tctggcctat ttgcagatct ggacaacaac tttctcctgg ctgtgatggc	360
ccttgaccgc tatgtggcca tcagccatcc tctccattat gccctaacca tgaactcca	420
acgtgtgtgc ctgttgggtg ctgtgtcatg ggtgatcact attttacatg ccctagtga	480
tacctctcta gtgaccaggc tttccttctg tgggtccaaat attatccctc acttcttctg	540
tgatctgggc ccactcctga agctggcctg ctccagtact tgtgtcaatg atctgggtct	600
catccttctg gcaggaacac tgctgattgc gccctttgtc tgcattcctta tgcctactt	660
ttacattgca ttggccatcc tgagaattga ttccccaagg ggtaagcaaa gggccttctc	720
cagctgcact tcccacctct ctgtagtctc tctgttctat agcacagcta tcggtgtcta	780
tttatgtcct ccatcatccc actcagatgg aaaggacaga gtcttctcag tcatgtacac	840
gggtgtgact cccatgttga accccttcat ctacagcctg aggaacaggg atatgaaggg	900
ggcactggga aaactgcttg gaataaaaac atcctaacac ccttactcaa ga	952

&lt;210&gt; 604

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g453 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 604

cattttagt ggtgcgtgtt cagatactcg ggtattgtgg tggagataca catagtcttt	60
tgaacattcc gttgtaggtc gctggtagct ggatatgtcc tttaaacttt tgtggcaatt	120
catttgagaa gaaacgcagc tttttctatt gaggttctat gctataagta aaggatgcaa	180
gacattaatt agacaaaata aggtaaaatt ttgtattcgc ttagagagtt taagaggcta	240
ttagccacta gtctctatag tgcctaagta aatcgattct gcttaataaa ctgctacctg	300
gcttagtaag taaacaaatt gaaacttatt ttaggaaaga aatatatatt cttatatcta	360
catcagattc tcttatgtag aaacactaga ggggtgaatga ggagttaatg taagcagcat	420
catatttttg ctcatctcct tctctatgat ttctgcttct tctgtccaaa ttctgtgagg	480
tgtcctctag atgaaattat cacaggcatg gaaaagggtc ttttccactt ggtccatcct	540
catgattgca gttgtaacat actgggactc attcattttc acatatgtat atgagactta	600
aatcatccac atttcaggcc aggttaagtt tctagaaata ttctatgctt tccttgact	660
tacactcaat cctgtcgtct acagcgttgg cactgacagt gttctgggtg caatgaaaaa	720
tatgtcttag agcaacattc tacataaaaa aaag	754

&lt;210&gt; 605

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g454 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 605

atggaccaga	tcaaccacac	taatgtgaag	gagtttttct	tcctggaact	tacacgttcc	60
cgagagctgg	agtttttctt	gtttgtggtc	ttcttttgctg	tgatgtage	aacagtcctg	120
ggaaatgcac	tcattgtggt	cactattacc	tgtgagtcce	gcctacacac	tcctatgtac	180
tttctctgc	ggaacaaatc	agtccctggac	atcgtttttt	catctatcac	cgtccccaag	240
ttcctgggtg	atctttttatc	agacaggaaa	accatctcct	acaatgactg	catggcacag	300
atctttttct	tccactttgc	tggtggggca	gatatttttt	tcctctctgt	gatggcctat	360
gacagatacc	ttgcaatcgc	caagcccctg	cactatgtga	ccatgatgag	gaaagagggtg	420
tggtgtggcct	tggtgggtggc	ttcttgggtg	agtgggtggt	tgcatccaat	catccaggta	480
attctgatgc	ttccattccc	cttctgtggc	cccaacacac	tggatgcctt	ctactgttat	540
gtgctccagg	tggtaaaact	ggcctgcact	gacacctttg	ctttggagct	tttcatgac	600
tctaacaacg	gactggtgac	cctgctctgg	ttcctctgc	tcctgggctc	ctacactgtc	660
attctggtga	tgctgagatc	ccactctggg	gagggggcga	acaaggccct	ctccacgtgc	720
acgtcccaca	tgctggtggt	gactcttcac	ttcgtgcctt	gtgtttacat	ctactgccgg	780
cccttcatga	cgctgcccac	ggacacaacc	atatccatta	ataacacggt	cattaccccc	840
atgctgaacc	ccatcatcta	ttccctgaga	aatcaagaga	tgaagtcagc	catgcagagg	900
ctgcagagga	gacttggggc	ttccgagagc	agaaaatgg			939

&lt;210&gt; 606

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g455 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 606

atggaaagaa	tcaaccacac	cagcagtgct	tccgagttta	tcctcctggg	actctcctcc	60
cggcctgagg	accaaaaagac	actctttggt	ctcttcctca	tcgtgtacct	ggtcaccata	120
acaggggaacc	tgctcatcat	cctggccatt	cgcttcaacc	cccatcttca	gacccctatg	180
tattttcttct	tgagttttct	gtctctcact	gatatttgct	ttacaacaag	cgttgtcccc	240
aagatgctga	tgaacttcct	gtcagaaaag	aagaccatct	cctatgctgg	gtgtctgaca	300
cagatgtatt	ttctctatgc	cttgggcaac	agtgcagact	gccttctggc	agtcatggcc	360
tttgaccgct	atgtggccgt	ctgtgacctt	ttccactatg	tcaccaccat	gagccaccac	420
cactgtgtcc	tgctgggtggc	cttctcctgc	tcatttctc	acctccactc	actcctgcac	480
acacttctgc	tgaatcgtct	caccttctgt	gactccaatg	ttatccacca	ctttctctgt	540
gacctcagcc	ctgtgctgaa	attgtcctgc	tcttccatat	ttgtcaatga	aattgtgcag	600
atgacagaag	cacctattgt	tttgggtgact	cgttttctct	gcattgcttt	ctcttatata	660
cgaatcctca	ctacagttct	caagattccc	tctacttctg	ggaaacgcaa	agccttctcc	720
acctgtggtt	tttacctcac	cggtgtgacg	ctcttttatg	gaagcatctt	ctgtgtctat	780
ttacagcccc	cateccaccta	cgctgtcaag	gaccacgtgg	caacaattgt	ttacacagtt	840
ttgtcatcca	tgctcaatcc	ttttatctac	agcctgagaa	acaaagacct	gaaacagggc	900
ctgaggaagc	ttatgagcaa	gagatcc				927

&lt;210&gt; 607

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g456 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 607

atggccaatg	tcaccttggt	gacaggattt	cttcttatgg	ggttttctaa	tatccagaag	60
ctgcggtatt	tatatggtgt	gctcttcccta	ctgatttacc	tgccagccct	aatgagtaac	120
cttctcatca	ttactctcat	taccctggac	gtaaagctcc	aaacacccat	gtacttcttc	180
ctgaagaact	tatccttttt	ggatgtcttc	ctgggtgctg	ttccaatccc	aaaattcatt	240
gtcaacaacc	taaccacaaa	caattccatt	tccattctag	gatgtgcctt	ccagctactt	300
ttaatgactt	ccttctcagc	aggagagata	tttatcctca	ctgccatgtc	ctatgaccgc	360
tatgtagcca	tctgctgtcc	cctgaactac	gaggtaatca	tgaatactgg	agtcgtgtgt	420

ttaatggcaa	gtgtttcctg	ggccattgga	gggctctttg	gtactgcgta	cacagctggc	480
acattttcca	tgcttttctg	tggtccag	gtgattccac	agtttttctg	tgatgttcc	540
tcattactaa	ggattttcctg	ttctgaaaca	ctaattggtaa	tttatgcagg	tattggaggt	600
ggtgcatggt	taagcatttc	ttgtttcatc	tgtattgtga	tctcttacat	ttatatcttc	660
tccactgtac	tgaagatccc	taccactaaa	ggtcagtcca	aagctttttc	cacatgcttc	720
ccccatctca	ctgtttttcac	tggtttttatc	ataactgctt	attttgttta	tcttaagcca	780
ccttcaaatt	caccatctgt	tattgacagg	ctgcttttctg	tgatctacac	tgtgatgcct	840
ccagtattta	accctgtaac	ctacagcctg	cggacaatg	acatgaaatg	tgctctgata	900
aggttgctgc	agaaaacata	tggtcaggag	gcttacttc			939

&lt;210&gt; 608

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g457 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 608

atggctgtag	gaaggaacaa	cacaattgtg	acaaaattca	ttctcctggg	actttcagac	60
catcctcaaa	tgaagatttt	ccttttcatg	ttattttctg	ggctctacct	cctgacgttg	120
gcctggaact	taagcctcat	tgccctcatt	aagatggact	ctcacctgca	catgcccctg	180
tacttcttcc	tcagtaacct	gtccttcctg	gacatctgct	atgtgtectc	caccgcccct	240
aagatgctgt	ctgacatcat	cacagagcag	aaaaccattt	cctttgttgg	ctgtgccact	300
cagtactttg	tcttctgtgg	gatggggctg	actgaatgct	ttctcctggc	agctatggcc	360
tatgaccggg	atgtgcaat	ctgcaacccc	ttgctttaca	cagtcctcat	atcccataca	420
ctttgtttaa	agatgggtgg	tggcgccctat	gtgggtggat	tccttagttc	tttcattgaa	480
acatactctg	tctatcagca	tgatttctgt	gggccctata	tgatcaacca	ctttttctgt	540
gacctccctc	cagtcctggc	tctgtcctgc	tctgatacct	tcaccagcga	gggtggtgacc	600
ttcatagtca	gtgttgctgt	tggaatagtg	tctgtgctag	tggtcctcat	ctcttatggt	660
tacattgttg	ctgctgttgt	gaagatcagc	tcagctacag	gtaggacaaa	ggccttcagc	720
acttgtgcct	ctcacctgac	tgctgtgacc	ctcttctatg	gttctggatt	cttcattgtac	780
atgcgaccca	gttccagcta	ctccctaaac	agggacaagg	tggtgtccat	attctatgcc	840
ttggtgatcc	ccgtgggtgaa	tcccatcatc	tacagtttta	ggaataagga	gattaaaaat	900
gccatgagga	aagccatgga	aagggacccc	gggatttctc	acgggtggacc	attcattttt	960
atgaccttgg	gc					972

&lt;210&gt; 609

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g458 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 609

atgaccaatc	agacacagat	gatggaattc	ttgcttgtga	gatttactga	gaattgggtg	60
ctcctgaggg	tgcatgcttt	gctcttctca	ctgatctacc	tcacggctgt	gctgatgaat	120
ttagtcatca	ttctcctcat	gattctggac	catcgtctcc	acatggcaat	gtactttttc	180
ctccgacatt	tgctcttctt	agacctgtgt	ctcatttctg	ccacagtccc	caaatccatc	240
ctcaactctg	tcgctccac	tgactccatc	tccttcctgg	gggtgtgtgt	gcagctcttc	300
ttggtgggtac	tgctggctgg	atcagagatt	ggcctcctta	ctgccatgtc	ctatgaccgc	360
tatgctgcca	ctctgtgccc	cctacactgt	gaggctgtca	tgagcagagg	gctctgtgtc	420
cagttgatgg	ctctgtcctg	gctcaacaga	ggggccttgg	gactcttgta	cacagctgga	480
acattctctc	tgaattttta	tggtctgtgat	gagctacatc	agttcttctg	cgatgtccct	540
gccctactaa	agctcacttg	ttctaaagaa	catgccatca	ttagtgtcag	tgtggccatt	600
ggggtctgtt	atgcattttc	atgttttagt	tgcatgttag	tttcctatgt	gtacattttc	660
tctgtgtgt	taaggatata	acagagacag	agacaatcca	aagccttttc	caactgtgtg	720
cctcacctca	ttgtgtgcac	tgtgtttctt	gtaacagggtg	ctgttgctta	tttaaagcca	780
gggtctgatg	caccttctat	tctagacttg	ctgggtgtctg	tggtctatct	tgctcgacct	840
ccaaccttga	accctgttat	ctactgtctg	aagaacaagg	acattaaatc	cgctctgagt	900

aaagtcctgt ggaatgtag aagcagtggg gtaatgaaaa ga

942

<210> 610

<211> 921

<212> DNA

<213> Unknown (H38g459 nucleotide)

<220>

<223> Synthetic construct

<400> 610

atgaatcaca	gcgttgtaac	tgagttcatt	attctgggcc	tcacaaaaaa	gcctgaactc	60
cagggaatta	tcttctctt	ttttctcatt	gtctatcttg	tggtttttct	cggcaacatg	120
ctcatcatca	ttgccaaaat	ctataacaac	accttgcata	cgcccatgta	tggtttcctt	180
ctgacactgg	ctggttgagg	catcatctgc	acaacaagca	tcataaccgaa	gatgctgggg	240
accatgctaa	catcagaaaa	taccatttca	tatgcaggct	gcatgtccca	gctcttcttg	300
ttcacatggt	ctctggggagc	tgagatgggt	ctcttcacca	ccatggccta	tgaccgctat	360
gtggccattt	gtttccctct	tcattacagt	actgttatga	accaccatat	gtgtgtagcc	420
ttgctcagca	tggtcatggc	tattgcagtc	accaattcct	gggtgcacac	agctcttatc	480
atgaggttga	ctttctgtgg	gccaaacacc	attgaccact	tcttctgtga	gataacccca	540
ttgctggctt	tgctctgtag	ccctgtaaga	atcaatgagg	tgatgggtga	tggtgctgat	600
attaccctgg	ccatagggga	ctttattctt	acctgcatct	cctatgggtt	tatcattggt	660
gctattctcc	gtatccgcac	agtagaaggc	aagagggaag	ccttctcaac	atgctcatct	720
catctcacag	tggtgaccct	ttactattct	cctgtaatct	acacctatat	ccgccctgct	780
tccagctata	catttgaaag	agacaagggt	gtagctgcac	tctatactct	tgtgactccc	840
acattaaacc	cgatgggtga	cagcttccag	aatagggaga	tgcaggcagg	aattaggaag	900
gtgtttgcat	ttctgaaaca	c				921

<210> 611

<211> 810

<212> DNA

<213> Unknown (H38g460 nucleotide)

<220>

<223> Synthetic construct

<400> 611

atggaagtga	gtgggaacca	cacctctgtg	gccatgtttg	ttctcctagg	actctcagat	60
gaaaaagagc	tgacgtcat	cctctttcca	gtcttcttg	tgatctacct	tgtagccctg	120
atttggaaca	tggtcttat	catcctcatc	agaatagact	ctcatctgaa	cacacccatg	180
tacttttttc	tcagtttctt	ctcatttaca	gacatctgct	attcttctac	catcagccca	240
aggatgcttt	cagacttctt	aaaagataag	aagacaattt	ccttccttgc	ctgtgccact	300
cagtattttc	ttggggcctg	gatgagtctg	gctgagtgtc	gcctcttggt	catcatggcc	360
tgtagacagat	atgtggccat	tgacagcccc	ctgcagtact	cagcaatcat	ggcccttagt	420
atctgttggg	agatggtagc	tgaggtctgt	gggggtggat	tccttagtag	cttagttcat	480
acagtccctt	gctttaatct	ctactactgt	gggccaaaata	tcattcaaca	tttcttctgt	540
aacacacttc	agattatttc	cttgtcttgc	tccaaccctt	ttatcagcca	aatgattctt	600
tttctggaag	ctatttttgt	tggttggtgg	tcttctgttg	ttatcctttt	gtcttatggg	660
ttcattgtag	cttccatact	gaaaatatca	tcaacaaaat	gttggtgcaa	ggccttcaat	720
acctgtgcct	cccacctggc	agctgtggct	ctcttctatg	gcacagccct	ttctgtgtac	780
atgcatacta	gctctagcca	ctccatgaag				810

<210> 612

<211> 988

<212> DNA

<213> Unknown (H38g461 nucleotide)

<220>

<223> Synthetic construct

<400> 612

tactccaaag	aaattataga	ataatgtact	tccaatgata	ttataaaatg	tggttagcat	60
aataagatta	ctttttttac	tgtttatcct	tttagagttc	acagaagatt	tggtgttaca	120
gcaagtgtc	tttttcatct	ttctcatcat	ttatgtcatc	agcctctcag	gcaacatcat	180
tctgaattct	ctcatctgtg	ctgattcttg	gccctacaca	cccatgtatt	tcttctactg	240
aaaccgggtc	cttctggatc	tctggtatc	ctctgtccac	atccccgata	tctgtctgac	300
ttgcatttct	gatgacaaaa	ccatctcctt	tctgtgctgc	cttgctcagt	tcttctctgc	360
tgtgttggtc	taaaatgagt	gctatatgat	ggcttccatg	gcttatgacc	gctacatggc	420
aatctccaa	cccctgcttt	attccccggc	cacattccca	gagttatgtg	ccagtcttgt	480
tgaggcttca	caccttggcg	gctttgtaaa	ctcaaccatc	atcaccagt	agacacctac	540
cttgagcttc	tgtggcagca	atatcattga	tgatttcttc	tgtgatctgc	ccccacttgt	600
aaagttggtg	tgtgatgtga	aggagcgcta	ccaggctgtg	ctgcatttta	tgcttgccctc	660
caatcatcac	tcccactgca	cttattcttg	cgctcatctc	ttcatcattg	cagccatctc	720
gaagatccgt	tccattaagg	gccgcctcca	ggcttctctc	acttgtgggt	ctcccccgac	780
ggctctcacc	ttgtactatg	gtgcaatctt	ctttatttac	tcccaaccaa	gaactagcta	840
tgcttataaa	atggataaat	tggggtcagt	gttctatact	gtgggtgattc	caatgctaaa	900
ccccttgatc	tatagcttaa	gaaataagga	tgtcaaagat	gccttgaaga	aaatgttaga	960
tagacttcag	tttcttaaag	aaaaatat				988

&lt;210&gt; 613

&lt;211&gt; 1049

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g462 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 613

atggagcaga	gcaattattc	cgtgtatgcc	gactttatcc	ttctgggttt	gttcagcaac	60
gcccgtttcc	cctggcttct	ttgccctcat	tctcctggtc	tttgtgacct	ccatagccag	120
caacgtggtc	aagatcattc	tcattccacat	agactcccg	ctccacaccc	ccatgtactt	180
cctgtctcag	cagctctccc	tcaggagcat	cttgtatatt	tccaccattg	tgcccaaaat	240
gctggctgac	caggatgatga	gccagagagc	catttccctt	gcaggatgca	ctgcccaca	300
cttctcttac	ttgaccttag	caggggctga	gttcttctc	ctaggactca	tgtcctgtga	360
tcgctacgta	gccatctgca	accctctgca	ctatcctgac	ctcatgagcc	gcaagatctg	420
ctgggttgatt	gtggcgccag	cctggctggg	agggtctatc	aatgggttct	tgctcacccc	480
cgctaccacg	cagttccctt	tctgtgcctc	tcgggagatc	aaccacttct	tctgcgaggt	540
gcctgccctt	ctgaagctct	cctgcacgga	cacatcagcc	tatgagacag	ccatgtatgt	600
ctgctgtatt	atgatgctcc	tcattccctt	ctctgtgac	tcgggctctt	acacaagaat	660
tctcattact	gtttatagga	tgagcgaggc	agaggggagg	cgaaaggctg	tggtccacctg	720
ctctctcac	atgggtggtg	tcagcctctt	ctatggggct	gccatgtaca	catacgtgct	780
gcctctatct	taccacaccc	ctgagcagga	caaagctgta	tctgccttct	acaccatcct	840
cactcccatg	ctcaatccac	tcatttacag	ccttaggaac	aaggatgtca	cgggggccct	900
acagaagggt	gttgggaggt	gtgtgtctc	aggaaaggta	accactttct	aaacaaattg	960
catatgctgc	tagagacttg	aaatgaagga	tacaagactt	tatcattgcc	cttgagttta	1020
aatattctct	gcctggaaac	aagtgacct				1049

&lt;210&gt; 614

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g463 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 614

atgggtgttc	acaatttgtt	cacggtgact	cagtttatcc	ttatagggtc	ctcttacttc	60
tccaatgagc	actaccttct	ttttgtggcc	cttgccatta	tctgtcaggt	gttcttgggtg	120
cgaagtggag	acattctctt	ggccattggg	actgtgatta	agttgcacac	tactcatgta	180
ttattttttg	gcaaatgtgt	ccatcttaga	catattgtgt	tcattcagcta	ctatacctaa	240
gatgcctaag	attctctaga	ctgaggatca	cagcatttct	tttgttaggt	gagctttgca	300
gccctatttc	ctagtggcct	gggctgggaa	gaaagcttct	tcactgttac	ggcttatgac	360



tggtgtgtgg	tcacatgttt	ctccctttgt	tacatcctga	tcatgaacaa	attggctctg	420
tccagctggt	ttatgggacc	tgagcagctg	ggtttctaaa	tttctcctc	ctccacgtag	480
tgtctaccct	ctgcctgtct	ttctgcaagc	ctgatcgagt	taaccagtat	tactgtgata	540
tctcaccgat	gggggccctg	ttgtgccagt	ccatgcacct	ggcaaacatg	cttggttttag	600
tggaatcagt	tatcttgggg	atcagtgcct	ttctggctgc	ctttaacttt	tacatatata	660
tcatctccac	tatcctaaag	atccagtgtg	tagagtggag	tgcaaagtgc	ttctctacat	720
gcacttccca	cctccttacg	gtctgtttgt	tctatggcat	attgacattt	acctacattt	780
actccttctc	cagtcaacac	tcacatgtct	aaggcaagcc	cagatctagc	cacagacagg	840
ctcatctcta	tgctatacag	agttattacc	ctgatgttta	acttcatcac	tgacaacctg	900
agaaacacag	aggtaaaagg	agcctcagaa	aggttttatg	tcattgaaca	tgtttat	957

&lt;210&gt; 615

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g464 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(840)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 615

atgtacctga	ccacgggtgct	ggggaacctg	ctcatcatgc	tgctcatcca	gctggactct	60
caccttcaca	cccccatgta	cttcttcctc	agccacttgg	ctctcactta	tttttccttt	120
tcatctgtca	ctgtccctaa	gatgctgatg	gacatgcgga	ctaagtacaa	atcgatcctc	180
tatgaggaat	gcatttctca	gatgtatttt	tttatatttt	ttactgacct	ggacagcttc	240
cttattacat	caatggcata	tgaccgatat	gttgccatat	gtcaccctct	ccactacact	300
gtcatcatga	gggaagagct	ctgtgtcttc	ttagtggctg	tatcttggat	tctgtcttgt	360
gccagctccc	tctctcacac	ccttctcctg	acccggctgt	ctttctgtgc	tgcgaaacacc	420
atcccccatg	tcttctgtga	ccttgtctgc	ctgtcgaagc	tgctcctgtc	agatatcttc	480
ctcaatgagc	tggtcatggt	cacagtaggg	gtgggtggca	ttaccctgcc	attcatgtgt	540
atcctgggtat	catatggcta	cattggggcc	accatcctga	gggtcccttc	aaccaaaggg	600
atccacaaag	cattgtccac	atgtggctcc	catctctctg	tggtgtctct	ctattatggg	660
tcaatatttg	gccagtacct	tttcccgact	gtaagcagtt	ctattgacaa	ggatgtcatt	720
gtggctctca	tgtacacggg	ggtcacaccc	atgttgaacc	cctttatcta	cngcattngg	780
aacagggaca	tgaaagaggc	ccttgggaaa	ctcttcagta	gagcaacatt	tttctcttgg	840

&lt;210&gt; 616

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g465 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 616

atgaattcat	caagtgactg	aagacaacca	gtgatggacg	gggtgaatga	tagctccttg	60
cagggctttg	ttctgatggg	catatcagac	catccccagc	tggagatgat	cttttttata	120
gccatcctct	tctctatatt	gtgacccta	cttgggaact	caaccatcat	cttgctttcc	180
cgcttgagg	cccggctcca	tacacccatg	tacttcttcc	tcagcaacct	ctcctccttg	240
gaccttgctt	tcgctactag	ttcagtcccc	caaatgctga	tcaatttatg	gggaccaggc	300
aagaccatca	gctatgggtg	ctgcataacc	cagctctatg	tcttcctttg	gctgggggcc	360
accgatgca	tctgtctggt	ggatgatgca	tttgaccgct	acgtggcagt	gtgccggccc	420
ctccgctaca	ccgccatcat	gaacccccag	ctctgctggc	tgctggctgt	gattgcctgc	480
ctgggtggct	tgggcaactc	tgtgatccag	tcaacattca	ctctgcagct	cccatttgtt	540
gggaccggga	gggtggaggg	attcctctgc	gaggtgcctg	ccatgatcaa	actggcctgt	600
ggcgacacaa	gtctcaacca	ggctgtgctc	aatgggtgct	gcaccttctt	cactgcagtc	660
ccactaagca	tcactgtgat	ctcctactgc	ctcattgtct	aggcagtgct	gaaaatccgc	720
tctgcagagg	ggaggcgaaa	ggcgttcaat	acgtgcctct	cccatctgct	ggtgggtgtc	780

ctctttctatg gctcagccag ctatgggtat ctgcttccgg ccaagaacag caaacaggac	840
cagggcaagt tcatttcctt gttctactcg ttgggtcacac ccatgggtgaa tccccctatc	900
tacacgctg	909

<210> 617  
 <211> 926  
 <212> DNA  
 <213> Unknown (H38g466 nucleotide)

<220>  
 <223> Synthetic construct

<400> 617	
atgcagagga gcaatcacac agtgactgag ttcacacctgc tgggcttcac cacagatcca	60
gggatgcaac tgggcctctt tgtgggtgtc ctgggtgtgt actgtctgac tgtggtagga	120
agtagcacc tcacgtgtt gatctgtaat gactcccacc tacacacacc catgtatttt	180
gtcattggaa atctgtcatt tctggatctc tgggtattctt ctgtctacac cccaaagatc	240
ctagtgcact gcatctctga agacaaaagc atctcctttg ctggctgcct gtgtcagttc	300
ttctctgcca ggctggccta tagtgagtgc tacctactgg ctgccatggc ttatgaccac	360
tacgtggcca tctccaagcc cctgctttat gctcagacca tgccaaggag attgtgcatc	420
tgtttggttt tatattccta tactgggggt tttgtcaatg caataatatt aaccagcaac	480
acattcacat tggatttttg tggtgacaat gtcattgatg actttttctg tgatgtccca	540
cccctcgtga agctggcatg cagtgtgaga gctaccaggc tgtgctgcac ttccttctgg	600
cctccaatgt catctcccct actgtgtcga tccctgcctc ttacctctcc atcatcacca	660
ccatcctgag gatccactct acccagggcc gcatcaaagt cttctccaca tgctcctccc	720
acctgatctc cgttacctta tactatggct ccattctcta caactactcc cggccaagtt	780
cagctactc cctcaagagg gacaaaatgg tttctacctt ttatactatg ctgttcccca	840
tgttgaatcc catgatctac agtctgagga ataaagacat gaaagacgct ctgaaaaaat	900
tcttcaagtc agcataatcc aaagtc	926

<210> 618  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g467 nucleotide)

<220>  
 <223> Synthetic construct

<400> 618	
atggacggg tgaatgatag ctccctgcag ggctttgttc tgatgagcat atcgaccat	60
ccccagctgg agatgatctt ttttatagcc atcctcttct cctatttgct gaccctactt	120
gggaactcaa ccatcatctt gctttcccgc ctggaggccc ggctccatac acccatgtac	180
ttcttctca gcaacctctc ctccctggac ctgtcttcg ctactagtgc agtccccaa	240
atgctgatca atttatgggg accaggcaag accatcagct atgggtggctg cataaccag	300
ctctatgtct tcccttggtt gggggccacc gagtgcaccc tgctgggtgt gatggcattt	360
gaccgctacg tggcagtgtg ccggcccctc cgctacaccg ccatcatgaa cccccagtc	420
tgctggctgc tggctgtgat tgcctggctg ggtggcttg gcaactctgt gatccagtc	480
acattcactc tgcagctccc attgtgtggg caccggaggg tggagggatt cctctgcgag	540
gtgcctgcca tgatcaaact ggctgtggc gacacgagtc tcaaccaggc tgtgctcaat	600
ggtgtctgca ccttcttcac tgcagtccca ctaagcatca tctgtatctc ctactgcctc	660
attgctcagg cagtgtgaa aatccactct gcagagggga ggcgaaaggc gttcaatacg	720
tgctctccc atctgtggt ggtgttctc ttctatggct cagccagcta tgggtatctg	780
cttcgggcca agaacagcaa acaggaccag ggcaagttca tttccctgtt ctactcgtg	840
gtcacacca tgggtgaatcc cctcatctac acgtgcgga acatggaagt gaaggcgca	900
ctgaggaggt tgctggggaa aggaagagaa gttggc	936

<210> 619  
 <211> 247  
 <212> DNA  
 <213> Unknown (H38g468 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 619

ggtgagaggc	ttaagacact	caacacatgt	gtgtcacata	tctatgcagt	gctgatcttc	60
tatgtgccta	tggttagtgt	gtccatggtt	catcgatttg	ggaggcatgc	tcctgaatat	120
gtgcacaagt	tcatgtctct	ttgtacctcc	aatgctctac	ccaattatct	attccatcaa	180
gactaaggag	attcgcagga	gactacacaa	gatgttattg	ggagctaagt	tctgatcaag	240
gaaaact						247

&lt;210&gt; 620

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g469 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 620

atggaagtgg	gaaattgcac	catcctgact	gaattcatct	tggtgggttt	ctcagcagat	60
tcccagtggc	agccgattct	atttggagtg	tttctgatgc	tctatttgat	aaccttgta	120
ggaaacatga	ccttggttat	cttaatccga	actgattccc	acttgcatat	acctatgtac	180
tttttcattg	gcaatctgtc	ttttttggat	ttctggtata	cctctgtgta	tacccccaaa	240
atcctggcca	gttgtgtctc	agaagataag	cgcatttccc	tggttggtat	tggttggtat	300
ctgttttttt	cctgtgttgt	agcctacact	gaatgctatc	tcttggtcag	catggcatat	360
gaccgcccag	cagcaatttg	taaccatttg	ctttattcag	gtaccatgtc	caccgcccct	420
tgtactgggc	ttgttgctgg	ctcctacata	ggaggatttt	tgaatgccat	agcccatact	480
gccaatatct	tccgcctgca	tttttgggtg	aaaaatatca	ttgaccactt	tttctgtgat	540
gcaccaccat	tggtaaaaat	gtcctgtaca	aacaccaggg	tctacgaaaa	agtctgtgct	600
ggtgtggtgg	gcttcacagt	actctccagc	attcttgcta	tcttgatttc	ctatgtcaac	660
atcctcctgg	ctatcctgag	aatccactca	gcttcaggaa	gacacaaggc	attctccacc	720
tgtgcttccc	acctcatctc	agtcattgct	ttctatggat	cattgttggt	tatgtattca	780
aggcctagtt	ccacctactc	cctagagagg	gacaaaagtag	ctgctctggt	ctacaccgtg	840
atcaaccac	tgctcaaccc	tctcatctat	agcctgagaa	acaaagatat	caaagaggcc	900
ttcaggaaag	caacacagac	tatacaacca	caaaca			936

&lt;210&gt; 621

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g470 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 621

atgcctactg	taaaccacag	tggtactagc	cacacagtct	tccacttgct	gggcatccct	60
ggcctacagg	accagcacat	gtggatttct	atcccattct	tcatttccta	tgtaaccgcc	120
cttcttggga	acagcctgct	catcttcatt	atcctcaca	agcgagcct	ccatgaaccc	180
atgtacctct	tccctctgat	gctggctgga	gcagacattg	tccctccac	gtgcaccatt	240
cctcaggcct	tagctatctt	ctgggtccgt	gctggggaca	tctccctgga	tcgttgcatc	300
actcagctct	tcttcaccca	ttccaccttc	atctctgagt	cagggatctt	gctgggtgat	360
gcctttgacc	actatattgc	catatgctac	ccactgaggt	acaccaccat	tcttacaaat	420
gctctgatca	agaaaatttg	tgtgactgtc	tctctgagaa	gttatggtag	aattttccct	480
atcatatttc	ttttaaaaag	attgactttc	tgccagaata	atattattcc	acacaccttt	540
tgtgaacaca	ttggcctagc	caaataatga	tgtaatgaca	ttcgaataaa	catttggtat	600
gggttttcca	ttctaattgc	gacgggtggt	ttagatgttg	tactaatttt	tatttcctat	660
atgctgattc	tccatgctgt	cttccacatg	ccttctccag	atgcttgcca	caaagctctc	720
aacacatttg	gctcccatgt	ctgcatcatc	atcctctttt	atgggtctgg	catcttcaca	780
atccttacc	agagggttgg	acgccacatt	ccaccttgta	tccacatccc	gttggttaat	840
gtctgcattc	tggtccacc	tatgctgaat	cccattattt	atgggatcaa	aaccaagcaa	900
atccaggaa	aggtggttca	gtttttgttt	ataaaacaga	aaataacttt	ggtt	954

<210> 622  
 <211> 942  
 <212> DNA  
 <213> Unknown (H38g471 nucleotide)

<220>  
 <223> Synthetic construct

<400> 622  
 atggaggctg ccaatgagtc ttcagagggga atctcattcg ttttattggg actgacaaca 60  
 agtcctggac agcagcggcc tctctttgtg ctgttcttgc tcttgatgt ggccagcctc 120  
 ctgggtaaat gactcattgt ggctgccatc caggccagtc cagcccttca tgcacccatg 180  
 tacttcctgc tggcccacct gtcccttctgt gacctctgtt tcgcctccgt cactgtgccc 240  
 aagatgttgg ccaacttgtt ggcccatgac cactccatct cgctggctgg ctgcctgacc 300  
 caaatgtact tcttctttgc cctgggggta actgatagct gtcttctggc ggccatggcc 360  
 tatgactgct acgtggccat ccggcacccc ctcccctatg ccacgaggat gtcccgggcc 420  
 atgtgcgcag ccctgggtggg aatggcatgg ctgggtgtccc acgtccactc cctcctgtat 480  
 atcctgtctc tggctcgctt gtcccttctgt gcttcccacc aagtgcacca cttcttctgt 540  
 gaccaccagc ctctcttaag gctctcgtgc tctgacaccc accacatcca gctgctcatc 600  
 ttcaccgagg gcgcgcagct ggtggtcact cccttctctg tcatcctcgc ctccatggg 660  
 gccatcgag ctgccgtgct ccagctgccc tcagcctctg ggaggctccg ggctgtgtcc 720  
 acctgtggct cccacctggc tgtggtgagc ctcttctatg ggacagtcac tgcagtctac 780  
 ttccaggcca catcccagc cgaggcagag tggggccgtg tggccactgt catgtacact 840  
 gtagtcaccc ccatgctgaa ccccatcatc tacagcctct ggaatcgca tgtacagggg 900  
 gcaactccag cccttctcat tgggcgaagg atctcagcta gt 942

<210> 623  
 <211> 946  
 <212> DNA  
 <213> Unknown (H38g472 nucleotide)

<220>  
 <223> Synthetic construct

<400> 623  
 atctctatgt tctcctgcaa caccagcact tctggtcagt ctaccttctt cctcactggg 60  
 ttccaggcc tggaaagcctc tcatcattgg gtttccatcc ccatcaacct cttctgtgtg 120  
 gtttccatcc tgggtaataa tatcatctc tctctgatcc acacagatcc agccttacat 180  
 gaacccatgt atatcttctt gtccatgttg gcagcctctg atctgggcct ctgtgcctct 240  
 accttccccca ctatgggtgcg tctcttcttg ctgggagctc gtgagctgcc ctttgatctc 300  
 tgtgcagcac agatgttctt catccatacc ttcacctatg tggagtccgg tgtactgctg 360  
 gccatggcct tcgatcgctt tattgccatc cgggaccctc tgcattatgc cataatcatt 420  
 acctgctcag tcacagccga ggtgggaact gccattctgg tgagggtgt tctgctcaac 480  
 ctcccgggac ctatcctcct gcagcagctg ctctttccca agatcagcgc tctctgtcac 540  
 tgctactgcc tgcactgtga ccttgtgggg ttggcctgct cagacacca gatcaatagc 600  
 ctgggtggcc tggtttccat cctcttctca ctgtgccttg actccttctt catcatgctt 660  
 tcatatgccc tgatcctatg aactgtgctg ggcattgcat cacctgggga gcggctcaag 720  
 gcaactcaaca cgtgtgtctc acacctctgc attgttctca tcttttattt gcccacacgg 780  
 gctgtctgtc ttgcaccgag taaagaagca tgactaccct gctctggcag tgctcatggc 840  
 caacctacac ttcttggctc cacccttcat gaacccatt gtgtattgca tcaagtctag 900  
 gcagatccgt cagagcctcc taaagcactt ccagcagaag aggatt 946

<210> 624  
 <211> 960  
 <212> DNA  
 <213> Unknown (H38g473 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 624

cacacagagc	catggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcccg	cctcgctggg	ttgtcccggt	ccatgtatct	ggatcatggtg	120
ctgaggaacc	tgtcatcat	cctggctgtc	agctctgact	cccacctcca	cacccccatg	180
tactttcttc	tctccaacct	gtgctgggct	gacatcggtt	tcacctcggc	catggttccc	240
aagatgattg	tggacatgca	gtctcatagc	agagtcattc	cttatgctgg	ctgcctgaca	300
cggatgtctt	tcttgggtcc	ttttgcatgt	atagaagaca	tgctcctgac	tgcatgggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcategt	gaatcctcac	420
ctctctgtct	tcttagtttt	ggtgtccttt	ttccttagcc	tggtggattc	ccagctgcac	480
agttagattg	tgttacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	agcttctcaa	ccttgccctg	tctgacagcg	tcataaatag	catattctta	600
tatttcgata	gtactatgtt	tggttttctt	cccatttcaa	ggatcctttt	gtcttactat	660
aaaattgtcc	cctctattct	aaggatttca	tcgtcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	accccccagg	agtgggtgtg	tggcgtcagt	gatgtacgct	840
gtggtcaccc	ccatgctgaa	ccctttcatc	tatagcctga	gaaacagaga	cattcaaagc	900
gccctctgga	ggctgctgag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

&lt;210&gt; 625

&lt;211&gt; 985

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g474 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 625

atgaaactca	taaaccatac	catcagaacc	caacctcctt	tctgctcatg	ggaattccag	60
gcccgaggc	atcccacttt	tggattgctt	ttcccttctg	ctccatgtat	gccctggcag	120
tgtctggaaa	catgggtggt	ctgctagtgg	tacattcaga	gcctgtattg	caccagccca	180
tgtacctgtt	cctctgcatg	ctatccacca	ttgacctggt	cctctgcacc	tccactgtgc	240
ccaagctcct	tgcacttttt	tgggcaaagg	atgctgagat	caactttggg	gcctgtgctg	300
cccagatgtt	ctttatccat	ggcttctcag	ctgtagaatc	tggtataact	ctagcaatgg	360
cctttgaccg	ctacttagcc	atttgctggc	ctctgcacta	tgggtcattg	ctctccccag	420
agtctgtagg	caagctgggg	gctgcagcgt	gcttcgtgg	ttgggactca	tgacccact	480
acactgctta	ctggcaagac	tgagctactg	cagtcgagtg	gtggccact	cctactgtga	540
acacatggct	gtggtaaagc	tggcttgtgg	aggaacacag	ccaaacaaca	tctatggcat	600
cactgctgcc	acactgggtg	tgggcactga	ctccatctgt	attgctgtct	cctatgcact	660
catcctccga	gctgtgttag	gtctttcctc	caaggaggca	agggttaaga	cctttggcac	720
ttgtggctcc	cacctgggtg	tcatacttct	cttctacaca	ccaggactct	tctccttcta	780
cacacagcgg	tttggccagc	acgtgccccg	gcacatccac	atccttctag	ctgacctcta	840
cctgggttgg	ccacccatgc	tcaacctcat	catctatggc	atgaagacca	qacagatctg	900
ggatggggcc	ctccggcttc	tgaagtgggg	ccctgctcag	tcataaagtc	ttcaacccca	960
ccctgaaacc	tttatcttct	ttgcc				985

&lt;210&gt; 626

&lt;211&gt; 989

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g475 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 626

cacacagagc	cacggcatct	cacaggtgtg	tgagaattcc	tcctcgtggg	actctcagag	60
gatccagaac	tgcagcctgt	cctcggtggg	gtgtccctgt	ccatgtatgg	ggtcacagtg	120
ataaggaacg	tgtcatcat	cctgggtgtg	agctctgact	cccacctcca	cacccccatg	180
tttttttctt	ctccaacgtg	tgggtgggctg	acatcagttt	cacgtcggcc	ggggttccca	240
agatgacggg	ggacatgcag	tcgcatagca	gagtcattcta	ttatgctggc	tgcatgactc	300
ggatgtcttt	tttcgtcctt	ttagcatgta	tagaagacat	gctcgtgtgt	gtgatggcat	360
aggagtgcct	tgtagccatg	tgtcgccctg	tgcaatacac	agttattgta	aatcctcacc	420

tgtgtgtttt	cagagtggg	gtgtccttc	tccagagcgt	gttgattcc	caggtgcaca	480
gatagagtgt	gtcacattc	actttttca	agaatgtgga	aatctctcat	tttgtgtgtg	540
agccatctca	atttctccac	tttgctgtt	gtgacagttt	catcaagagc	atattcatgt	600
atttcgatag	taatatgttt	ggttttcttc	ccatcacagg	gatctttttg	tcttaatata	660
aaagtgtccc	ctccattata	aggatttcat	cgtcagatgg	aaagtataaa	gctttctcca	720
cgtgtggctc	tcacgtggca	gttgtttgct	tattatatgg	aacaggcatt	ggggtgtaca	780
tgacttcagg	tgtggcacca	ccccccagca	atgggtgtgt	ggcatcagtg	aagtacgcgg	840
tggtcacccc	catgctgacc	cctttcatct	acagcgtgag	aaacagggac	attcaaagcc	900
ccctgtggag	tgtgtgcagc	agcacagtta	aatcttttga	tgtgtcccat	cttttttgtg	960
tgtgggtaag	aaagggcacc	cacattaaa				989

&lt;210&gt; 627

&lt;211&gt; 512

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g476 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 627

cacacacagc	cacggggctc	cacacgtgtg	tgagaattcc	tcctcctggg	actctcacag	60
gatccacaac	tgacgtgtg	ctctctgggc	tgccctgtg	catgtgtctg	ggcacacagc	120
tggggaacct	gctgcatcat	cctgggtgtg	agctctgact	cccacctcca	cacccccatg	180
tactcttttc	tctccaacct	gtgctggggc	tgacatcagt	ttcacctcca	ccacggggcc	240
caagttgatt	gtggacatcc	actcttacac	cagagacatc	tcctatgcac	gctgtctgac	300
tcacacacct	ctctttgcc	tttttgagg	cgtgggaaag	agacatgctc	ctgagagtga	360
tgggctatga	ccgcgttgta	gacatctgtg	accctctata	tcattcacac	gccatgaacc	420
cctgtgtctg	tggtctctta	gatttgtggt	ctcttttttt	tctcacactt	ttatacaccc	480
acctgcacaa	ctcgattgcc	ttacacatga	cc			512

&lt;210&gt; 628

&lt;211&gt; 967

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g477 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 628

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagtcca	60
agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	ccaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	taccctaaa	240
atgattgcag	actttctggt	tgagcacaag	actatttctt	ttgatgccc	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtc	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgttgtgc	tcttccctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcactg	ttaatctgcc	attttgtggt	cctaataagg	tagatagttt	ttttctgtga	540
ccttccctcta	tgaccaagt	tagcctgcat	agacacttat	gttgtcagcc	tactaatagt	600
tgagatagtg	ggctttcttt	ctctgagttc	ctttctcttc	ttggttgtct	cctacactgt	660
aatacttggt	acagtttagga	atagctcttc	tgtaagcatg	gtgaaggcct	gctccacatt	720
gactgtctcac	atcactgtgg	tcactttatt	ctttggaccg	tgtattttca	tctatgtgtg	780
gcccttcagc	agttactcag	ttgacaaaagt	ccttgctgta	ttctacacca	tcttcacgtc	840
tatttttaaac	cctgtaatct	acatgctaag	aaacaaagaa	gtgaaggcag	ctatgtcaaa	900
actgaagagt	cggtatcaga	agcttggtca	ggtttctgta	gtcataagaa	acgttctttt	960
cctagaa						967

&lt;210&gt; 629

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g478 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 629

atggaggggt	ttaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agatattctt	ttttgtggtg	ttttctgtct	tctatttaat	gaccatgttg	120
ggcaactgcc	tgattttact	cactgtccta	tccacctcac	accttcactc	tcgcacgtac	180
ttcctgctca	gcaacctgtc	tcattgacat	gtgcctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgtct	tgcgtaagac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgctg	ctgatctcca	tgtcttttga	360
caggatattt	gccatatgta	aacctctccg	ctattcaaca	attatgagcc	aaagagtgtg	420
tgttgagctt	gtggcagttt	cttgttggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcccttgg	tcattccagt	agcttgtata	gatatttatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgactgc	tcttacaagt	tttctgcttt	tgctcacctc	ctacatcatt	660
gttcttaata	ctatcagggg	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcacatt	ttattgttgt	gttaatgttc	tttgggccct	gtattttcat	ttatgtgtgg	780
ccttccacaa	acttccctgt	agacaaaatt	ctctctgttt	tctataccat	cttcaactcc	840
tttctgaatc	cacttatcta	tactttgaga	aaccagggaag	tgaagacagc	aatgaagaag	900
aaactgaata	ttcagtattt	cagtcttggg	aaaactgtct	cg		942

&lt;210&gt; 630

&lt;211&gt; 595

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g479 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 630

atgaaccctg	gtttgtgtgg	cttttagagtt	gtgggtgtctt	ttttttttca	cagtctttta	60
ggcgacacag	tgacaaactt	gagcgctcca	caaatgacgt	gtttcgagta	tgtggaaatt	120
cataatttct	tgtgtgccct	ttctcaactc	ccccatcggt	catgggtgtga	cactttcccc	180
aataacataa	tcgtgtattt	tctgtctgcc	atatttggtt	ttcttcccat	cgcggggacc	240
ccttttctct	taatatgaaa	gtgtttcctc	cattgagagg	gtttcatcat	aagggtggaga	300
gtataaggct	ttccccacgt	gtgggtctca	cctctcagtc	gtttgctgat	tatatggcac	360
aggcggttga	gggcacctca	gttcagatgt	gtcatcttcc	ccgagaaagt	ctgcggtggc	420
ctcagtgatg	tacactgtgg	tcacccccat	gctgaaccct	ttcatctaca	gcatgagaaa	480
caggataact	aaaagtgtcc	tgcgggcgcc	gcacggcagc	acgggtgta	tttgatatct	540
tcttatctgt	ccatttcctt	ttgtagtgtg	ggttaaaaaa	ggcagaaagg	tcaaa	595

&lt;210&gt; 631

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g480 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 631

atgctgggtc	tcaatggcac	ccccttccag	ccagcaacac	tccagctgac	aggcattcct	60
gggatacaaa	caggcctcac	ctgggttgcc	ctgattttct	gcatcctcta	catgatctcc	120
attgtaggga	acctcagcat	tctcactctg	gtgttttggg	agcctgctct	gcatcagccc	180
atgtactact	tcctctctat	gtctgctctc	aatgatctgg	gagtgtcctt	ttctacactt	240
cccactgtga	tttctacttt	ctgcttcaac	tacaaccatg	ttgcgtttaa	tgcttgcttg	300
gtccagatgt	tcttcatcca	cactttctcc	ttcatggagt	caggcatact	gctggccatg	360
agcttggatc	gctttgtggc	tatttgttat	ccattacgct	atgtcactgt	gctcactcac	420
aaccgtatat	tggtcatggg	tctgggcatt	cttaccaga	gtttcaccac	tctcttcctt	480
ttcccttttg	tggtgaaacg	actgcccttc	tgcaaggcca	atgttttgca	tcactcctac	540
tgtctccatc	cagatctcat	gaaagtagca	tgtggagaca	tccatgttaa	caacatttat	600

```

gggctcttgg tgatcatttt tacctatggt atggactcaa ctttcatcct gctttcctac 660
gcattgatcc tgagagccat gctgggtcatc atatcccagg aacagcggct caaggcactc 720
aacacctgca tgtcacacat ctgtgcagtg ctggcctttt atgtgcccat aattgctgtc 780
tccatgattc accgcttctg gaaaagtgtc ccacctgttg ttcattgtcat gatgtccaat 840
gtctacctgt ttgtaccacc catgtctaac cctatcatct acagtgtgaa aaccaaggag 900
atccgcaaaag ggattctcaa gttcttccat aaatcccagg cc 942

```

&lt;210&gt; 632

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g481 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 632

```

atggggttgt tcaatgtcac tcaccctgca ttcttctctc tgactggtat ccctgggtctg 60
gagagctctc actcctggct gtcaggggcc ctctgcgtga tgtatgctgt ggcccttggg 120
ggaaatacag tgatcctgca ggctgtgcga gtggagccca gcctccatga gcccatgtac 180
tacttcctgt ccattgtgtc cttcagtgtg gtggccatat ccattggccac actgcccact 240
gtactccgaa ccttctgcct caatgccgc aacatcactt ttgatgctg tctaattcag 300
atgtttctta ttacttctt ctccatgatg gaatcaggta ttctgctggc catgagtttt 360
gaccgctatg tggccatttg tgacccttg cgctatgcaa ctgtgtcac cactgaagtc 420
attgtgtcaa tgggtttagg tgcagtgtc cgaagcttca tcaccctttt cctcttccc 480
tttcttatta agaggctgcc tatctgcaga tccaatgttc tttctcactc ctactgctg 540
caccagaca tgatgaggct tgccctgtgt gatatcagta tcaacagcat ctatggactc 600
tttgttcttg tatccacctt tggcatggac ctgtttttta tcttctctc ctatgtgtc 660
attctgcgtt ctgtcatggc cactgcttcc cgtgaggaa gcctcaaagc tctcaacaca 720
tgtgtgtcac atatcctggc tgtacttgca ttttatgtgc caatgattgg ggtctccaca 780
gtgcaccgct ttgggaagca tgtcccatgc tacatacatg tctcatgtc aaatgtgtac 840
ctatttgtgc ctctgtgtc caacctctc atttatagcg ccaagacaaa ggaaatccgc 900
cgagccattt tccgcatgtt tcaccacatc aaaata 936

```

&lt;210&gt; 633

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g482 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(467)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 633

```

atggaaagca atcagacctg gatcacagaa gtcacctgt tgggattcca ggtggaccga 60
gctctggagt tgttctctt tgggtttttc ttgctattct acagcttaac cctgatggga 120
aatgggatta tcctggggct catctacttg gactctagac tgcacacacc catgtatgtc 180
ttctgtcac acctggccat tgtggacatg tcctatgcct cgagtactgt ccctaagatg 240
ctagcaaatc ttgtgatgca caaaaaagtc atctcctttg ctcttgcat acttcagact 300
tttttgtatt tggcgtttgc tattacagag tgtctgattt tgggtgatgat gtgctatgat 360
cggatgtgtg caatctgtca ccccttgca atacaccnt cattatgaac tggagagtgt 420
gcactgtcct ggctcaact tgctggatat ttagctttct cttggct 467

```

&lt;210&gt; 634

&lt;211&gt; 988

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g483 nucleotide)

&lt;220&gt;



<223> Synthetic construct

<221> misc\_feature

<222> (1)...(988)

<223> n = A,T,C or G

<400> 634

atggaatgca accagacatg gatcacagac atcaccctgc tgggattcca ggttgggtcca	60
gcactggcga ttctcatctn gtgaactctt ctctgtcttc tatacactca ccctgctggg	120
gaatgggggc atctttggga ttatctgcct ggactctaag cttcacacac ccatgtactt	180
cttctctca caccctggcca tcattgacat gtcctatgct tccaacaatg ttcccaagat	240
gttggcaaac ctaatgaacc agaaaagaac catctccttt gttccatgca taatgcagac	300
ttttttgtat ttggcttttg ctgttacaga gtgcctgatt ttggtggtga tgcctatga	360
taggtatgtg gccatctgcc accctttcca gtacactgtc atcatgagct ggagagtgtg	420
cacgatcctg gttctcacgt cctggctcatg tgggtttgcc ctgtccctgg tacatgaaat	480
tctcttcta aggttgccct tctgtgggcc cgggatgtg aaccacctct tctgtgaaat	540
tctatctgtc ctcaagctgg cctgtgctga cactgggtt aaccaagtgg tcatatttgc	600
tacctgtgtg tttgtcttag tcgggcctct ttccttgatt ctggtctcct acatgcacat	660
cctcggggcc atcctgaaga tccagacaaa ggagggccgc ataaaggcct tctccacctg	720
ctctctccac ctgtgtgtgg ttggactatt ctttggcata gccatggtgg ttacatggt	780
cccagactct aatcaacgag aggagcagga gaaaatgctg tccctgtttc acagtgtctt	840
gaacccaatg ctgaaccccc tgatctacag cctgaggaat gctcagttga agggcgccct	900
ccacagagca ctccagagga agaggtccat gagaacggtg tatgggcttt gcctttaaaa	960
catgtggttt gctgaagcaa gaattttg	988

<210> 635

<211> 941

<212> DNA

<213> Unknown (H38g484 nucleotide)

<220>

<223> Synthetic construct

<400> 635

atgggagtca accaatcatg gtcaccagaa ttcctcctgg tggaaatcca gctcagtgcc	60
gagatggaag tgctcctctt ttagatcttc tccctgttat acatcttcag cctgctggca	120
aatggcatga tcttgggact catctgtctg gaccacattc tgcttacctc catgtacttc	180
ttctctcac acctggccat cattgacatg tcctatgctt ccaacaatgt tcccaagatg	240
ttggcaaatc tgatgaacaa gaaaagaacc atctcctttc ttccatgcat aatgcagacc	300
tatttgtatt tctcttttgc tgctacagag tgtctgattt tgggtggtgat gtcctatgat	360
aggatgtgg ccatttgcca cctctccag tacactgtca tcatgagctg gagagtgtgc	420
acgatcctgg ctctcacatc ctggctcatgt ggggtttgcc tgctcctggt acatgcaatt	480
cttcttctaa ggttgccgtt ctgcccggcc cgggatgtga accacctctt ctgtgaaatt	540
ctgtctgtcc tcaagctggc ctgttctgac acctgggggt aaccacagtg gtcataattg	600
ctacctgtgt gtttgtctta gttggacctc tttgtttgat gcttgtctcc tacatgcaca	660
tcctctggcc atcctaaaga tccagacaaa ggaagccgca taaaggcctt ctgcacctgc	720
tctctccacc tgtgtgtggt tggactcttc ttgtggcata gccactggtg gtttacatag	780
tcccagactc taatcaacga gaggagcagg agaaaatgct gtccctgttt cacagtgtct	840
tgaacccaat tctgaacccc ctgatctaca gtctgaggaa tgctcaggtg aaggcgcccc	900
tccacagagc actgcagagg acgctgtcta tgtaaggagt g	941

<210> 636

<211> 1002

<212> DNA

<213> Unknown (H38g485 nucleotide)

<220>

<223> Synthetic construct

<400> 636

atgtgttatc tttctcagct atgcctcagc cttgggggaa acactttaca tatgggggat	60
---	----

gtgagacata	ccaatgagag	caacctagca	ggtttcatcc	ttttaggggt	ttctgattat	120
cctcagttac	agaaggttct	atttgtgctc	atattgatcc	tgtattttact	aactattttg	180
gggaataacca	ccatcattct	ggtttctcgt	ctggaacca	agcttcata	gccgatgtat	240
ttcttctctt	ctcatctctc	cttcctgtac	cgctgcttca	ccagcagtg	tattccccag	300
ctcctggtaa	acctgtggga	acccatgaaa	actatcgcc	atgggtggctg	tttgggtcac	360
ctttacaact	cccatgccct	gggatccact	gagtgcgtcc	tcccggctgt	gatgtcctgt	420
gaccgctatg	tggctgtctg	ccgtcctctc	cattacactg	tcttaatgca	tatccatctc	480
tgcattggcct	tggcatctat	ggcatggctc	agtggaaatag	ccaccaccct	ggtacagtcc	540
accctcacc	tgcagctgcc	cttctgtggg	catcgccaag	tggatcattt	catctgcgag	600
gtccctgtgc	tcatcaagct	ggcttgtgtg	ggcaccacgt	ttaacgaggc	tgagcttttt	660
gtggctagta	tctttttcct	tatagtgcct	gtctcattca	tcttggctctc	ctctggctac	720
attgcccacg	cagtgttgag	gattaagtca	gctaccagga	gacagaaagc	attcggggacc	780
tgttctctcc	acgtgacagt	ggtcaccatc	ttttatggaa	ccatcatctt	catgtatctg	840
cagccagcca	agagtagatc	cagggaccag	ggcaagtgtg	tttctctctt	ctacactgtg	900
gtaacccgca	tgcttaaccc	tcttatttat	accttgagga	tcaaggaggt	gaaaggggca	960
ttaaagaaa	ttctagcaaa	ggctctggga	gtaaataattt	ta		1002

&lt;210&gt; 637

&lt;211&gt; 510

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g486 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 637

atggaaggca	acaagacatg	gatcacagac	atcaccttgc	cgcgattcca	ggttgggtcca	60
gcactggaga	ttctcctctg	tggacttttc	tctgccttct	atacactcac	cctgctgggg	120
aatgggggtca	tctttgggat	tatctgcctg	gactgtaagc	ttcacacacc	catgtacttc	180
ttcctctcac	acctggccat	tgttgacata	tcttatgctt	ccaactatgt	ccccaagatg	240
ctgacgaatc	ttatgaacca	ggaaagcacc	atctcctttt	ttccatgcat	aatgcagaca	300
ttcttgtatt	tggcttttgc	tcacgtagag	tgtctgattt	tgggtgggtgat	gtcctatgat	360
cgctatgcgg	acatctgcca	ccccttacgt	tacaatatcc	tcatgagctg	gagagtgtgc	420
actgtcctgg	ctgtggcttc	ctgggtgttc	agcttcctcc	tggctctggg	cccgtttagt	480
tctcagtcgc	tgagggtgcat	gaacgtactg				510

&lt;210&gt; 638

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g487 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 638

atggacacag	gcaacaaaac	tctgccccag	gactttctct	tactgggctt	tcttgggtct	60
caaactcttc	agctctctct	ctttatgctt	tttctgggtga	tgtacatcct	cacagttagt	120
ggtaatgtgg	ctatcttgat	gttgggtgagc	acctcccatc	agttgcatac	ccccatgtac	180
ttctttctga	gcaacctctc	cttcctggag	atttgggtata	ccacagcagc	agtgcccaaa	240
gcactggcca	tcctactggg	gagaagtcag	accatatcat	ttacaagctg	tcttttgcag	300
atgtactttg	ttttctcatt	aggctgcaca	gagtacttcc	tcttggcagc	catggcttat	360
gaccgctgtc	ttgccatctg	ctatccttta	cactacggag	ccatcatgag	tagcctgtct	420
tcagcgcagc	tggccctggg	ctcctgggtg	tgtgggttctg	tggccattgc	agtgccca	480
gccctcatca	gtggcctgtc	cttctgtggc	ccccgtgcca	tcaaccactt	cttctgtgac	540
attgcaccct	ggattgccct	ggcctgcacc	aacacacagg	cagtagagct	tgtggccttt	600
gtgattgctg	ttgtgggttat	cctgagttca	tgcctcatca	cctttgtctc	ctatgtgtac	660
atcatcagca	ccatcctcag	gatccctct	gccagtggcc	ggagcaaagc	cttctccacg	720
tgtcctctgc	atctcacctg	ggtgctcatt	tggatgtggg	ccacagtttt	ccttcacgtc	780
cgcacctcta	tcaaagatgc	cttggatctg	atcaaagctg	tccacgtcct	gaacactgtg	840
gtgactccag	ttttaaaccc	cttcatctat	acgttctgta	ataaggaagt	aagagagact	900
ctgtgaaga	aatggaaggg	aaaa				924

<210> 639  
 <211> 669  
 <212> DNA  
 <213> Unknown (H38g488 nucleotide)

<220>  
 <223> Synthetic construct

<400> 639  
 aaagaaatgg gatgtcacca atcaatggtc acagaattca tcctgggtggg attccagctc 60  
 agtgcctgaga tggaagtgc cctcttttgg agcttctccc ttggaatagc cttggaactc 120  
 atctgtctgg accacagtct gcacactctc atacttcttc ctctcacacc tggccgctcat 180  
 tgacatggcc tatgcttcca acaatgttcc caagatgctg gtggatcttg caaactagaa 240  
 aagcaccatg tgcttttttc catgcataat gcagacattc ttgtatttgg cttttgctca 300  
 catagagtgt ctgattttgg tggttttgtc ctatgatcgc tatgtggcca tctgccaccc 360  
 cttacgttac aatgtcctca tgagctggag agagtgcact gtccctggctg tggcttcctg 420  
 ggtgttcagc ttctcctcgg ctctgggtcca tttagtcttc attctgaggc tgcccttcag 480  
 tgggctcatg aaatcaacca ctactgtgaa atcctgtctg tcctcaagtt ggcctgtgct 540  
 gacacctggc tcaaccaggt ggtcatcttt gcaagctgca tgttcacct ggtagggtga 600  
 ctctgcctgg tgctgggtctc ttacttgggc atctggcggc atctgagatc agttgcgaag 660  
 ccaaaaagg 669

<210> 640  
 <211> 927  
 <212> DNA  
 <213> Unknown (H38g489 nucleotide)

<220>  
 <223> Synthetic construct

<400> 640  
 atgggattgg gcaatgagag ttccctaattg gatttcatcc ttctaggctt ctgagaccac 60  
 cctcgtctgg aggcgttct ctttgtattt gtctttttct tctacctcct gacccttggtg 120  
 ggaaacttca ccataatcat catctcatat ctggatcccc ctcttcatac cccaatgtac 180  
 ttttttctca gcaacctctc ttactggac atctgcttca ctactagcct tgctcctcag 240  
 accttagtta acttgcaaag accaaagaag acgatcactt acggtgggtg tgtggcgcaa 300  
 ctctatattt ctctggcact gggtccact gaatgtatcc tcttggctga catggccttg 360  
 gatcggtaca ttgctgtctg caaacccctc cactatgtag tcatcatgaa cccacggctt 420  
 tgccaacagc tggcatctat ctctggctc agtgggttgg ctagtccct aatccatgca 480  
 acttttacct tgcaattgcc tctctgtggc aaccataggc tggaccattt tatttgcgaa 540  
 gtaccagctc ttctcaagtt ggcttgtgtg gacaccactg tcaatgaatt ggtgcttttt 600  
 gttgttagtg ttctgtttgt tgcattcca ccagcactca tctccatctc ctatggcttc 660  
 ataactcaag ctgtgctgag gatcaaatca gtagaggcaa ggcacaaagc cttcagcacc 720  
 tgctcctccc accttacagt ggtgattata ttctatggca ccataateta cgtgtacctg 780  
 caaccttagt acagctatgc ccaggaccaa ggggaagtta tctccctctt ctacaccatg 840  
 gtgaccccca ctttaaattc tatcatctat actttaagga acaaggatat gaaagaggct 900  
 ctgaggaaac ttctctcggg aaaattg 927

<210> 641  
 <211> 1012  
 <212> DNA  
 <213> Unknown (H38g490 nucleotide)

<220>  
 <223> Synthetic construct

<400> 641  
 tctacagacc cacagaatct aacagatgtc tctgtattcc tctcctaga actacagagg 60  
 atccagaacg gcagccggtc ctcaactggc tgttctgtc catgtgctg gtcattggtc 120  
 tggggaacct gctcatcatc ctggccatca gccctgactc ccacctccac atccccatgt 180

```

acttcttctt ctccaacctg tcttgctg acatcggttt cacctccacc acggtcccca 240
agatgattgt ggacatccag tctcacagca gagtcattct ctatgcaggc tgcctgactc 300
agatgtctct ctttgccatt tttggaggca tggaaagagag acatgctcct gagtgtgatg 360
gcctatgacc ggtttgtagc catctgtcac cctctatatc attcagccat catgaacccg 420
tgttctgtg gcttcctagt tttgtgtct tttttttct gtcctcagtc ttttagactc 480
ccagctgcac aacttgattg ccttacaagt gacctgcttc aaggatgtgg aaattcctaa 540
tttcttctgt gaccttctc aactcccca tcttgcatgt tgtgacacct tcaccaataa 600
gataatcatg tatttcctg ctgccatatt tgggtttctt cccatctcag ggaccctttt 660
ctcttactct aaaattgttt cctccattct gagggtttca tcatcagggt ggaagtataa 720
agccttctcc acctgtgggt ctcacctgtc agttgtttgc tgagtttatg gaacaggcgt 780
tggaggttac ctcagttcag atgatgtgtc atcttcccc agaaagggtg cagtggcctc 840
atgatgttac acggtggtca ccccatgccc gaacccttc atctacagcc tgagaaacag 900
ggatattaaa agtgtcctgc ggcggccgca cggcagcaca gtctaattct aatatcttct 960
tatctgttcc attccttttg tagtgtgggt taaaaaggc agaaagggtca aa 1012

```

&lt;210&gt; 642

&lt;211&gt; 879

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g491 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 642

```

atgggatttt cgaattcctg ggatattcag attgtacatg ctgctctatt ctccctagtt 60
tacctggcag ctgtcatagg aaatctccta atcatcatac ttaccactct ggatgttcac 120
ctccaaaccc caatgtattt ctttttgaga aacttgctct tcttagattt ttgttacatc 180
tctgtcacia ttccaaaatc tattgttagt tccttgactc atgatacttc catttctttc 240
tttgggtgtg ctctgcaagc cttctttttc atggacttgg caactacgga ggtagccatc 300
cttacagtga tgccttatga ccgctatatg gccatctgcc ggcctttaca ttatgagggtc 360
atcataaacc aagggtgtctg tctgaggatg atggccatgt cgtgggtcag tgggggtgatc 420
tgtggattca tgcagtgtgat agcaacattc tcattaccat tctgtgggcg caatagaata 480
cgtcaatttt tctgtaatat tccacagctc ctaagcctct tagaccccaa agtaattacc 540
attgagattg gagtcattgt ttttggtaca agtcttctga taatctcctt tgttgtaatt 600
actctctcct acatgtacat tttttctgtc atcatgagga ttcttcttaa ggagggtaga 660
tcaaaaacat tttctacctg cattccacat cttgtggttg taacactctt tatgatattc 720
ggcagcattg cctatgtgaa gccaatattc aattctcccc ccgttctgga tgttttctctg 780
tctgcgttct acacagtcgt gcccccgacc ctgaaccccg tcatctatag tctgaggaat 840
agggacatga aggcagccct gagaaggcag tgtggtccc 879

```

&lt;210&gt; 643

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g492 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 643

```

atgatgggcc atcagaatca cactttcagc agtgatttca tacttttggg attgttctct 60
tcttcccaaa caagtgtggt cttcttctta gacaatttgt cattttcatt atgagtgtaa 120
cagaaaatac gctcatgac ctcctcatte gcagtactc ccgactccac actccaatgt 180
attttctgct cagccatctc tccttaatgg atatcttgca tgtttccaac atcgttccca 240
aaatggtcac taactttctg tcaggcagca gaactatttc atttgcagggt tgtgggttcc 300
aggtatttct gtccctcacc ctcttgggtg gtgagtgcct tctcctgggt gcaatgtcct 360
gtgatcgcta tgtggctatc tgtcaccgca tgcgctatcc gattcttatg aaggagtatg 420
ccagcgctct catggctgga ggctcctggc tcattgggggt tttcaactcc acagtccaca 480
cagcttatgc actgcagttt cccttctgtg gctctagggc aattgatcac ttcttctgtg 540
aagtcctgca catgttgaag ttgtcctgtg cagacacaac acgctatgaa cgagggtgtt 600
gtgtaagtgc tgtgatcttc ctgctgatcc ctttctcctt gatctctgct tcttatggcc 660
aaattattct tactgtcttc cagatgaaat catcagaggc aaggaaaaag tcattttcca 720

```

cttggttcctt	ccacatgatt	gtgggtcacga	tgtactatgg	gccatttatt	tttacatata	780
tgagacctaa	atcataccac	actccaggcc	aggataagtt	cctggcaata	ttctatacga	840
tcctcacacc	cacactcaac	cctttcatct	acagcttttag	gaataaagat	gttctggcgg	900
tgatgaaaaa	tatgctcaaa	agtaactttc	tgcacaaaaa	aatgaatagg	aaaattcctg	960
aatgtgtgtt	ctgtctattt	ctatgttaaa	tgcctgaagg	atactcatga	gaggtttcct	1020

&lt;210&gt; 644

&lt;211&gt; 932

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g493 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 644

atgaagtggg	caaaccagac	agctgtgacg	gaatacgtcc	tgatgggggt	acacgagcac	60
tgtaacctgg	agggtgtcct	gtttgtgttc	tgcctgggca	tctactccgt	gaatgtgttg	120
gggaacgccc	tcctcatagg	gctgaacgtg	ctgcaccctc	gcctgcacaa	ccccatgtac	180
ttctcagcaa	cctctccctc	atggacatct	gcggcacctc	ctcctttgtg	cctctcatgc	240
tagacaattt	cctggaaacc	cagaggacca	tttccttccc	tggctgtgcc	ctgcagatgt	300
acctgacctt	ggcgctggga	tcaacggagt	gcctgtgtct	ggctgtgatg	gcatatgacc	360
gttatgtggc	tatctgccag	ccgcttaggt	acccagagct	catgagtggg	cagacctgca	420
tgcagatggc	agcgctgagc	tgggggacag	gctttgccaa	ctcactgcta	cagtccatcc	480
ttgtctggca	cctccccttc	tgtggccacg	tcatacaacta	cttctatgag	atcttggcag	540
tgctaaaact	ggcctgtggg	gacatctccc	tcaatgcgct	ggcattaatg	gtggccacag	600
ccgtcctgac	actggccccc	ctcttgtctc	tctgcctgtc	ttaccttttc	atcctgtctg	660
ccatccttag	ggtaccctct	gctgcaggcc	ggtgcaaagc	cttctccacc	tgctcagccc	720
accgcacagt	ggtggtgggt	ttttatggga	caatctcctt	catgtacttc	aaaccaagg	780
ccaaggatcc	caacgtggat	aagactgtcg	cattgttcta	cggggttgtg	acgccctcgc	840
tgaaccccat	catttacagc	ctgaggaatg	cagaggtgaa	agctgccgtc	ctaactctgc	900
tgagaggagg	tttgcctctc	aggaaagcat	cc			932

&lt;210&gt; 645

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g494 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 645

atgatggaaa	tagccaatgt	gagttctcca	gaagtctttg	tcctcctggg	cttctccaca	60
cgaccctcac	tagaaactgt	cctcttcata	gttgtcttga	gtttttacat	ggtatcgatc	120
ttgggcaatg	gcatcatcat	tctggctctc	catacagatg	tgcacctcca	cacacctatg	180
tactttcttc	ttgccaaact	ccccttctcg	gacatgagct	tcaccacgag	cattgtccca	240
cagctccttg	ctaacctctg	gggaccacag	aaaaccataa	gctatggagg	gtgtgtggtc	300
cagttctata	tctcccattg	gctgggggca	accgagtgtg	tcctgctggc	caccatgtcc	360
tatgaccgct	acgctgccat	ctgcaggcca	ctccattaca	ctgtcattat	gcatccacag	420
ctttgccttg	ggctagcttt	ggcctccttg	ctgggggggc	tgaccaccag	catgggtggc	480
tccacgtcca	ccatgctcct	accgctgtgt	gggaacaatt	gcatcgacca	cttcttttgc	540
gagatgcccc	tcattatgca	actggcttgt	gtggatacca	gcctcaatga	gatggagatg	600
tacctggcca	gctttgtctt	tgttgctctg	cctctggggc	tcatectggt	ctcttacggc	660
cacattgccc	gggcccgtgt	gaagatcagg	tcagcagaag	ggcggagaaa	ggcattcaac	720
acctgttctt	cccacgtggc	tgtggtgtct	ctgttttacg	ggagcatcat	cttcatgtat	780
ctccagccag	ccaagagcac	ctcccatgag	cagggcaagt	tcatagctct	gttctacacc	840
gtagtcactc	ctgcgctgaa	cccacttatt	tacaccctga	ggaacacgga	ggtgaagagc	900
gccctccggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

&lt;210&gt; 646

&lt;211&gt; 792

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g495 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 646

atgatgggtc	tgagtatcgt	tttgacctcc	ctgtttggca	attccctcat	gatttctctg	60
attcactggg	accaccggtt	ccacacgccc	atgtacttcc	tcctgagcca	actttccctc	120
atggacgtga	tgtctggttc	caccactgtg	cccaaaatgg	cggtcgacta	cttgaccgga	180
agtaaggcca	tctcccgcgc	tggtgtgtgt	gcgcagatct	tcttctctcc	cacactgggt	240
ggtaggagag	gcttccctct	agcagccatg	gcctatgacc	gctatgcggc	tgtctgccac	300
ccactccgat	atcccactct	catgagctgg	cagctgtgcc	tgaggatgaa	cctgtcgtgt	360
tggtctctgg	gtgcagctga	cgggctcctg	caggctgttg	ctaccctgag	cttcccatat	420
tgcgggtgac	acgagatcga	tcacttcttc	tgcgagaccc	ccgtgtgtgt	gcgtttggct	480
tgtgtctgaca	cttcagtctt	cgaaaacgcc	atgtacatct	gctgtgtgtt	aatgtctctg	540
gtccccctttt	ccctcatcct	gtcctcctat	ggtctcatcc	tcgtgtgtgt	tctgcacatg	600
cgctctacag	aagcccgcaa	gaaggccttt	gccacctgct	cttcacatgt	ggctgtgggt	660
ggactctttt	atggagctgc	catttttacc	tatatgagac	ccaaatccca	caggctccact	720
aaccacgaca	aggttgtgtc	agccttctat	actatgttca	cccctttact	aaacccctc	780
atctacagtg	tg					792

&lt;210&gt; 647

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g496 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 647

aatctgtctt	tcttagatct	ctgctttaca	gcaagcattg	cccctcagct	gctgtggaac	60
ctgggggggc	cagagaagac	catcacctac	cacggctgtg	tggcccaact	ctacatctac	120
atgatgctgg	gtccaccga	gtgcgtcttc	ctggtgtgca	tgtcccatga	ccgctatgtg	180
gccgtctgcc	ggtccctgca	ctacatggca	gtcatgcgcc	cacatctctg	cctgcagctg	240
gtgactgtgg	cctggtgctg	tggcttcta	aactccttca	tcattgtgtc	tcagacgatg	300
cagctctccc	ggtgtggacg	tcgcagggtg	gaccacttcc	tgtgtgagat	gcctgtctct	360
attgccatgt	cttgtgagga	aaccatgctg	gtagaagcga	ttcacctttg	ccctgggggt	420
ggctctcttc	ctggtgccgc	tctccctcat	cctcatctcc	tacggcgtga	ttgcagccgc	480
ggtgctgagg	atgaagtcag	cagcagggcg	aaagaaagcc	ttccacacct	gctcttctca	540
cctcacagtg	gtctctctct	tctacggaac	catcatctac	ggtgtacctg	aagccggcca	600
acagctactc	ccaagatcag	gggaagtcc	tgactctctt	ctacaccatc	gtcattccca	660
gc						662

&lt;210&gt; 648

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g497 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 648

atggagccgc	tcaacagaa	agagggtgtc	gagttctttc	tgaaaggatt	ttctggctac	60
ccagccctgg	agcatctgct	cttccctctg	tgtctagcca	tgtacctggt	gaccctcctg	120
gggaacacag	ccatcatggc	ggtgagcgtg	ctagatatcc	acctgcacac	gcccggtgtac	180
ttcttctctg	gcaacctctc	taccctggac	atctgtctaca	cgccacacct	tgtgcctctg	240
atgctgggtc	acctcctgtc	atcccgggaag	accatctcct	ttgtgtctct	tgccatccag	300
atgtgtctga	gctgtccac	gggtctccacg	gagtgacctg	tactggccat	cacggcctat	360
gaccgtacc	tggccatctg	ccagccactc	aggtaaccag	tgctcatgag	ccaccggctc	420
tgcgtgctgc	tgatgggagc	tgctgggtgc	ctctgcctcc	tcaagtcggt	gactgagatg	480
gtcatctcca	tgaggctgcc	cttctgtggc	caccacgtgg	tcagtcactt	cacctgcaag	540

atcctggcag	tgctgaagct	ggcatgcggc	aacacgtcgg	tcagcgaaga	cttcctgctg	600
gcggtgctca	tctgtgctgt	gcctgtaccc	ctggcattca	tctgcctgtc	ctacttgctc	660
atcctggcca	ccatcctgag	ggtgccctcg	gcgccaggt	gctgcaaagc	cttctccacc	720
tgcttggcac	acctggctgt	agtgtgtctt	ttctacggca	ccatcatctt	catgtacttg	780
aagcccaaga	gtaaggaagc	ccacatctct	gatgaggtct	tcacagtcct	ctatgccatg	840
gtcacgacca	tgctgaaccc	caccatctac	agcctgagga	acaaggaggt	gaaggaggcc	900
gccaggaagg	tgtggggcag	gagtcgggcc	tccagg			936

&lt;210&gt; 649

&lt;211&gt; 940

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g498 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 649

atggaaaggg	gaaattggac	attggtgact	gagtttattc	ttgtggggat	accaaccacc	60
agagcccttg	ggggcctcct	ctttgtgatt	ttttatcagc	ctatttgggtg	acagtccttg	120
gaaacaccct	tattattatc	ctgattcttg	tggattacag	gctccactca	cccatgtatt	180
tcttctcag	caatctctct	ttcagtgaag	cattaacccat	aacctgtgct	gttcctaaga	240
tgctggaggg	cttcccgtcg	gaaaggaaga	gcatcacaag	tggcgaatgc	tctgcacagt	300
cctatttcta	ttttctttcc	ggatgcaactg	agtttattcc	ttttgctgtc	atgtcctatg	360
accgctatgt	ggcattttgc	agtcctcttc	agtaccctgc	aattatgacc	agctcactct	420
gtgcccacct	cgtcactctc	tcttgggttg	gtggctttct	cctcatgctc	ccatccacca	480
tcctcaaggc	aggactgcca	cactgtgtgc	ccaacgtgat	tgagcacttt	ttctgtgaca	540
gcgcccctct	cctccacctg	gcctgtgctg	acattcgtgc	tattgagctg	ttggactttc	600
tcagctcact	ggtcctgac	ctcagctccc	tctcactcac	agtggctctc	tatgtttaca	660
tcactctccac	cattctgaag	ataccctcag	gccaagggtca	acgcaaagcc	tttgccacct	720
gtgcctctca	cttcacggtg	gtctccgtgg	gctatgggat	ctccatcttt	gtctatgttc	780
accctcaca	gaagagcagc	ctgcacctca	acaagatcct	ctttatcctc	tccagcatca	840
tcacaccct	cctgaatccc	ttcgtcttca	gtctgtggaa	tgaacccatg	aaagatgcac	900
tgaaggacgc	ctcgcccgga	ggacagagct	tgctcaaagg			940

&lt;210&gt; 650

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g499 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 650

atggcaaatc	tcacaatcgt	gactgaattt	atccttatgg	ggttttctac	caataaaaat	60
atgtgcattt	tgcattcgat	tctcttcttg	ttgatttatt	tgtgtgccct	gatggggaat	120
gtcctcatta	tcatgatcac	aactttggac	catcatctcc	acaccccggt	gtatttcttc	180
ttgaagaatc	tatctttctt	ggatctctgc	cttatttcag	tcacggctcc	caaactctatc	240
gccaattctt	tgatacacia	caactccatt	tcatctcttg	gctgtgtttc	ccagggtcttt	300
ttgttgcttt	cttcagcatc	tgcagagctg	ctcctctca	cgggtgatgtc	ctttgaccgc	360
tatactgcta	tatgtcaccc	tctgcactat	gatgtcatca	tggacaggag	cacctgtgtc	420
caaagagcca	ctgtgtcttg	gctgtatggg	ggctgtattg	ctgtgatgca	cacagctggc	480
accttctcct	tatcctactg	tgggtccaac	atgggtccatc	agttcttctg	tgacattccc	540
cagttattag	ctatttcttg	ctcagaaaat	ttaataagag	aaattgcact	catccttatt	600
aatgtagttt	tggatttctg	ctgttttatt	gtcatcatca	ttacctatgt	ccacgtcttc	660
tctacagtca	agaagatccc	ttccacagaa	ggccagtcac	aagcctactc	tatttgcttt	720
ccacacttgc	tggttgtgtt	atttctttcc	actggattca	ttgcttatct	gaagccagct	780
tcagagtctc	cttctatttt	ggatgctgta	atttctgtgt	tctacactat	gctgccccca	840
acctttaatc	ccattatata	cagtttgaga	aacaaggcca	taaagggtggc	tctgggggatg	900
ttgataaagg	gaaagctcac	caaaaag				927

&lt;210&gt; 651

<211> 942  
 <212> DNA  
 <213> Unknown (H38g500 nucleotide)

<220>

<223> Synthetic construct

<400> 651

atgggggatg tgaatcagtc ggtggcctca gacttcattc tgggtgggct cttcagtcac	60
tcaggatcac gccagctcct cttctccctg gtggctgtca tgtttgtcat aggccttctg	120
ggcaaacacc ttcttctctt cttgatccgt gtggactccc ggctccacac acccatgtac	180
ttcctgtctc gccagctctc cctgtttgac attggctgtc ccatgggtcac catccccaag	240
atggcatcag actttctgcg gggagaaggt gccacctcct atggagggtg tgcagctcaa	300
atattcttcc tcacactgat ggggtgtggc gagggcgctc tgttggctcct catgtcttat	360
gaccgttatg ttgctgtgtg ccagcccctg cagtatcctg tacttatgag acgccaggta	420
tgtctgtctg tgatgggctc ctccctgggtg gtaggtgtgc tcaacgcctc catccagacc	480
tccatcacc tgcattttcc ctactgtgcc tcccgtattg tggatcactt cttctgtgag	540
gtgccagccc tactgaagct ctccgtgtgc gatacctgtg cctacgagat ggcgtgtcc	600
acctcagggg tgctgatact aatgtccctt ctttccctca tcgccacctc ctacggccac	660
gtgttgacag ctgttctaag catgcgtctc gagggaggca gacacaaggc tgtcaccacc	720
tgctcctcgc acatcacggt agtggggctc ttttatgggt ccgcctgtgt catgtacatg	780
gtgccttgcg cctaccacag tccacagcag gataacgtgg tttccctctt ctatagcctt	840
gtcaccctca cactcaaccc ccttatctac agtctgagga atccggagggt gtggatggct	900
ttggtcaaag tgcttagcag agctggactc aggc aaatgt gc	942

<210> 652

<211> 936

<212> DNA

<213> Unknown (H38g501 nucleotide)

<220>

<223> Synthetic construct

<400> 652

atggatctta aaaatggatc tctagtgacc gagtttattt tactaggatt ttttggacga	60
tgggaacttc aaattttctt ctttgtgaca ttttccctga tctacgggtg tactgtgatg	120
ggaaacattc tcattatggg cacagtgcac tgtaggtcaa cccttcattc tccctgttac	180
ttctccttg gaaatctctc ttttttggac atgtgtctct ccaactgccac aacacccaag	240
atgatcatag atttgtctac tgaccacaag accatctctg tgtggggctg cgtgaccag	300
atgttcttca tgcacttctt tgggggtgct gagatgactc ttctgataat catggccttt	360
gacaggtatg tagccatatg taaacccctg cactatagga caatcatgag ccacaagctg	420
ctaaaggggt ttgcgatact ttcatggata attggttttt tacactccat aagccagata	480
gttttaacaa tgaacttgcc tttctgtggc cacaatgtca taaacaacat attttgtgat	540
cttccccttg tgatcaagct tgcttgcat gaaacatata ccctggaatt atttgtcatt	600
gctgacagcg ggctgtctc tttcacctgt ttcacctctt tgcttgtttc ttacattgtc	660
atcctgggtc gtgtaccaaa aaaatcatca catgggctct ccaaggcgct gtccacattg	720
tctgccaca tcattgtggg cactctgttc tttggacctt gtatttttat ctatgtttgg	780
ccattcagta gtttggcaag caataaaact cttgccgtat tttatacagt tatcacacc	840
ttactgaatc cgagtattta taccctgaga aataagaaaa tgcaagaggc cataagaaaa	900
ttacggttcc aatatgttag ttctgcacag aatttc	936

<210> 653

<211> 972

<212> DNA

<213> Unknown (H38g502 nucleotide)

<220>

<223> Synthetic construct

<400> 653

atgccaacag acaaacaaat ggaaaaacaa aatcagtcca tgggtgcctga atttattttg	60
--	----



ttgggattca	aaaatctcat	gagctacaga	ttttctttat	cttatttttc	cattctctac	120
atatccataa	ttaagtaacc	taatcattat	ctttgtagtg	aaactggatc	ctcaattgca	180
tttctccatg	tacttcctac	tggccaacct	gtcatctact	gatatgcccc	tggcctcctt	240
tgctactcct	aagaaaatcg	ataatgtaat	tagtgaatat	aggaccatct	cctatgaagg	300
ctgcatgaca	tagagatttt	tccttcactt	tttaagtgga	agtgagatgg	ttttactcct	360
agccatggca	atcgatagat	aatttgccat	atgcaaacc	ctccattaca	agtccattgc	420
atcggacttg	ctcctcgctc	ctggactatg	gatttcatgc	acaccatgag	ccaaattgtt	480
ctcacagtga	ctttgccatt	ctgtggtctc	agtgttggtg	atatttttgt	gtgtgtgtga	540
tctgccttgt	gataaaactt	gcctgtacag	acacttacat	cttggagcta	tgagtcattg	600
cagacagtgg	actactttct	ttgctgtgtt	tcattgtttc	gttaatctcc	tatagcaccg	660
tcctgattat	tatttgacat	cattcctcca	gggggtcttc	caaaactctg	tccacgcttt	720
cagcccacat	tatggtgggtg	gtactgttct	ttggagcttg	catctttacc	tgtgaaagac	780
cattcagcac	tgctcccat	gatgtctgtg	ttttaacta	ttttgtctcc	ccttttaaat	840
ccaatcatct	acacattcag	gaataacgac	atgaagaaag	cattaagaaa	aatgaagatt	900
aactttgtga	gttctagatc	aacttgataa	ctaaaatatt	ataatcacta	aaagcatcat	960
cattattggt	gt					972

&lt;210&gt; 654

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g503 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 654

atggatgaag	ccaatcactc	tgtggtctct	gagtttgtgt	tcctgggact	ctctgactcg	60
cggaagatcc	agctcctcct	cttccctctt	ttctcagtg	tctatgtgtc	aagcctgatg	120
ggaaatctcc	tcattgtgct	aactgtgacc	tctgaccctc	gtttacagtc	ccccatgtac	180
ttcctgctgg	ccaacctttc	catcatcaat	ttggtatttt	gttccctccac	agctcccaag	240
atgatttatg	accttttcag	gaagcacaag	accatctctt	ttgggggctg	tgtagttcag	300
atcttcttta	tccatgcagt	tgggggaact	gagatggtgc	tgctcatagc	catggctttt	360
gaccgatatg	tggccatag	taagcctctc	cactacctga	ccatcatgaa	cccacaaagg	420
tgcattttgt	ttttagtcac	ttcctggatt	ataggtatta	ttcactcagt	gattcagttg	480
gcttttgttg	tagacctgct	gttctgtggc	cctaataaat	tagatagttt	cttttgtgat	540
cttctcgat	ttatcaaact	ggcttgcata	gagacctaca	cattgggatt	catggttact	600
gccaatagtg	gatttatttc	tctggcttct	tttttaattc	tcataatctc	ttacatcttt	660
attttgggtga	ctgttcagaa	aaaatcttca	ggtggtatat	tcaaggcttt	ctctatgctg	720
tcagctcatg	tcattgtggt	ggttttgggtc	tttgggccat	taatcttttt	ctatattttt	780
ccatttccca	catcacatct	tgataaattc	cttgccatct	ttgatgcagt	tatcactccc	840
gttttgaatc	cagtcactct	tacttttaga	aataaagaga	tgatggtggc	aatgagaaga	900
cgatgctctc	agtttgtgaa	ttacagtaaa	atcttt			936

&lt;210&gt; 655

&lt;211&gt; 967

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g504 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 655

atgaataggg	acaaccagtc	tgtggtgtct	gaattcgtgt	tgctgggact	ctcaaattct	60
tgggagactc	aagatttttc	ttttttgctt	ttcttgtctt	ttctatgtgt	ccggtgtgat	120
ggcaaaccct	attgtagtgg	tcattgtaac	ctctgaccct	tacttgcaat	cctccttgta	180
tattttgctg	gccaacctct	ctgtcattga	tctcacattt	tgctccattg	cagcacgcaa	240
gatgatttgt	gatattttca	ggaaacagaa	agtcatttcc	ttttggggct	gtgtagctca	300
gatcttcttt	agccatgctg	ttggggggcac	tgagatgggtg	ctgctcatag	ccatggcctt	360
tgacagatat	gttgccgtat	gtaagccctt	tactacctg	accatcatgc	atccaagaat	420
gtgcattttg	attctagtgg	cttcttgggc	cattggtctc	attcactcat	tggtccaatt	480
gtcttttgta	gtaaaactgc	ccttctgtgg	ccctaattgt	ttggacagct	tttactgtga	540

catacctcag	ctcatcaaac	ttgcttgac	aaatacctat	aaactgcagt	tcatgggttac	600
tgctaatagt	gggttcattt	ccttgagtgc	tttcttcttg	ctcatcctct	cttacatctt	660
cattctggcc	actcttcaga	aacactcctc	aggaggctca	tccaaggctg	tctctactct	720
gtcagctcat	attactgttg	tggttttatt	ccttggtcca	ctgatttttt	tctatgtatg	780
gccctctcct	ccaacacatc	tgaataaatt	tctagccata	tttgatgcca	tttctactcc	840
ttttctgaat	ccagtcactc	acacattcag	gaacagggaa	atgaagattg	caataaggag	900
agtgttcggt	caatttatgg	gttttagaaa	aactacttaa	gtggctttat	taaaacacag	960
aatttcc						967

&lt;210&gt; 656

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g505 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 656

atggttgagg	caaatcactc	cgtgggtgca	gagtttgtgt	tcttgggact	caccaattcc	60
tgggagatcc	gacttctcct	ccttggtgtc	tcttccatgt	tttacatggc	cagtatgatg	120
ggaaactctc	tcatTTTgct	cactgtgact	tctgaccctc	acttgcactc	ccccatgtat	180
tttctgttag	ccaacctctc	cttcattgac	ctgggtgttt	cctctgtcac	ttctcccaaa	240
atgatttatg	acctgttcag	aaagcacgaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tggcgggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccatatg	taagccctc	cagtacctga	ccattatgag	cccaagaatg	420
tgcatgttct	tcttagtggc	tgccctgggtg	accggcctta	tccactctgt	agttcaattg	480
gtttttgtag	taaacttgcc	cttctgtggt	cctaattgat	cggacagctt	ttactgtgac	540
cttctctcgt	tcatcaaaact	tgccctgcaca	gacagctacc	gactggagtt	catgggttaca	600
gccaacagtg	gattcatctc	tctgggctcc	ttcttcatac	tgatcatttc	ctatgtggtc	660
atcattctca	ctgttctgaa	acactcttca	gctgggttat	ccaaggctct	gtccaccctt	720
tcagctcacg	tcagtgtggt	agttttgttc	tttggctcct	tgatttttgt	ctatacgtgg	780
ccactctcct	ccacacacct	ggataagttt	ctggccatct	ttgatgcagt	tctcactcct	840
gttttaaatc	ctatcatcta	cacattcagg	aat			873

&lt;210&gt; 657

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g506 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 657

atgaatggaa	tgaatcactc	tgtggtatca	gaatttgtat	tcatgggact	caccaactca	60
cgggagattc	agcttctact	ttttgttttc	tctttgttgt	tctactttgc	gagcatgatg	120
ggaaaccttg	tcattgtatt	cactgtaacc	atggatgtct	atctgcactc	ccccatgtat	180
ttctctcctg	ctaacctctc	aatcattgat	atggcatttt	gctcaattac	agcccctaag	240
atgatttggtg	atattttcaa	gaagcacaa	gccatctcct	ttcggggatg	tattactcag	300
atcttcttca	gccatgctct	tgggggcact	gagatgggtgc	tgctcatagc	catggccttt	360
gacagataca	tggccatatg	taaacctctc	cactacctga	ccatcatgag	cccaagaatg	420
tgtctatact	ttttagccac	ttcctctatc	attggcctta	tccactcatt	ggtccaatta	480
gtttttgtgg	tagatttacc	ttttgtggt	cctaatatct	ttgacagttt	ttactgtgat	540
ctccctcggc	tctcagact	tgccctgtacc	aacacccaag	aactggagtt	catgggtcact	600
gtcaatagtg	gactcatttc	tgtgggctcc	tttgtcttgc	tggttaatttc	ctacatcttc	660
attctgttca	ctgtttggaa	acattcttct	ggtgggtctag	ccaaggccct	ctctaccctg	720
tcagctcatg	tcactgtggt	catcttgttc	tttgggccac	tgatgttttt	ctacacatgg	780
ccttctccca	catcacacct	ggataaatat	ccttgctattt	ttgatgcatt	tattactcct	840
tttctgaatc	cagttatcta	cacattcagg	aacaaagaca	tgaaagtggc	aatgaggaga	900
ctgtgcagtc	gtcttgcgca	ttttacaaag	atctttg			936

&lt;210&gt; 658

<211> 980  
 <212> DNA  
 <213> Unknown (H38g507 nucleotide)

<220>  
 <223> Synthetic construct

<400> 658  
 atggagcaaa ggaaaaatgt gactgagttt gtccttgtgg ggctcactca gagccccag 60  
 ggacagaaaa tattatttct tgtgttcttg ctcatctacg ttgtgacaat ggtaggcaac 120  
 atattcattg ttgtgactgt ggtggtcagc ccaactttgg atgccccatg tacttcttcc 180  
 ttggctactt atcatttatg gatgctgttc attctactac agttaccca aatatgatta 240  
 tagacttact ctatgagaag aaaaccattt cgttccaagc ttgattacc agatttttat 300  
 aggacacctt tttgggggtg ctgagatttt actccttgtt gtcatggcct atgatggcta 360  
 cgtgaccatc tgcaaacccc tgcattattt gaccatcatg aaccaacggg tgtgcattct 420  
 actgctgtcg ttggcctggg ctggagggtt cttgcatgct gtagttcaac ttctttttgt 480  
 ttacaacctt cccttctgtg gccccaatgt cattgaccat ttcatctgtg acatgtaccc 540  
 tttattaaaa cttgcctgca ctgacacctt tgttactggc ctactgtgg ttgccaatga 600  
 tggggcaatc tgtgtggtea tctttatgct cttactcttc tcctatgggg tcattctgca 660  
 ctccctgaag aatcttagtc aggaaggag gcacaaagcc ttatccacct gtggctcca 720  
 tatcatgtg gtgatcctct tctttgtccc ttgtattttc atgtatgtga gacctccttt 780  
 gaccttacct attgataaat ccttgactgt gttttacact gttatcacac ctatgttgaa 840  
 ccctctaate tatactttaa gaaatgcaga gatgaaaaat gctatgaaga agctctggac 900  
 tagaaaaaga aaatgaggtg gcagacaaat gtatcatcta ttttcagtga agagttgctc 960  
 cctccaggaa agccatttgt 980

<210> 659  
 <211> 917  
 <212> DNA  
 <213> Unknown (H38g508 nucleotide)

<220>  
 <223> Synthetic construct

<400> 659  
 atgaatctta aaaatggatc tctagtgaac gagtttattt tactaggatt ttttggacga 60  
 tgggaacttc aaattttctt ctttgtgaca ttttcctga tctacggtgc tactgtggtg 120  
 ggaaacattc tcattatggg cacagtgaac tgtagtgcga cccttcattc tcccttgta 180  
 tttctccttg gaaatctctc ttttttgga atgtgtctct ccactgccac aacacccaag 240  
 atgatcacaa gaccatctct gtgtggggct gcgtgacca gaagttcttc atgcacttct 300  
 ttgggagtg tgagatgact cttctgataa tcatggcctt tgacaggat gtagccatat 360  
 gtaaacccct gactatagg acaatcatga gccacaagct gctaaagggg tttgcgatac 420  
 tttcatggat aattggtttt ttacactcca taagccagat agttttaaca atgaacttgc 480  
 ctttctgtgg ccacaatgtc ataaacaaca tattttgtga tcttccctt gtgatcaagc 540  
 ttgcttgcac tgaaacatac accctggaat tatttgcac tgctgacagc gggctgctct 600  
 ctttcacctg tttcatcctc ttgcttgttt cttacattgt catcctggc agtgtacca 660  
 aaaaatcac acatgggctc tccaaggcgc tgtccacatt gtctgccac atcattgtgg 720  
 tcaactctgt ctttggacct tgtattttta tctatgtttg gccattcagt agtttgga 780  
 gcaataaaac tcttgcgtga ttttatacag ttatcacacc gttactgaat ccgagtattt 840  
 ataccctgag aaataagaaa atgcaagagg ccataagaaa attacgggtc caatatgtta 900  
 gttctgcaca gaatttc 917

<210> 660  
 <211> 1008  
 <212> DNA  
 <213> Unknown (H38g509 nucleotide)

<220>  
 <223> Synthetic construct

<400> 660

tctacagacc	cacagaatct	aacagatgtc	tctatattcc	tcctcctaga	acctcagagg	60
atccagaatg	acagccggtc	ctcgctgggc	tggttcctgtc	catgtgcctg	gtcacgggtgc	120
tggggaacct	gctcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acatcttctt	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
agatgactgt	ggacatccag	tctcacagca	gagtcattctc	ctatgcaggc	tgccctgactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgttcct	gagtgtgatg	360
gcctatgacc	ggtttgtagc	catctgtcac	cctctatatc	attcagccat	catgaacccg	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttt	ctctcagtct	tttagacgtc	480
cagctgcgca	acttgattgc	cttacaaatg	acctgcttca	aggatgtgga	aattcctaata	540
ttcttctgtg	acccttctca	actcccccat	cttgcatgtt	gtgacacctt	caccaataac	600
ataatcctgt	atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gaccttttc	660
tcttactata	aaatcgtttt	ctccattctg	agggtttcat	catctggtgg	gaagtataag	720
gccttctcca	cctgtgtgtc	tcacctgtca	gtggtttgc	gatttttatg	aacaggcggt	780
ggagggtacc	tcagttcaga	tgtgtcatct	ccccgagaa	aggctgcagt	ggcctcagt	840
atgtacacgg	tggtcacccc	catgctgaac	cccttcatct	acagcctgag	aaacagggat	900
attaaaagt	tcctgcggcg	gccgcacagc	agcacggtct	aatcttgata	tcttcttctc	960
tgttccattc	cttttgtagt	gtgggttaaa	aaaggcagca	aggtcaaa		1008

&lt;210&gt; 661

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g510 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 661

atgatggaaa	tagccaatgt	gagttctcca	gaagtctttg	tcctcctggg	cttctccaca	60
cgacctcac	tagaaactgt	cctcttcata	gttgtcttga	gtttttacat	ggtatcgatc	120
ttgggcaatg	gcatcatcat	tctggctctc	catacagatg	tgacctcca	cacacctatg	180
tacttcttct	ttgccaacct	ccccttctg	gacatgagct	tcaccacgag	cattgtccca	240
cagctcctgg	ctaacctctg	gggaccacag	aaaaccataa	gctatggagg	gtgtgtgtgc	300
cagtctctata	tctcccattg	gctgggggca	accgagtgtg	tcctgctggc	caccatgtcc	360
tatgaccgct	acgtgccat	ctgcaggcca	ctccattaca	ctgtcattat	gcatccacag	420
ctttgccttg	ggctagcttt	ggcctcctgg	ctgggggggc	tgaccaccag	catggtgggc	480
tccacgctca	ccatgctcct	accgctgtgt	gggaacaatt	gcatcgacca	cttcttttgc	540
gagatgcccc	tcattatgca	actggcttgt	gtggatacca	gcctcaatga	gatggagatg	600
tacctggcca	gctttgtctt	tgttgtcctg	cctctggggc	tcactcctggt	ctcttacggc	660
cacattgccc	gggccgtgtt	gaagatcagg	tcagcagaag	ggcggagaaa	ggcattcaac	720
acctgttctt	cccacgtggc	tgtggtgtct	ctgttttacg	ggagcatcat	cttcatgtat	780
ctccagccag	ccaagagcac	ctcccatgag	cagggcaagt	tcatagctct	gttctacacc	840
gtagtcactc	ctgcgctgaa	cccacttatt	tacaccctga	ggaacacgga	ggtgaagagc	900
gcctccgggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

&lt;210&gt; 662

&lt;211&gt; 912

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g511 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 662

atggaaagag	caaaccattc	agtggatatc	gaatttattt	tggtgggact	ttccaaatct	60
caaaatcttc	agattttatt	cttcttggga	ttctctgtgg	tcttcgtggg	gattgtgtta	120
ggaaacctgc	tcattcttgg	gactgtgacc	tttgattcgc	tccttcacac	accaatgtat	180
tttctgctta	gcaacctctc	ctgcattgat	atgatcctgg	cttcttttgc	tacccttaag	240
atgattgtag	atttctccg	agaacgtaag	accatctcat	ggtggggatg	ttattccag	300
atgttcttta	tgcacctcct	gggtgggagt	gagatgatgt	tgcttgtagc	catggcaata	360
gacaggatg	ttgcatatg	caaaccctc	cattacatga	ccatcatgag	cccacgggtg	420
ctcactgggc	tactgttatc	ctcctatgca	gttggatttg	tgcactcatc	tagtcaaatg	480

gctttcatgt	tgactttgcc	cttctgtggt	cccaatgtta	tagacagctt	tttctgtgac	540
cttccccttg	tgattaaact	tgccctgaag	gacacctaca	tcctacagct	cctgggcatt	600
gctgacagt	ggctcctgtc	actggctctg	ttcctcctct	tgcttgtctc	ctatggagtc	660
ataatattct	cagttaggta	ccgtgctgct	agtcgatcct	ctaaggcttt	ctccactctc	720
tcagctcaca	tcacagttgt	gactctgttc	tttgcctcgt	gtgtctttat	ctacgtctgg	780
cccttcagca	gatactcggg	agataaaatt	ctttctgtgt	tttacacaat	tttcacacct	840
ctcttaaatc	ctattattta	tacattaaga	aatcaagagg	taaaagcagc	cattaaaaaa	900
agactctgca	ta					912

&lt;210&gt; 663

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g512 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 663

atgggtcaatt	tgacttcaat	gagtggattc	cttcttatgg	ggttttctga	tgagcgtaag	60
cttcagattt	tacatgcatt	ggatatttctg	gtgacatacc	tgetggcctt	gacaggcaac	120
ctcctcatta	tcaccatcat	taccgtggac	cgctgctctc	attcccccat	gtattacttt	180
ttaaagcacc	tctctcttct	ggacctctgc	ttcatctctg	tcacagtccc	ccagtccatt	240
gcaaattcac	ttatgggcaa	cggttacatt	tctcttgttc	agtgcatctc	tcagggtttc	300
ttcttcatag	ctctggcctc	atcagaagtg	gccattctca	cagtgatgtc	ttatgacagg	360
tacgcagcaa	tctgtcaacc	acttcattat	gagactatta	tggatccccg	tgctgtagg	420
catgcagtga	tagctgtgtg	gattgctggg	ggcctctctg	ggctcatgca	tgctgccatt	480
aacttctcca	tacctctctg	tgggaagaga	gtcattcacc	aattcttctg	tgatgttcc	540
cagatgctga	aactagcctg	ttcttatgaa	ttcattaatg	agattgcact	ggctgcattc	600
acaacgtctg	cagcatttat	ctgtttgatc	tccattgtgc	tctcctacat	tcgcatcttc	660
tctacagtgc	tgagaatccc	atcagctgag	ggccggacca	aggtcttctc	cacctgccta	720
ccacacctat	ttgtagccac	cttctttctt	tcagctgcag	gctttgagtt	tctcagactg	780
ccttctgatt	cctcatcgac	tgtggacctt	gtattctccg	tattctatac	tgtgatacct	840
ccaacactca	atccagtcac	ttatagctta	cggaaatgatt	ccatgaaggc	agcactgagg	900
aagatgctgt	caaaggaaga	gcttctctcag	agaaaaatgt	gcttaaaagc	catgtttaaa	960
ctc						963

&lt;210&gt; 664

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g513 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 664

atgggacccac	agaactattc	cttgggtgtca	gaatttgtgt	tgcatggact	ctgcacttca	60
cgacatcttc	aaaatttttt	ctttatatatt	ttctttgggg	tctatgtggc	cattatgctg	120
ggtaaccttc	tcatttttgt	cactgtaatt	tctgatccct	gcctgcactc	ctccccatg	180
tacttctctg	tggggaacct	agctttcctg	gacatgtggc	tggcctcatt	tgccactccc	240
aagatgatca	gggatttcct	tagtgatcaa	aaactcatct	cctttggagg	atgtatggct	300
caaatcttct	tcttgcactt	tactgggtgg	gctgagatgg	tgctcctggg	ttccatggcc	360
tatgacagat	atgtggccat	atgcaaacc	ttgcattaca	tgactttgat	gagttggcag	420
acttgcacat	ggctgggtgct	ggcttcattg	gtcgttggat	ttgtgcactc	catcagtcaa	480
gtggctttca	ctgtaaaatt	gccttactgt	ggccccaatg	aggtagacag	cttcttctgt	540
gacctccctc	tgggtgatcaa	acttgccctg	atggacacct	atgtcttggg	tataattatg	600
atctcagaca	gtgggttgct	ttccttgagc	tgttttctgc	tcctcctgat	ctcctacacc	660
gtgatccctc	tcgctatcag	acagcgtgct	gccggtagca	catccaaagc	actctccact	720
tgctctgcac	atatcatggg	agtgacgctg	ttctttggcc	cttgcathtt	tgtttatgtg	780
cggcctttca	gtaggttctc	tgtggacaag	ctgctgtctg	tgttttatac	catttttact	840
ccactcctga	accctattat	ctacacattg	agaaatgagg	agatgaaagc	agctatgaag	900
aaactgcaaa	accgacgggt	gacttttcaa				930

<210> 665  
 <211> 957  
 <212> DNA  
 <213> Unknown (H38g514 nucleotide)

<220>  
 <223> Synthetic construct

<400> 665  
 atggaagaa agaatcaaac agctataact gaattcatca tcttgggatt ctccaaccta 60  
 aatgaattgc agtttttact attcaccatc ttctttctga cttatttctg tactttggga 120  
 ggaaatatat taattatctt gacgactgtg actgateccac acctgcatac acctatgtat 180  
 tattttcttag ggaacttggc ctttattgac atctgctaca ccaccagcaa tgtccccag 240  
 atgatgggtgc acctcctctc aaagaaaaaa agcatttctt atgtgggggtg tgtggttcaa 300  
 ctttttgcac ttgttttctt tgtaggatca gagtgtctcc tactggcagc aatggcatat 360  
 gatcggtaca ttgcaatctg caatccttta aggtattcag ttattctgag caaggttcta 420  
 tgcaatcaat tagcagcctc atgctgggct gctgggttcc ttaactcagt ggtgcataca 480  
 gtgttgacat tctgcctgcc cttctgtggc aacaatcaga ttaattactt cttctgtgac 540  
 atccccctt tgctgatctt gtctgtgga aacacttctg tcaatgagtt ggcactgcta 600  
 tccactgggg tcttcattgg ttggactcct ttctttgta tctactttc ctacatttgc 660  
 ataactcca ccattctgag gatccagtc ttagagggaa gacgaaaagc cttttctaca 720  
 tgtgcctccc acctggccat tgtctttctc ttttatggca gcgccatctt tacatatgta 780  
 cggccatct caacttactc attaaagaaa gataggttgg ttccagtgtt gtacagtgtt 840  
 gttaccoccca tgctaaaccc tataatttac acattgagga ataaggacat caaagaagct 900  
 gtcaaaacta tagggagcaa gtggcagcca ccaatttctt ctttggatag taaactc 957

<210> 666  
 <211> 910  
 <212> DNA  
 <213> Unknown (H38g515 nucleotide)

<220>  
 <223> Synthetic construct

<400> 666  
 atgagagaat ttttcttgte agggttctca cagacaccat ctattgaagc agggctatctt 60  
 gtactatttc ttttcttcta tatgtccatt tgggttggca atgtcctcat catggtcaca 120  
 gtagcatctg ataaatacct gaattcatca cccatgtatt tccttcttgg caacctctca 180  
 tttctggacc tatgttatte aacagtaacg acccctaagc ttctggctga cttctttaat 240  
 catgaaaaac tcatttccta tgaccaatgc attgtgcaac tcttcttctt gcattttgta 300  
 ggggcagctg agatgttcct gctcacagtg atggcgtagc atcgctatgt tgcaatctgt 360  
 cgcccgtgc actacaccac tgtcatgagt cgggggttat gctgtgtgtt ggttgctgcc 420  
 tctggatgg gaggatttgt gcactccact gtccagacca ttctcactgt ccatctacct 480  
 ttttgtgggc caaatcaggt ggaaaacttt tttttgtgat gttccccctg tcatcaaat 540  
 tgcttgtgct gacacttttg tcattgaatt gctcatggta tctaacagtg ggttgatctc 600  
 caccatctcc tttgtggtgc tgatttctc ctacaccact atcctagtca agattcgctc 660  
 caaggaagga aggcgaaagg cactctccac gtgtgcctct cactcatgg ttgtaacact 720  
 gtttttttga ccctgtatct tcatctacgc tctcctttc tctacatttt ctgtggacaa 780  
 gatggtgtct gtactctaca atgttattac ccaatgcta aacccccctc tctacacact 840  
 tcggaacaaa gaggtaaagt cagccatgca gaagctctgg gtcagaaatg ggcttacttg 900  
 gaaaaagcag 910

<210> 667  
 <211> 945  
 <212> DNA  
 <213> Unknown (H38g516 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 667

atggagaatg	tcactacaat	gaatgagttt	cttctacttg	gcctgactgg	tggtcaggag	60
ctgcagcctt	tcttcttttg	gattttctta	atcatttacc	tgataaactt	gattggaaat	120
ggatctatat	tggtgatggg	tggtttggaa	ccacaactcc	actcccttat	gtattttttt	180
ctgggaaacc	tttcttgtct	ggatatttct	tattcttcag	tgacactgcc	caagctgctc	240
gtaaacctcg	tgtagcagtcg	cagggtctata	tcttttctag	gctgtatcac	ccagctacac	300
ttcttccact	ttttgggaag	cacagaggcc	attttactgg	ctatcatggc	ctttgaccgt	360
tttgttgcca	tctgcaatcc	tcttcgctac	actgtcatca	tgaacccccca	ggtgtgtatt	420
ctgttggcag	ctgcggcctg	gctcatcagc	ttcttttacg	ctctgatgca	ttctgtcatg	480
actgcacacc	tgagtttttg	tggtcttcag	aaactcaatc	acttcttcta	cgatgtcaag	540
ccgtctttag	aattggcctg	tagtgacaca	ttactcaatc	aatggcttct	ttccattgtc	600
acaggcagca	tatccatggg	agctttcttt	ctgactcttc	tctcctgctt	ctatgtaatt	660
ggcttccttc	tgtttaagaa	caggtcctgc	agaatactcc	acaaggctct	gtccacttgt	720
gcctccatt	ttatggtggt	atgtcttttc	tatggacctg	tgggcttcac	atatattcgt	780
cctgcttcag	ccacctccat	gattcaggac	cggataatgg	ccatcatgta	tagcgccgtc	840
acccctgtac	tgaatccact	aatctacacc	cttaggaaca	aagaagtgat	gatggctctg	900
aagaaaatct	ttggtaggaa	gttgtttaaa	gactggcagc	aacac		945

&lt;210&gt; 668

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g517 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 668

atgaatgaga	caaatcattc	tcgggtgaca	gaatttgtgt	tgctgggact	gtctagttca	60
agggagctcc	aacctttctt	gtttcttaca	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatacatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttttgc	taccctaaa	240
atgattgcag	actttctggt	tgagcgcaag	actatttctt	ttgatgcctg	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtgc	tcctagtttc	catggcctat	360
gaccgttatg	ttgttatatg	caaacctctc	cactacatga	cagtcatgag	ccgtcgtgta	420
tgtgttggtc	tcgtccctcat	ttcatggttt	gtgggcttca	tccatactac	cagccagttg	480
gcattcactg	ttaatctgcc	attttgtggt	cctaataagg	tagacagttt	tttctgtgac	540
cttctcttag	tgaccaagtt	agcctgcata	gacacttatg	ttgtcagctt	actaatagtt	600
gcagatagtg	gctttctttc	tctgagttcc	tttctcctct	tggttggtctc	ctacactgta	660
atacttggtta	cagttaggaa	tcgtcctctc	gcaagcatgg	cgaaggcccg	ctccacattg	720
actgttcaca	tcactgtggt	cactttatct	tttggaccat	gcattttcat	ctatgtgtgg	780
cccttcagca	gttactcagt	tgacaaagtc	cttgctgtat	tctacaccat	cttcacgctt	840
attttaaac	ctgtaatcta	cacgctaaga	aacaaagaag	tgaaggcagc	tatgtcaaaa	900
ctgaagagtc	ggtatctgaa	gcctagtcag	gtttctgtag	tcataagaaa	tggtcttttc	960
ctagaa						966

&lt;210&gt; 669

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g518 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(594)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 669

gnnccgctac	tactacccat	gtactgtttc	ctgnctatac	tgtccgccac	tgacctcggc	60
ctgtccatat	ccactctggt	caccatgctg	agtatattct	ggttcaatgt	gagggaaatc	120
agctttaatg	cctgcttgtc	ccacatgttc	tttattaaat	tcttcactgt	catggaatcc	180

tcagtgcgtg	tggccatggc	ttttgatcgt	tttgtggccg	tctctaatacc	ccttaggtat	240
gccatgattt	taactgactc	cagaatagct	caaattggag	tggcaagtgt	catcaggggg	300
ctcctaatac	tgacaccaat	ggtagcactt	cttataagac	tttctactg	ccacagcccg	360
agtactccac	cactcctact	gctaccaccc	tgatgtgatg	aagttctcat	gcacagacgc	420
cagaatcaac	agtgcagttg	ggctgactgc	catgtttctt	actggttggt	gtagacttac	480
ttctcatcct	cctttcttat	gttttgatca	ttaggactgt	ccttancgtt	gcttccccag	540
aagagaggaa	ggaaaccctt	cagtacatgt	gtctcccaca	ttgggggctt	ttgc	594

&lt;210&gt; 670

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g519 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 670

atgagccctg	agaaccagag	cagcgtgtcc	gagttcctcc	ttctgggcct	ccccatccgg	60
ccagagcagc	aggctgtgtt	cttcaccctg	ttcctgggca	tgtacctgac	cacgggtgctg	120
gggaacctgc	tcatcatgct	gtcatccag	ctggactctc	accttcacac	ccccatgtac	180
ttcttctcca	gccacttggc	tctcactgac	atctcctttt	catctgtcac	tgtccctaag	240
atgctgatgg	acatgcggac	taagtacaaa	tcgatcctct	atgaggaaatg	catttctcag	300
atgtattttt	ttatattttt	tactgacctg	gacagcttcc	ttattacatc	aatggcatat	360
gaccgatatg	ttgccatatg	tcaccctctc	cactacactg	tcatcatgag	ggaagagctc	420
tgtgtcttct	tagtggtgtg	atcttggatt	ctgtcttgtg	ccagctccct	ctctcacacc	480
cttctcctga	ccggctgtgc	tttctgtgct	gcgaacacca	tcccccatgt	cttctgtgac	540
cttctgtccc	tgctcaagct	gtcctgtcca	gatattcttc	tcaatgagct	ggcatgttgc	600
acagtatggg	tggtggtcat	taccctgcca	ttcatgtgta	tcctgggtac	atatgggtac	660
attggggcca	ccatcctgag	ggctccctca	accaaaggga	tccacaaagc	attgtccaca	720
tgtggctccc	atctctctgt	ggtgtctctc	tattatgggt	caatatttgg	ccagtacctt	780
ttcccgactg	taagcagttc	tattgacaag	gatgtcattg	tggctctcat	gtacacggtg	840
gtcacacca	tggtgaaccc	ctttatctac	agccttagga	acagggacat	gaaagaggcc	900
cttgggaaac	tcttcagtag	agcaacattt	ttctcttgg			939

&lt;210&gt; 671

&lt;211&gt; 586

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g520 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 671

ckactactac	tacctatgta	ttttttctk	kgcaacctgt	cactgttaga	tctctgcctt	60
ccttcaatacc	ctgtgcccac	gatgctgcag	aatttattaa	ctcaaaggta	aaccatctct	120
atgtggtaact	gcattgtcca	gagtttcttt	ctcatattct	ctgggagcac	agaagcctgc	180
ctactccttg	ccatggcctg	tgatcactct	acttccaact	gccaccctcg	gctcaacgat	240
gtggttatga	atcagcctgt	ctgtgtcagg	atgggtattg	cagcatgggc	agtgggatcc	300
ctaaactcct	tgacaaagaa	tcttttcatt	tacaacttac	acttctgtgg	ccccagtgtc	360
atccctcact	tctgtgtgga	gctgccttca	ctctccctc	tctcttgat	tgatccagct	420
gccagtgagg	tccttctctg	tgggtcatgt	acattgctag	gatttgtgac	ttgccgctgg	480
tcctcttttc	ttactctaac	accatctctg	cctcctagcc	atttgktttt	ctgagggtca	540
aggcaaagcc	ttctccacct	gtccttccca	cctcaccgtg	gtgctt		586

&lt;210&gt; 672

&lt;211&gt; 918

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g521 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 672

atgagccctg	agaaccagag	cagcgtgtcc	gagttccctc	tcctgggcct	ccccatccgg	60
ccagagcagc	aggccgtgtt	cttcgccctg	ttcctgggca	tgtacctgac	cacgggtgctg	120
gggaacctgc	tcatactgct	gtcatccag	ctagactctc	accttcacac	ccccatgtac	180
ttcttcctta	gccacttggc	cctcactgac	atctcctttt	catctgtcac	tgcccttaag	240
atgctgatga	acatgcagac	tcagcaccta	gccgtctttt	acaagggatg	catttcacag	300
acatactttt	tcatactttt	tgctgactta	gacagtttcc	ttatcacttc	aatggcatat	360
gacaggatg	tggccatctg	tcatacctta	cattatgcca	ccatcatgac	tcagagccag	420
tgtgtcatgc	tgggtggctgg	gtcctgggtc	atcgcttggt	cgtgtgctct	tttgcatacc	480
ctcctcctgg	cccagctttc	cttctgtgct	gaccacatca	tcctcacta	cttctgtgac	540
cttgggtgcc	tgctcaagtt	gtcctgctca	gacacctccc	tcaatcagtt	agcaatcttt	600
acagcagcat	tgacagccat	tatgcttcca	ttcctgtgca	tcctggtttc	ttatgggtcac	660
attgggggtca	ccatcctcca	gattccctct	accaagggca	tatgcaaagc	cttgtccact	720
tgtggatccc	acctctcagt	gggtgactatc	tattatcgga	caattattgg	tctctatttt	780
cttcccccat	ccagcaaac	caatgacaag	aacataattg	cttcagtgat	atacacagca	840
gtcactccca	tgttgaaccc	attcattttac	agtctgagaa	ataaagacat	taagggagcc	900
ctaagaaaac	tcttgagt					918

&lt;210&gt; 673

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g522 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 673

ctactactac	cyatgtat	ttttcttggc	aacctstccc	tcattggacat	ctgcggcacc	60
tcctcctttg	tgctctcat	rtagacaat	ttcctggaaa	cccagaggac	catttccttc	120
cctggctgtg	ccctgcagat	gtacctgacc	ctggcgctgg	gatcaacgga	gtgcctgctg	180
ctggctgtga	tggcatatga	ccgttatgtg	gctatctgcc	agccgcttag	gtacycagag	240
ctcatgagtg	ggcagacctg	catgcagatg	gcagcgctga	gctggggggac	aggctttgcc	300
aactcactgc	tacagtccat	ccttgtctgg	cacctcccct	tctgtggcca	cgatcatcaac	360
tacttctatg	agatcttggc	agtgtctaaa	ctggcctgtg	gggacatctc	cctcaatgcg	420
ctggcattaa	tgggtggccac	agccgtcctg	acactggccc	ccctcttgct	catctgcctg	480
tcttaccttt	tcatactgtc	tgccatcctt	agggtaccct	ctgctgcagg	ccgggtgcaaa	540
gccttctcca	cctgctcagc	ccaccgcaca	gtggtggtgg	ttttttatgg	g	591

&lt;210&gt; 674

&lt;211&gt; 985

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g523 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 674

gttaatggat	ggagtaataa	atcagtgggt	actgaattca	atgtgttggg	gctgtctagc	60
tcttgggaac	tccaagtctt	ctttttcttt	atcttctctg	tgttttatgg	agctgcagtg	120
ttgggaacaa	tccttatcat	catcacagta	attatagact	ctcatttgca	ttccccaatg	180
tactttcttc	ttagcaatct	ctcttccatc	gatgtgtgtc	aggctacatt	tgccactccc	240
aagatgattg	cagacttcct	caacgaacac	aagaccacca	ctttccaggg	atgcatgtca	300
caaactcttt	tcttgcatgt	ttttgggggt	agtgtgatgg	tgcttcttgt	tgccatggcc	360
tatgatagat	acattgctat	atgcaaacct	ctgcaactaca	tgaccatcat	gaaccggagg	420
gtgtgaaactg	ttctggtggg	ggtttctctg	gccattggca	tctcacactc	agccacccac	480
ctggcattca	aagtcaatct	gcctttctgt	ggaccacaaca	gggtagacaa	ttttttctgt	540
gacctcctcc	tagtgatcaa	gcttgccctg	ttagacacct	atggttttga	gatactgggtg	600
ctcactaaca	gtggctgtgct	ctcacttatg	tggttctctc	ttttgtctat	ttctgacact	660
atcatccttg	ctactgtgca	tcgccaagcc	tctgatggga	tgtccaaggc	cctttccact	720
ctgtctgccc	acattactgt	tgtgcttctc	ttctttggcc	cattaatatt	catctatatt	780

tggccctttg	aaagcttccc	aattgataaa	tttatctctg	tgttttttta	ctgtcttcac	840
tcctctcctt	aaccccatga	tttatactct	gaggaataaa	gatataaagg	aagccatgag	900
gaagctaagg	agatgacatg	tgggttccaa	gcagggtttt	tagacaacta	caaagaagta	960
atacaaattc	ctacttttgg	gctttt				985

&lt;210&gt; 675

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g524 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(780)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 675

atgtatttct	tcttgagttt	tttgtctctc	actgatattt	gctttacaac	aagcgttgct	60
cccaagatgc	tgatgaactt	cctgtcagaa	aagaagacca	tctcctatgc	tgggtgtctg	120
acacagtatg	tattttctct	atgccttggg	caacagtgac	agctgccttc	tttcgtaant	180
gcctttgacc	gctatgttgc	cgtctgtgac	cctttccact	atgtcaccac	catgagccac	240
caccactgtg	ttctgctggt	ggccttctcc	tgctcattta	cttaccttca	ctcactcctg	300
cacacacttc	tgctgaatcg	tctcaccttc	tgctgactcca	atgttatcca	ccactttctc	360
tgtgacctca	gccctgtgct	gaaattgtcc	tgctcttcca	tatttgtaa	tgaaattgtg	420
cagatgacag	aagcacctat	tgttttgggt	actcgttttc	tctgcattgc	tttctcttat	480
atacgaatcc	tcactacagt	tctcaagatt	ccctctactt	ctgggaaacg	caaagccttc	540
tccacctgtg	gtttttacct	caccgtgggt	acgctctttt	atggaagcat	cttctgtgtc	600
tatttacagc	ccccatccac	ctacgctgtc	aaggaccacg	tggcaacaat	tgtttacaca	660
gttttgtcat	ccatgtctaa	tccttttatc	tacagcctga	gaaacaaaga	cctgaaacag	720
ggcctgagga	agcttatgag	caagagatcc	taggaagcac	cctcttgaaa	aactcgtaag	780

&lt;210&gt; 676

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g525 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 676

tactactact	accctatgta	tttttttctt	tgcaacctgt	ccttcctgga	catgagcttc	60
accacgagca	ttgtcccaca	gtctctggct	aacctctggg	gaccacagaa	aaccataagc	120
tatggagggt	gtgtgggtcca	gttctatata	tccattggc	tgggggcaac	cgagtgtgtc	180
ctgctggcca	ccatgtccta	tgaccgctac	gctgccatct	gcaggccact	ccattacact	240
gtcattatgc	atccacagct	ttgccttggg	ctagctttgg	cctcctggct	gggggggtctg	300
accaccagca	tggtggggtc	cacgctcacc	atgctcctac	cgctgtgtgg	gaacaattgc	360
atcgaccact	tcttttgcga	gatgccctc	attatgcaac	tggttgtgtg	ggataaccagc	420
ctcaatgaga	tgggagatgt	acctggccag	ctttgtcttt	gttgtcctgc	ctctgggggt	480
catcctgggtc	tcttacggcc	acattgccgg	gccgkgttga	agaacaagtc	agcagaaggg	540
cggagaaagg	cattcaacac	ctgttctttc	cacgtg			576

&lt;210&gt; 677

&lt;211&gt; 929

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g526 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 677

atggatataa	gaaacagctc	aataataatc	tgagtttgtt	ttgttagaat	tcacagcac	60
ttgggaactt	gaaattttgt	ttcttaaata	tttttgttgg	cctatgcagc	aatcatggca	120
ggaaacctca	ctgcaatcgc	tgtaacctcc	aatcctcccc	tttgctcaac	acctatgtac	180
ttcctccttg	gaaatctctc	ctttctcagt	atgtttatct	ccacagtcac	aatctctaag	240
atgggtccaga	cgttctcagg	gagaataaaa	ccacttcctc	atggggctgt	atgggtcaga	300
tctccacttc	ttaggaggca	gtgagatgac	tcttctcata	tttatggctg	ttgatcagca	360
cattgcaata	tgacagacct	ttcactgcag	aaccatcacg	aactgcaggg	tactcatggc	420
cactcatggg	ctctgtgctg	ctatcacggg	ctgttggttt	tgtgcatact	ataagccaga	480
ttgtttttat	tatcaccttg	cccttctgtg	gccccagtg	ggtggacaat	ttattttgag	540
accttcctct	agttctgaag	cttgctgca	ctgagactta	tgatctggag	ttgctggtaa	600
ttgctaaaag	tggacagtgt	tctttcatct	gcttcatagt	cttgctcatt	ttctacacta	660
ttattctggt	aactgtgcag	catcgatcct	ctgatgcact	ctccaaggct	ctgtccacac	720
tgtctgctca	tatcactgca	gtcactctat	ttttatgagc	catgtgtcta	catttacact	780
tggccattta	ggagcttttc	agtggataca	tttctttctg	tgttttattc	agttacaccc	840
ttactgaacc	ccattactta	cagtctgaga	tgaagcatc	tatacatcaa	ctgaggaccc	900
aacacatcat	ctccagacaa	accttctct				929

&lt;210&gt; 678

&lt;211&gt; 595

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g527 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 678

ctactactac	ccatgtattt	ttttctgtgc	aacctgtccc	tggtggactt	tggttattcc	60
tcagctgtca	ctcccaaggt	gatggtgggg	tttctcacag	gagacaaatt	catattatat	120
aatgcttgtg	ccacacaatt	cttcttcttt	gtagccttta	tactgcaga	aagtttcttc	180
ctggcatcaa	tggcctatga	ccgctatgca	gcattgtgta	aaccctgca	ttacaccacc	240
accatgacaa	caaagtgtatg	tgctcgctcg	gccataggct	cctacatctg	tggtttctctg	300
aatgcacca	ttcatactgg	gaacactttc	aggctctcct	tctgtagatc	caatgtagtt	360
gaacactttt	tctgtgatgc	tcctcctctc	ttgactctct	catgttcaga	caactacatc	420
agtgagatgg	ttattttttt	ttgtgggtgg	attcaatgac	ctcttttcta	tcctggtaat	480
cttgatctcc	tacttattta	tatttatcac	catcatgaag	atgcgctcac	ctgaaggacg	540
ccagaaggcc	ttttctactt	gtgcttccca	ccttactgca	gtttccatct	tttat	595

&lt;210&gt; 679

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g528 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 679

atggaggcca	tgaactatt	aatcaatct	caagtgtcag	aattcatttt	gctgggactg	60
accagctccc	aggatgtaga	gtttcttctc	tttgccctct	tctcgggtat	ctatgtgggc	120
acagttttgg	gtaaccttct	tattatagtc	acagtgttta	acacccctaa	cctgaatact	180
cccatgtatt	ttctccttgg	taatctctct	ttttagata	tgacccctgc	ttcttttgcc	240
accctaagg	tgattctgaa	cttgttaaaa	aagcagaagg	taatttcttt	tgctgggtgc	300
ttcactcaga	tatttctcct	tcacttactg	ggtgggggtg	aaatgggtact	gttgggtctcc	360
atggcttttg	acagatatgt	ggccatttgt	aagccctac	actacatgac	catcatgaac	420
aagaagggtat	gtgttttgct	tgtagtgacc	tcatggctct	tgggtctcct	tcactcaggg	480
tttcagatac	catttgctgt	gaacttgccc	ttttgtgggc	ccaatgtggg	agacagcatt	540
ttttgtgacc	tccttttggg	tactaaagct	gcctgtatag	acatatattt	tgtacaggta	600
gtcattgttg	ccaacagtgg	cataatctcc	ctgagctgtt	tcattatttt	gcttatctcc	660
tacagctctga	tcctcataac	cattaagaac	cactctccta	ctgggcaatc	taaagcccgt	720
tccactttga	ctgctcacat	cacagtgggt	attctcttct	ttggcccatg	catctttatc	780
tacatttggc	ccttcggcaa	ccactctgta	gataagttcc	ttgctgtgtt	ttataaccatc	840
atcactccta	tcttgaatcc	aattatctat	actctgagaa	acaaagaaat	gaagatatcc	900

atgaaaaaac tctggagagc ttttgtgaat tctagagaag atact 945

<210> 680

<211> 951

<212> DNA

<213> Unknown (H38g529 nucleotide)

<220>

<223> Synthetic construct

<400> 680

atggagcccc	aaaatacctc	cactgtgact	aactttcagc	tgtaggatt	ccagaacctt	60
cttgaatggc	aggccctgct	ctttgtcatt	ttcctgctca	tctactgcct	gaccattata	120
gggaatgttg	tcatcatcac	cgtggtgagc	cagggcctgc	gactgcactc	ccctatgtac	180
atgttcctcc	agcatctctc	ctttctggag	gtctggtaca	cgccaccac	tgtgcccctt	240
ctcctagcca	acctgctgtc	ctggggccaa	gccatctcct	tctctgcctg	catggcacag	300
ctctacttct	tcgtattcct	cggcgccacc	gagtgccttc	tcttggcctt	catggcctat	360
gaccgttacc	tggccatctg	cagccactc	cgctaccctt	ttctcatgca	tcgtgggcta	420
tgtgccagggt	tggtggtggt	ctcatggtgc	acaggggtca	gcacaggctt	tctgcattcc	480
atgatgattt	ccaggttgga	cttctgtggg	cgcaatcaga	ttaaccattt	cttctgcgac	540
ctcccgccac	tcatgcagct	ctcctgttcc	agagtttata	tcaccgaggt	gaccatcttc	600
atcctgtcaa	ttgccgtgct	gtgcatttgt	ttttttctga	cactggggcc	ctatgttttc	660
attgtgtcct	ccatattgag	aatcccttcc	acctctggcc	ggagaaagac	cttttccaca	720
tgtggctccc	acctggctgt	tgctactctc	tactacggga	ccatgatctc	catgtatgtg	780
tgtccagtc	cccactgtt	gcctgaaatc	aacaagatca	tttctgtctt	ctacactgtg	840
gtcacaccac	tgctgaacc	agttatctac	agcttgagga	acaaagactt	caaagaagct	900
gttagaaagg	tcattgagaag	gaaatgtggt	attctatgga	gtacaagtaa	a	951

<210> 681

<211> 1005

<212> DNA

<213> Unknown (H38g530 nucleotide)

<220>

<223> Synthetic construct

<400> 681

tctacagacc	cacagaatct	aacagatgtc	tctatatctc	tcttcctaga	agctcagagg	60
atccagaatg	gcagccggtc	ctcactgggc	tgtgctgtgc	catgtgcctg	gtcacgggtgc	120
tggggaacct	gtcatcatc	ctggccgtca	gccctgactc	ccacctccac	atccccatgt	180
acttcttctc	ctccaacctg	tccctgcttg	acatcggttt	cacctccacc	acgggtcccca	240
agatgattgt	ggacatccag	tctcacagca	gagtcactc	ctacgcaggc	tgcctgactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgtcctt	gagtgtgata	360
gcctatgagc	ggttttagc	catctgtcac	cctctatatc	attcagccat	catgaaccca	420
tgtttctgtg	gctttctagt	tttgtgtctt	ttttttttt	ctcagtcttt	tagacgcccc	480
gctgcacaac	ttgattgcct	tacaaaggac	ctgcttcaag	gatgtggaaa	ttcctaattt	540
cttctgtgac	ccttctcaac	tccccatctt	gcataattgtg	gcaccttcac	caataacata	600
atcatgtatt	tccctgccgc	catatttggg	tttcttccca	tctcggggac	gcttttctct	660
tacgataaaa	ttgttttctc	cattctaagg	gtttcatcat	caggtgggaa	gtataaggcc	720
ttctccacct	gtgggtctca	cctgtcagtt	gtttgtgat	tttatggaac	aggcattgga	780
ggctacctga	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcagtggc	ctcagtgatg	840
tacacgggtgc	tcattccccat	gccgaacccc	ttcatctaca	gcctgagaaa	cagggatatg	900
aaaagtgtcc	tgacgcggcc	acatggcagc	acgatctcat	ctcaatatct	tcttatttgt	960
tccattcctt	ttgtagtgtg	ggttaaaaaa	ggcagcaagg	tcaaa		1005

<210> 682

<211> 990

<212> DNA

<213> Unknown (H38g531 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 682

cacacagagc	cacagaatct	cacagggtatc	tgagaattcc	tcctcctggg	actctcagag	60
gattccagaac	tgagccgggt	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgaggaacc	tgctcagcac	cctgggtgtc	agctctgact	ccccctcca	cacccccatg	180
tactttcttc	tctccaacct	gtgctgggct	gacatcggtt	tcaccttggc	catagtctcc	240
aagatgactg	tgacatgca	gtctcatagc	agagtcactc	ctcatgcggg	ctgcctgaca	300
cagatgtctt	tcttggtcct	ttttgcatgt	atagaagaca	tgttcctgac	tgtgatggcc	360
tatgacagat	ttgtagccat	ctgtcgccct	ctttactacc	cagtcactcat	aaatcctcac	420
ctctgtgtct	tcttcgtttt	ggtgtccttt	ttccttagcc	tggtggattc	ccagctgcac	480
agttggattg	tgtgacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttctcta	ccttgccctg	tctgacagca	tcatcaatag	catattcata	600
tattttgata	gtactatgtt	tggttttctt	ccattttcaa	ggatcctttt	gtcttactat	660
aaaattgtcc	cctccattct	aaggatttca	tcgtcagatg	ggaagtataa	agccttcacc	720
acctgtggct	ctcacctagc	agttgtttgc	ttatttgatg	gaacaggcat	tgcatgttac	780
ctgacttcag	ctgtggcacc	acccccagg	aatgggtgtg	tggtgcagct	gatgtacgct	840
gtggtcacc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacagggg	cattcaaaac	900
accctgtgga	ggctgcgcag	cagaagagtg	gaatctcatg	atctgttcca	tccttttttt	960
gtgtgggtga	gaaagggcaa	ccacattaaa				990

&lt;210&gt; 683

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g532 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 683

tctacagacc	cacaaaatct	aatagatgtc	tttgatttcc	tcctcctgga	acctcagagg	60
atccagaacg	gcagctgggc	cttgctgggc	tgttcctgtc	catgtgcctg	gtcacgggtg	120
tggggaacct	gtctcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
actttcttct	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
agttgattgt	ggacatccaa	tcttacagca	gagtcacttc	ctatgcagge	tgcttgactc	300
agacgtctct	ctttgccatt	tttgagggca	tggaagagag	acatgctcct	gagtggtgatg	360
gtctatgacc	ggtttgtagc	catctgtcac	cctctatatc	attcagccgt	catgaacccc	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttc	tcagtctttt	agacgcccag	480
ctgcacaact	tgattgcctt	acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	540
ttctgtgacc	cttctcaact	cccccatctt	gcatgttgtg	acaccttcac	caataacata	600
atcatgtatt	ttcctgctgc	catatttggt	tttcttccca	tctcggggac	ccttttctct	660
tactatgaaa	ttgtttcctc	cattctgagg	gtttcatcat	aagggtgggaa	gtataaggcc	720
ttcgccacct	gtgggtctca	cctgtcagtc	gtttgctgat	tttatggaa	aggcggttgg	780
gggtacctca	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcgggtggc	ctcagtgatg	840
tacactgtgg	tcacccccat	gctgaacccc	ttcatctaca	gcctgagaaa	cagggatact	900
aaaagtgtcc	tgcggcggcc	gcacggcagc	acggtgtaat	cttgatatct	tcttatctgt	960
tccattcctt	ttgtagtgtg	ggttaaaaaa	ggcagaaagg	tcaaa		1005

&lt;210&gt; 684

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g533 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 684

cacacagagc	cacggcatct	cacagggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgagcctgt	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacagtg	120
ctaagggaacc	gtctcatcat	cctggctgtg	agctctgact	ccacctcca	cacccccatg	180
tactttcttc	tctccaacct	gtgctgggct	gacatcagtt	tcacctcggc	cacggttccc	240

aagatgacgg	tggacatgca	gtcgcatagc	agagtcacat	cttatgcggg	ctgcctgaca	300
cggatgtctt	tcttcgtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
taggactgct	ttgtagccat	ctgtcgccct	ctgcactacg	cagtcacgt	gaatcctcac	420
ctctgtgtct	tcttagtttt	gggtgccttt	ttccttagcc	tgttggtatc	ccagctgcac	480
agttagattg	tgttacaatt	cacctctctc	aagaatgtgg	aaatctctca	ttttgtctgt	540
gagccatctc	aacttctcaa	ccttgccctgt	tctgacagct	tcatcaatag	catattcatg	600
tatttcgata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaattgtcc	cctccattct	aaggatttca	tctgcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtggcacc	accccccagc	aatgggtgtg	tggcatcagt	gaagtacacc	840
gtggtcaccc	ccatgtgaa	ccctttcatc	tacagcctga	gaaacaggga	cattcaaagc	900
acccgtgga	ggctgtgcag	cagaacagtt	aaatctcttg	atctgttcca	ttctttttct	960

&lt;210&gt; 685

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g534 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 685

atttccttcc	ttttctgggt	ccttctcttg	gtcatttcta	gagttttggt	agccatggca	60
tgaggaaaca	gcactgaagt	gactgaattc	tgtcttctgg	gatttgggtg	ctagcaagag	120
ttttgggtga	tcctcttcat	tatattcctt	ctcatctatg	tgacctccat	aatgggtaat	180
agtgaataaa	tcttactcat	caacacagat	tccagatttc	aaacacccat	gtactttttt	240
ctacaacatt	tggcttttgt	tgatattctg	tacacttctg	ctatcactcc	caagatgctc	300
caaagcttca	cggaaagaaa	gaatttgata	tcattttggg	gctgcatgat	acaattattg	360
gtttatgcaa	catttgcaac	cagtgcactg	tatctcctgg	ctatgatagc	agtggaccat	420
tatgtttgaa	tctgtaagcc	ccttcactat	accgtaatca	cgtcccaaac	agtcctgcatc	480
catttggtag	ctggttcata	catcatgggc	tcaataaatg	cctctgtaca	tacaggtttt	540
gcattttcac	tgtctttctg	caagtccaat	aacatcaacc	actttttctg	tgatggctcc	600
ccaattcttg	ccctttcatg	ctccaatatt	gacatcaaca	tcatgctact	tgttgtcttt	660
gtgggattta	acttgatgtt	cactgggttg	gtagtcatct	tttctacat	ctacatcatg	720
gccaccatcc	tgaaaatgtc	ttctagtga	ggaaggaaaa	aatccttctc	aacatgtgcc	780
tcccacctga	ccacagttgc	cattttctat	gggacactct	cttacatgca	cttaccagtc	840
tcattctaata	aattcccagg	agaatatgaa	agtgccctct	atattttatg	gcactgttat	900
tcccatgttg	aatcctttaa	tctatagctt	gagaaataag	gaagtaaaag	aagctttaaa	960
attgataggg	aaaaagtctt	tt				982

&lt;210&gt; 686

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g535 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 686

atgacactag	gaaacagcac	tgaagtcact	gaattctatc	ttctgggatt	tgggtgccag	60
catgagtttt	ggtgtatcct	cttcattgta	ttccttctca	tctatgtgac	ctccataatg	120
ggtaaatagtg	gaataatctt	actcatcaac	acagattcca	gatttcaaac	actcacgtac	180
ttttttctac	aacatttggc	ttttgttgat	atctgtttaca	cttctgctat	cactcccaag	240
atgtccaaaa	gcttcacaga	agaaaagaat	ttgatgttat	ttcagggtcg	tgtgatacaa	300
ttcttagttt	atgcaacatt	tgcaaccagt	gactgttatc	tcctggctat	gatggcagtg	360
gatccttatg	ttgccatctg	taagccctt	cactatactg	taatcatgtc	ccgaacagtc	420
tgcattccgtt	tggtagctgg	ttcatacatc	atgggtcaca	taaatgcttc	tgtacaaaaca	480
ggtttttacat	gttcaactgtc	cttctgcaag	tccaatagca	tcaatcactt	tttctgtgat	540
gttcccccta	ttcttgcctt	ttcatgtctc	aatgttgaca	tcaacatcat	gctacttggt	600
gtctttgtgg	gtctaaactt	gatattcact	gggttggtcg	tcatcttttc	ctacatctac	660
atcatggcca	ccatcctgaa	aatgtcttct	agtcaggaa	ggaaaaaatc	cttctcaaca	720

tgtgcttccc	acctgaccgc	agtcaccatt	ttctatggga	cactctctta	catgtatttg	780
cagtctcatt	ctaataattc	ccaggaaaat	atgaaagtgg	cctttatatt	ttatggcaca	840
gttattccca	tgtaaatacc	tttaatctat	agcttgagaa	ataaggaagt	aaaagaagct	900
ttaaaagtga	tagggaaaaa	gttattt				927

&lt;210&gt; 687

&lt;211&gt; 894

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g536 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 687

atgggtcgag	gaaacagcac	tgaagtgact	gaattccatc	ttctgggatt	tggtgtccaa	60
cacgaatttc	agcatgtcct	tttcattgta	cttcttctta	tctatgtgac	ctccctgata	120
ggaaatattg	gaatgatctt	actcatcaag	accgattcca	gacttcaaac	acccatgtac	180
ttttttccac	aacatttggc	ttttgttgat	atctgttata	cttctgctat	cactcccaag	240
atgctccaaa	gcttcacaga	agaaaataat	ttgataacat	ttcggggctg	tgtgatacaa	300
ttcttagttt	atgcaacatt	tgcaaccagt	gactgttacc	tcctagctat	tatggcaatg	360
gattgttatg	ttgccatctg	taagccccct	cgctatccca	tgatcatgtc	ccaaacagtc	420
tacatccaac	tcgtagctgg	ctcatatatt	ataggctcaa	taaatgcctc	tgtacataca	480
ggttttacat	tttcactgtc	cttctgcaag	tctaataaaa	tcaatcactt	tttctgtgat	540
ggctctccca	ttcttgccct	ttcatgtctc	aacattgaca	tcaacatcat	tctagatggt	600
gtctttgtgg	gatttgactt	gatgttcact	gagttggcca	tcactctttc	ctacatctac	660
attatggcca	ccatccctgaa	gatgtcttct	actgctggga	ggaaaaaatc	cttctccaca	720
tgtgcctccc	acctgacagc	agtaaccatt	ttctatggga	cactctctta	catgtactta	780
cagcctcagt	ctaataattc	tcaggagaat	atgaaagtag	cctctatatt	ttatggcact	840
gttattccca	tgttgaatcc	tttaatctat	agcttgagaa	ataaggaagg	aaaa	894

&lt;210&gt; 688

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g537 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 688

acgtacgacg	gcgcgagggg	ggctctctgta	ttgtttctta	caatacatgc	aaatctacaa	60
tgatgtcaat	aaaaattcaa	ttaaaaatac	atgtagtaaa	aatagttgct	aatctatgct	120
ggagtttact	tgaatgtcac	tatgctgac	gtcaccttca	agtacacaca	tatcttccat	180
catcctgagc	ttgccctctg	ctatgtgtct	ttttccgcag	ttgtcttcca	cctgacagct	240
gtcaccattt	tctttggagc	tctctcttac	atggacttac	aacctgaatc	tactgtgttt	300
caagagcaag	aaaagccagc	atccatattt	tgtyggcatta	tgactctcgt	gttaaaacttc	360
cttatctact	gcctgtgaaa	ttaggaagta	aaagaagctc	tacagttaac	aaggaaaaag	420
tattaataca	tgtagactga	gggt				444

&lt;210&gt; 689

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g538 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 689

atgctagtgt	cacaacagga	gcagcctctt	ctgtttggca	tcttccttgg	catgtacctg	60
gtcaccatgt	tggggaacct	gctcattatc	ctggccatca	gctctgaccc	acacctccat	120
actcccatgt	acttctttct	ggccaacctg	tcattaactg	atgcctgttt	cacttctgcc	180
tccatcccca	aaatgctggc	caacattcat	acccagagtc	agatcatctc	gtattctggg	240

tgtcttgcac	agctatatatt	cctccttatg	tttgggtggcc	ttgacaactg	cctgctggct	300
gtgatggcat	atgaccgcta	tgtggccatc	tgccaaccac	tccattacag	cacatctatg	360
agtcccccagc	tctgtgcact	aatgctgggt	gtgtgctggg	tgctaaccac	ctgtcctgcc	420
ctgatgcaca	cactgttgct	gacccgcgtg	gctttctgtg	cccagaaaagc	catccctcat	480
ttctattgtg	atcctagtgc	tctcctgaag	cttgctgctg	cagataccca	tgtaaacgag	540
ctgatgatca	tcaccatggg	cttgctgttc	ctcactgttc	ccctcctgct	gatcgtcttc	600
tcctatgtcc	gcattttctg	ggctgtgttt	gtcatctcat	ctcctggagg	gagatggaag	660
gccttctcta	cctgtgtgtc	tcatctcacg	gtggttctgc	tcttctatgg	gtctcttatg	720
gggtgtgtatt	tacttcctcc	atcaacttac	tctacagaga	gggaaagtag	ggctgctgtt	780
ctctatatgg	tgattattcc	cacgctaaac	ccattcattt	atagcttgag	gaacagagac	840
atgaaggagg	ctttgggtaa	actttttgtc	agtggaaaaa	cattcttt		888

&lt;210&gt; 690

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g539 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 690

atgaagaggg	agaatcagag	cagtgtgtct	gagttcctcc	tcctggacct	ccccatctgg	60
ccagagcagc	aggctgtgtt	cttcaccctg	ttcttgggca	tgtacctgat	cacgggtgctg	120
gggaacctgc	tcatcatcct	gtcctccgg	ctggactctc	accttcacac	cccatgttc	180
ttcttctca	gccacttggc	tctcactgac	atctcccttt	catctgtcac	tgtcccaaag	240
atgttattaa	gcattgcaaac	tcaggatcaa	tccattcttt	atgcagggtg	tgtaactcag	300
atgtattttt	tcatattttt	cactgatcta	gacaatttcc	ttctcacttc	aatggcatac	360
gatcgggatg	tggccatctg	tcacccctc	cgctacacca	ctatcatgaa	agagggactg	420
tgtaacttac	tagtcactgt	gtcctggatc	ctctcctgta	ccaatgccct	gtctcacact	480
ctcctcctgg	cccagctgtc	cttttgtgct	gacaacacca	tccccattt	cttctgtgat	540
cttgttgccc	tactcaagct	ctcatgtcca	gacatctccc	tcaatgagct	ggtcattttc	600
acagtgggac	aggcagtcac	tactctacca	ctaatatgca	tcttgatctc	ttatggccac	660
attgggggtca	ccatcctcaa	ggctccatct	actaagggca	tcttcaaagc	tttgtccacc	720
tgtggctctc	acctctctgt	gggtgtctctg	tattatggca	caattattgg	actgtatttt	780
ctccctcat	ccagtgcctc	cagtgcacag	gacgtaattg	cctctgtgat	gtacacgggtg	840
atcaccccat	tgtctgaatcc	cttcattttat	agcctaagga	acaggggacat	aaaggggagcc	900
ctggagagac	tcttcaacag	ggcaacagtc	ttatctcaa			939

&lt;210&gt; 691

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g540 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 691

atggaaaaacc	aatccagcat	ttctgaattt	ttcctccgag	gaatatcagc	gcctccagag	60
caacagcagc	ccctcttcgg	aattttctctg	tgtatgtatc	ttgtcacctt	gactgggaac	120
ctgctcatca	tcttgcccat	tggtcttgac	ctgcacctcc	acaccccat	gtactttttc	180
ttggccaacc	tgtcttttgt	tgacatgggt	ttaacgtcct	ccacagttac	caagatgctg	240
gtgaatatac	agactcgcca	tcacaccatc	tcctatacgg	gttgccctcac	gcaaattgat	300
ttctttctga	tgtttggtga	tctagacagc	ttcttctctg	ctgccatggc	gtatgaccgc	360
tatgtggcca	tttgccaccc	cctctgtctac	tcacagtcac	tgaggcccca	agtctgtgcc	420
ctaagtcttg	cattgtgctg	ggctcctcacc	aatatcgttg	ccctgactca	cacgttcctc	480
atggctcggc	tgtccttctg	tgtgactggg	gaaattgtct	actttttctg	tgacatcaact	540
cctgtcctga	agctgtcatg	ttctgacacc	cacatcaacg	agatgatggc	ttttgtcttg	600
ggaggcaccg	tactcatcgt	ccccctttta	tgcatgttca	cctcctacat	ccacattgtg	660
ccagctatcc	tgagggtccg	aacccgtggc	gggggtggca	aggccttttc	cacctgcagt	720
tccacacctc	gcgttggttg	tgtgttctat	gggacctctc	tcagtgccta	cctgtgtcct	780
ccctccattg	cctctgaaga	gaaggacatt	gcagcagctg	caatgtacac	catagtgtgact	840



cccatgttga acccctttat ctatagccta aggaacaagg acatgaaggg ggccctaaag 900  
 aggtctttca gtcacaggag tattgtttcc tct 933

<210> 692

<211> 945

<212> DNA

<213> Unknown (H38g541 nucleotide)

<220>

<223> Synthetic construct

<400> 692

atgggaggca agcagccctg gggtcacagaa ttcactcttg tgggattcca ggttggtcca 60  
 gcactggcga ttctcctctg tggactcttc tctgtcttct atacactcac cctgctgggg 120  
 aatgggggtca tctttgggat tatctgcctg gactctaagc ttcacacacc catgtacttc 180  
 ttctctctac acctggccat cattgacatg tcctatgctt ccaacaatgt tcccaagatg 240  
 ttggcaaacc taatgaacca gaaaagcacc atctcctttg ttccatgcat aatgcagact 300  
 tttttgtatt tggtcttttg tgttacagag tgcctgattt tgggtggtgat gtcctatgat 360  
 aggtatgtgg ccactctgcca ccctttccag tacactgtca tcatgagctg gagagtgtgc 420  
 acgatcctgg cctcaacatg ctggataatt agctttctca tggctctggt ccatataact 480  
 catattctga ggccgccttt ttgtggccca caaagatca accactttat ctgtcaaact 540  
 atgtccgtat tcaaattggc ctgtgctggc cctaggctca accaggtggt cctatatgcy 600  
 ggttctgcgt tcatcgtaga ggggcccgtc tgcctggagc tggctctcaa cttgcacatc 660  
 ctgtcgcgcc atcttgagga tccagtaatg gggaggccg cagaccgact tactcttct 720  
 gctccttccc acctttgcat ggtgggactc ctttttgga gcaccatggt catgtacatg 780  
 gccccaagt cccgccacc tgaggagcag cagaaggctc tttccctgtt ttacagcctt 840  
 ttcaaccgga tgctgaaccc cttgatctac agcctgagga acgcagaggt caagggtgcc 900  
 ctgaaaagag tggttgaggaa acagagatca aagtgaggga tgcca 945

<210> 693

<211> 575

<212> DNA

<213> Unknown (H38g542 nucleotide)

<220>

<223> Synthetic construct

<400> 693

ttgaagggtt attaaaaggc aatatgagtg cagaagcaag gtaagttttt tgtaataatt 60  
 ttttggttaaat aatgtgaaat gtaaggaaaa aatatacaac tttaagtttc tgactgtcct 120  
 gctagaaaact agttttgccc tgcagcgacc cctctgtggg aatctcattg atgacaagtg 180  
 aaattcttgya agtgctaaag ttagtttgct caagttcact gctcatggat atgatcatga 240  
 tgggtgggtca acattcttct cttgccaatt ccaatgtact tatttataac tatgtgtctt 300  
 gtaatcttat ttttaaagag atcttatggt aatcttccaa gggagttag tttctgcatt 360  
 tcctggatat atgggttttc gtatattgcc tggctataat ttttagagct ctttacaac 420  
 tcacaaagat atggggctca acaatgaatg aaattgtacg gtggatgtat tagtattaaa 480  
 cgtattagta ttaaattgtg tgacataaac tggctcttaa atataatcac aaattagtat 540  
 ctacaatgct tcaagcattg ttgtcctttt tgaaa 575

<210> 694

<211> 942

<212> DNA

<213> Unknown (H38g543 nucleotide)

<220>

<223> Synthetic construct

<400> 694

atggctgaag aaaatcatat catgaaaaat gagtttatcc tcacaggatt tacagatcac 60  
 cctgagctga agactctgct gtttggtgtg ttctttgcca tctatctgat caccgtggtg 120  
 gggaatatta gtttggtggc actgatattt acacaccgtc ggcttcacac accaatgtac 180

atctttcttg	gaaatctggc	tcttgtggat	tcttgtctgt	cctgtgctat	tacccccaaa	240
atgttagaga	acttcttttc	tgagaacaaa	aggatttccc	tctatgaatg	tgcagtacag	300
ttttatttcc	tttgactgtg	ggaaactgca	gactgcttcc	ttctggcagc	aatggcctat	360
gaccgctatg	tggccatag	caaccactg	cagtaccaca	tcattgatgtc	caagaaactc	420
tgatttcaga	tgaccacagg	ggccttcata	gctggaaacc	tgatttccat	gattcatgta	480
gggcttgtat	ttaggttagt	tttctgtgga	tcgaatcaca	tcaaccactt	ttactgtgat	540
attcttccct	tgtatagact	ctcttgtgtt	gatccttata	tcaatgaact	ggttctattc	600
atcttctcag	gttcagttca	agtctttacc	ataggttagt	tcttaatatc	ttatctctat	660
attcttctta	ctattttcaa	aatgaaatcc	aaagagggaa	gggccaagc	tttttctacc	720
tgtgcacccc	actttttgtc	agtttcatta	ttctatggat	ctcttttctt	catgtacgtt	780
agaccaaatt	tgctgaaga	aggggataaa	gatataccag	ctgcaatttt	atttacaata	840
gtagttccct	tactaaatcc	tttcatttat	agcctgagaa	ataggggaag	aataagtgtc	900
ttaagaaaaa	ttctgatgaa	agaaataatc	tcaagaagat	gg		942

&lt;210&gt; 695

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g544 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 695

atgcaaggag	aaaacttcac	catttggagc	atttttttct	tggagggatt	ttcccagtac	60
ccagggttag	aagtgttct	cttcgtcttc	agccttgtaa	tgtatctgac	aacgctcttg	120
ggcaacagca	ctcttatttt	gatcactatc	ctagattcac	gccttaaaac	ccccatgtac	180
ttattccttg	gaaatctctc	tttcatggat	atttgttaca	catctgcctc	tgttcctact	240
ttgctgggtg	acttgcgtgc	atcccagaaa	accattatct	tttctgggtg	tgctgtacag	300
atgtatctgt	cccttgccat	gggctccaca	gagtgtgtgc	tcctggccgt	gatggcatat	360
gaccgttatg	tggccatttg	taaccgcgtg	agatactcca	tcattcatgaa	caggtgcgtc	420
tgtgcacgga	tggccacggt	ctcctgggtg	acgggttgcc	tgaccgctct	gctggaaacc	480
agttttgccc	tgcagatacc	cctctgtggg	aatctcatcc	atcacttcac	gtgtgaaatt	540
ctggcgggtg	taaagttagc	ttgcacaagt	tcactgctca	tgaacaccat	catgctgggtg	600
gtcagcattc	tcctcttgcc	aattccaatg	ctcttagttt	gcattctctta	catcttcate	660
ctttccacta	ttctgagaat	cacctcagca	gaggggaagaa	acaaggcttt	ttctacctgt	720
gggtgcccatt	tgactgtggt	gattttgtat	tatggggctg	ccctctctat	gtacctaaag	780
ccttcttcat	caaatgcaca	aaaaatagac	aaaatcatct	cgttgcttta	cggagtgtct	840
acccttatgt	tgaaccccat	aatttacagt	ttaagaaaca	aggaagtcaa	agatgctatg	900
aagaaattgc	tgggcaaaat	aacattgcat	caaacacacg	aacatctc		948

&lt;210&gt; 696

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g545 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 696

atgatgggta	gaaggaataa	cacaaatgtg	gctgacttca	tccttatggg	actgacactt	60
tctgaagaga	tccagatggc	tctgtttatg	ctatttctcc	tgatatacct	aattactatg	120
ctgggggaatg	tggggatgat	attgataatc	cgcctggacc	tccagcttca	cactcccatg	180
tattttttcc	ttactcacct	gtcatttatt	gacctcagtt	actcaactgt	cgtcacacct	240
aaaaccttag	cgaacttact	gacttccaac	tatatttccct	ttacgggctg	ctttgcccag	300
atgttctttt	ttgccttctt	gggtactgct	gaatgttacc	ttctctcttc	aatggcccat	360
gatcgctatg	cagcgatctg	cagtcctcta	cactacacag	ttattatgtc	caaaaggctc	420
tgccctgcctc	tcattactgg	gccttatgtg	attggcttta	tagactcctt	tgtcaacgtg	480
gtttccatga	gcagattgca	tttctacgac	tcaaacgtaa	ttcatcactt	tttctgtgac	540
acttccccaa	ttttagctct	gtcctgcact	gatacataca	acaccgaaat	cctgatattc	600
attattgttg	gttccacctc	gatgggtgcc	cttttcacaa	tatctgcate	ctatgtgttc	660
attctcttta	ccatcctgaa	aattaattcc	acttcaggaa	agcagaaaag	tttctctact	720

tgcgtctctc atctcttggg agtcaccatc ttttatagca ctctgatttt tacttattta	780
aaaccaagaa agtccttattc cttgggaaga gatcaagtgg cttctgtttt ttatactatt	840
gtgattcccg tgctgaatcc actcatttat agtccttagaa acaaagaggt gaaaaatgct	900
gtcatcagag tcatgcagag aagacaggac tccagg	936

&lt;210&gt; 697

&lt;211&gt; 634

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g546 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 697

acaatgttct ataaaaattag tgctttgttc taatgttttg tatcacttta ttttagtaaa	60
aattgagtaa gcaaaaaata tactgggttc tgactatctt tggcttttta gaggcattca	120
ttgccatgaa taaattataa aagttatata gttctctaata atgtttatat tttataatat	180
gaatatttag ttctctaata tgtttatatt ttataaatag aatatttctg tacattattt	240
cctaaaatgt atttttttct tttgtatctg ttgtcttttag ctattaattt ttgatagttt	300
ttctaccat cctcctcttc ccctacttta agaggcagat atctgtgcaa attcctagcc	360
atgctacact aatactacag cttcctgatg acactttttac attatcctca acttttgcct	420
ctcttattga ccctctgtat catcgatgct ctatggaaga ctgttcctta tgtacttaat	480
gtcagaaaaa ttctcttgac acagacagga tggcctctgt cttctacaca gtagtcattc	540
ccatgttaaa cccattgatc tggagcccca ggaacaagga tgtgacattg ccctgaggaa	600
agtcatgggc aatagaaaaac aggcattatt ttgc	634

&lt;210&gt; 698

&lt;211&gt; 682

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g547 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 698

tgcattgttct ctttttattt taattttttac cattttttttt cccacatgaa aggtcttgca	60
gtcacttaga aatgctgaga taaattgact ggtataaagt aaggatctctg attaatgaaa	120
tttactctaa aactaattgg ctttttcatg gactataaga ctatgcacaa ccacttcgta	180
ctcaaacatg caattctctt tccaatgttg tatgaccag taccagctc ttcaaagcac	240
attttttttt cttggtagat ctcaggctctt cttctgttg ctgatggcct agacaactat	300
agggccatct gaaagtcctt gcagtatttg gttgtcatga agcaatggct gtgtgttggtg	360
ctgctggttg tgccctgggc tggaggattt ttgcacacag taattcaact tggccttatt	420
catgggctcc catcttatga cccaatgtc attggtcggt ttgtctgtga catggacccc	480
ttaatgaagc ttgtctgtga ctatacactc aacagatttg tctattttgc aggtcatgac	540
ttaaatacta ggttttatat atttcgttta tattcagact ggactgtttc cttttggtga	600
tttgactttg gtatcctttt gtaatttttt ccctagagga catgattcta taaatcttgt	660
tatacatagt tattatccct gt	682

&lt;210&gt; 699

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g548 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 699

atggagccaa ggaaaaatgt gactgacttt gtctctcttg gcttcacaca gaatccaaag	60
gagcagaaag tactttttgt tatgttcttg ctctctcaca ttttgaccat ggtgggcaac	120
ctgtcattg tagtgaccgt aactgtcagt gagaccctgg gctcaccaat gtccttcttt	180
cttgcctggct taacatttat agatatcatt tattcttcat ccatttcccc cagattgatt	240

tcagacttgt	tctttgggaa	taattccata	tccttccaat	ctttcatggc	ccagctcttt	300
atcgagcacc	tttttgggtg	gtcagaggtc	tttctcctgt	tggtgatggc	ctatgaccgc	360
tatgtggcca	tctgtaagcc	cttgcatatt	ttggttatca	tgagacaatg	ggtgtgtgtt	420
ttgctgctgg	tagtgtcctg	ggttggagga	ttctgtcaat	cagtatttca	acttagcatt	480
atttatgggc	tcccattctg	tggccccaat	gtcattgata	attttttctg	tgacatgtat	540
cccttattga	aactggcctg	cactgacacc	catgttattg	gcctcttagt	ggtggccaat	600
ggaggactgt	cttgcaactat	tgcgtttctg	ctcttactca	tctcttatgg	tgatcatcctg	660
cactctctaa	agaaacttag	tcagaaaggg	aggcaaaaag	cccactcaac	ctgcagttcc	720
cacatcactg	tggttgtctt	cttctttgtt	ccttgtatatt	ttatgtgtgc	tagacctgct	780
aggaccttct	ccattgacaa	atcagtgagt	gtgttttata	cagtcataac	cccaatgctg	840
aaccccttaa	tctacactct	gagaaattct	gagatgacaa	gtgctatgaa	gaagctt	897

&lt;210&gt; 700

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g549 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 700

atgagtcctg	atgggaacca	cagtagtgat	ccaacagagt	tcgtcctggc	agggctccca	60
aatctcaaca	gcgcaagagt	ggaattatct	tctgtgtttc	ttcttgtcta	tctcctgaat	120
ctgacaggca	atgtgttgat	tgtgggggtg	gtaagggctg	atactcgact	acagaccctt	180
atgtacttct	ttctgggtaa	cctgtcctgc	ctagagatac	tgtcacttcc	tgatcatcatt	240
caaagatgc	tgagcaatct	cctctcaagg	caacacacta	tttcctttgc	tgatgtatc	300
acccaattct	atttctactt	ctttctcggg	gcctccgagt	tcttactgtt	ggctgtcatg	360
tctgctggatc	gctacctggc	catctgtcat	cctctgcgct	accccttgct	catgagtggg	420
gctgtgtgct	ttcgtgtggc	cttggcctgc	tgggtggggg	gactcgtccc	tggtgttggg	480
cccacagtgg	ctgtggcctt	gcttcccttc	tgtaagcagg	gtgctgtggg	acagcacttc	540
ttctgcgaca	gtggcccact	gctccgcctg	gcttgaccca	acaccaagaa	gctggaggag	600
actgactttg	tctgtggcctc	cctcgtcatt	gtatcttccct	tgctgatcac	tgctgtgtcc	660
tacggcctca	ttgtgtgtgc	agtcctgagc	atcccctctg	cttcaggccg	tcagaaggcc	720
ttctctacct	gtacctccca	cttgatagtg	gtgacctctt	tctatggaag	tgccattttt	780
ctctatgtgc	ggccatcgca	gagtggttct	gtggacacta	actgggcagt	gacagtaata	840
acgacatttg	tgacaccact	gttgaatcca	ttcatctatg	ccttacgtaa	tgagcaagtc	900
aaggaagctt	tgaaggacat	gttttaggaag	gtagtggcag	gcgtt		945

&lt;210&gt; 701

&lt;211&gt; 772

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g550 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 701

gtactctgtg	tcatatcttg	taaataaaat	catcatataa	gtttattgag	tttttttgag	60
tacctaataa	cttaataaaa	aaaatatggg	agcatatgta	gtacctgctt	tgatcaataa	120
cggataaagt	atctggaagt	ctttgctgag	aatctttttg	tgctgctgag	attattccac	180
tgatgtggat	gggccatggc	tggttatgtg	cgtctgtac	tacatgacca	tcgtgaatca	240
atataggtgt	agccatctca	ctggaatggc	atgtactgaa	agctttatcc	aggcacagtt	300
tagatcctct	ccccagctctg	acttcccttc	tatgacccca	atgtcatagc	tcattcatgt	360
gtgacttaaa	cacttttttg	aaactcctct	gcatgggtac	tactaataca	attggtttct	420
ttgttgctgc	caatgggtggg	ttcaactacc	tgtaaacaat	cattttcttg	atggtttctt	480
aagtggccat	cctatgtact	ttgaaaactc	acagcttggg	ggaaagatgc	taaagttctc	540
tacctgcatc	tctcacacca	ccatggtcat	cttatctttg	agttctgtat	atctgtgtat	600
ctgtgccccag	tgaccttccc	ccaatcaata	aagcaatggc	tggtgttcat	accgtgataa	660
atcctatgtt	aaaaccttta	gtctaaccct	cagaaatgca	gaggtgaaaa	gtgctttgag	720
aaaggtctgg	gtcaaaagat	gacctgaaga	gagaaataat	ctaaacataa	ga	772

<210> 702  
 <211> 954  
 <212> DNA  
 <213> Unknown (H38g551 nucleotide)

<220>  
 <223> Synthetic construct

<400> 702

atggaatggg	aaaaccacac	cattctggtg	gaattttttc	tgaagggact	ttctggtcac	60
ccaagacttg	agttactctt	ttttgtgctc	atcttcataa	tgatgtgggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcatc	ttggaccctc	accttcacac	ccctatgtac	180
ttctttctg	ggaacctctc	cttcttggac	atctgctaca	ccaccacctc	tattccctcc	240
acgctagtga	gcttcctttc	agaaagaaag	accattttccc	tttctggctg	tgcatgtcag	300
atgttcctca	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcgt	gatggccttt	360
gaccgctatg	tggctatctg	caacctctctg	agatatccca	tcacatgag	taaggatgcc	420
tatgtaccaca	tggcagctgg	gtcctggatc	ataggagctg	tcaattctgc	agtacaaaca	480
gtgtttgtgg	tacaattggc	tttctgcagg	aataacatca	tcaatcattt	cacctgtgaa	540
attctagctg	tcataaaact	ggcctgtgct	gacatctcag	gcaatgagtt	catcctgctt	600
gtgaccacaa	cattgttcct	attgacacct	ttgttattaa	ttattgtctc	ttacacgtta	660
atcattttga	gcatcttcaa	aattagctct	tcggagggga	gaagcaaacc	ttcctctacc	720
tgctcagctc	gtctgactgt	ggtgataaca	ttctgtggga	ccatcttcct	catgtacatg	780
aagcccaagt	ctcaagagac	acttaattca	gatgacttgg	atgccactga	caaacttata	840
ttcatattct	acaggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaac	900
aaggatgtga	aggaggcagt	aaaacaccta	ctgagaagaa	aaaattttta	caag	954

<210> 703  
 <211> 999  
 <212> DNA  
 <213> Unknown (H38g552 nucleotide)

<220>  
 <223> Synthetic construct

<400> 703

atggaagga	ccaattggac	agagatagag	ttcattctgc	aaggactttc	agggtaccca	60
agagctgaaa	aattcctttt	cgtgatgtgc	ttagtgatgt	acctgggtgat	tctcctaggt	120
aatggcacct	tgatcattct	gacactcctg	gatgctcgtc	tccacacacc	catgtacttc	180
ttccttggga	atctttcctt	cctagacatt	tggtacacat	cctcctccat	cccctcaatg	240
ctgatacact	tcctatcaga	gaagaaaacc	atctccttca	ctagatgtgt	gattcaaagt	300
tctgtctctt	acactatggg	atccaccgag	tgtgtgcttc	tagcagtgat	ggcatatgac	360
cgttatgtag	ccatctgcaa	ccctctgaga	tatcccatca	tcattgggcaa	ggcactttgt	420
attcagatgg	tggctgtctc	ttggggacta	ggctttctca	actcattgac	agaaactgtt	480
cttgcaatac	ggttaccctt	ctgtggaaaa	aaatgtcatt	aatcattttg	tttgtgaaat	540
attggccttt	gtcaagctgg	cttgacacaga	tacttctctg	aatgagatta	ttataatgtt	600
gggcaatgta	atatttttgt	tttctccatt	actgctgatt	tgtatctcct	acatctttat	660
cctttctact	gtactaagaa	tcaattcagc	tgaaggaagg	aaaaaggcct	tttccacctg	720
ctcagcccac	atgacagtgg	tgattgtggt	ttatgggaca	atcctcttca	tgtacatgaa	780
ggcaagtc	aaagactctg	cttttgacaa	actgattgcc	ctgttctatg	gcatagtcac	840
ccccatgctc	aatcctatca	tctatagcct	gaggaatata	gaggtgcatg	gagctatgag	900
gaaattaatg	agtagaccct	ggttctggag	gaaatgatga	cacactgaca	cctttgagtt	960
tatgcacaaa	atacgctcac	aagtttgaga	caacacttt			999

<210> 704  
 <211> 966  
 <212> DNA  
 <213> Unknown (H38g553 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 704

cacacagagc	catggaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctttg	ctctccctgt	ccctgtccat	gtgtctggtc	120
atgggtgctg	ggaacctgct	cagcatcctg	gctgtcagct	ctgtctctcc	cctccacacc	180
cccgtgtact	tcttcctctc	taaaactgtc	tgggctgaca	tcggtttcac	cttgggccacg	240
gttcccaaga	tgattgtgga	catgcagtcg	catagcagag	tcattctctca	tgcgggctgt	300
ctgacgcaga	tgtctttctt	catccttttt	gcatgtatag	aaggcatgct	cctgacagtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccaggt	catcgtgaat	420
cctcacctct	gtgtctcctt	cctttttggt	tcctttttcc	ttagcatggt	ggattcccag	480
ctgcacagtt	gaattgtgtt	acaattcaca	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaactt	gcctgttctg	acagcgtcat	caatagcata	600
ttcatatatt	tcaatagtac	tatgtttggt	tttcttccca	tttcagggat	cctatggtct	660
tactgtaaaa	tcgtcccttc	cattctaagg	atttcatcat	cagatgggaa	gtataaagcc	720
ttctccacat	gtggctctca	cctagcagtt	gtttgctgat	tttatagaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaaatg	gtgtggtggc	gtcagcgatg	840
ttctctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgcgagggt	gctcagcaga	acagtcgaat	cttatgatct	gttccatcct	960
ttttct						966

&lt;210&gt; 705

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g554 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 705

atggctgggg	aaaaccatac	tacactgcct	gaattcctcc	ttctgggatt	ctctgacctc	60
aaggccctgc	agggccccct	gttctgggtg	gtgcttctgg	tctacctggg	caccttgctg	120
ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctctg	gccaaactctc	agtgggtggag	ctcttctaca	ccactgacat	cgtgcccagg	240
accctggcca	atctgggctc	cccgcatccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	tcttcattgt	cctggggcatc	tcggagtgtc	gcctgctcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgctatt	ccacctctt	gagcccacgg	420
gcctgcatgg	ccatggtggg	tacctcctgg	ctcacaggca	tcattcacggc	caccacccat	480
gcctccctca	tcttctctct	accttttcgc	agccaccgca	tcattccgca	ctttctctgt	540
gacatcctgc	cagtactgag	gctggcaagt	gctgggaagc	acaggagcga	gatctccgtg	600
atgacagcca	ccatagtctt	cattatgata	cccttctctc	tgattgtcac	ctcttacatc	660
cgcacctctg	gtgccatcct	agcaatggcc	tccaccacga	gccgccgcaa	ggtcttctcc	720
acctgtcctc	cccatctgct	cggtggtctc	tctcttcttt	ggaacagcca	gcatcaccta	780
catccggccg	caggcaggct	cctctgttac	cacagaccgc	gtcctcagtc	tcttctacac	840
agtcatcaca	ccatgctca	accccatcat	ctacaccctt	cggaacaagg	acgtgaggag	900
ggccctgcga	cacttggtga	agaggcagcg	ccccctca			937

&lt;210&gt; 706

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g555 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 706

atggctggca	acaatttcac	tgaggttacc	gtcttcatcc	tctctggatt	tgcaaatcac	60
cctgaattac	aagtcagctc	tttcttgatg	tttctcttca	tttatctatt	cactgttttg	120
ggaaacctgg	gactgatcac	gttaatcaga	atggattctc	agcttcacac	ccctatgtac	180
tttttctctg	gcaatttagc	atttattgac	atatcttact	cctctactgt	aacacctaaag	240
gcattgggtg	atttccaatc	caatcggaga	tccatctcct	ttgttggtctg	ctttgttcaa	300
atgtactttt	ttgttggtg	ggtgtgttgt	gagtgtttcc	ttctgggata	aatggcctac	360
aatcgctaca	tagcaatctg	caatccctta	ctgtattcag	tagtcatgtc	caaaaaagtg	420

tccaactggc	tgggagtaat	gccatatgtg	ataggcttca	caagctcgct	gatatctgtc	480
tgggtgataa	gcagtttggc	gttctgtgat	tccagcatca	atcatttttt	ttgtgacacc	540
acagctcttt	tagcactctc	ctgtgtagat	acattcggca	cagaaatggg	gagctttgtc	600
ttagctggat	tcactcttct	tagctctctc	cttatcatca	cagtcactta	tatcatcate	660
atctcagcca	tcctgaggat	ccagtcagca	gcaggcaggc	agaaggcctt	ctccacctgc	720
gcacccacc	tcattggctgt	aactatcttt	tatgggtctc	tgattttcac	ctatttgcaa	780
cctgataaca	catcatcgct	gacccaggcg	caggtggcat	ctgtattcta	tacgattgtc	840
attcccatgc	tgaatccact	catctacagt	ctgaggaaca	aagatgtgaa	aaatgctctt	900
ctgagagtca	tacatagaaa	actttttcca				930

&lt;210&gt; 707

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g556 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 707

atctgtagcc	ccttgctgta	cagtgtcatc	atatccaata	aggcttgctt	ttctctgatt	60
ttaggggtgt	atataatagg	cctggtttgt	gcatacagttc	atacaggctg	tatgtttagg	120
gttcaattct	gcaaatttga	tttgattaac	cattatctct	gtgatcttct	tcccctccta	180
aagctctctt	gctctagtat	ctatgtcaac	aaactactta	ttctatgtgt	tggtgcattt	240
aacatccttg	tcccagctt	gaccatcctt	tgctcttaca	tctttattat	tgccagcatc	300
ctccacattc	gctccactga	gggcagggtc	aaagccttca	gcactttag	ctcccacatg	360
ttggcggttg	taatcttttt	tggatctgca	gcattcatgt	acttgcagcc	atcttcaatc	420
agctccatgg	accaggggaa	agtatcctct	gtgttttata	ctattattgt	g	471

&lt;210&gt; 708

&lt;211&gt; 529

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g557 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 708

ctggcccgt	cctccagtct	ggccttgggg	acatggcggt	ggcaatggca	cagcatgact	60
gagcttggtt	tgttggtgct	ctcagggttt	ggttccgtcc	ggggccttct	gttttgggca	120
gtgctctgca	aacatctggt	gaccctgctg	gacaactccc	tgatcgctgt	cctcgccctg	180
gcagcctctg	cctgcgctgg	cccacgcact	tcctcctgca	ccacttctcc	ttaggggagg	240
tcccacgcca	cagcggcgga	gtctcggatg	caggccgatt	cccttcccc	gccgcactag	300
cccaccggta	ggcggtcttc	cgctgctggg	ttcttctgcc	ctccctggca	tcgccgaatg	360
cgcttgcgca	gggcatggc	ctccgcgct	gtgacgccat	ctgccggccg	ctgcattcta	420
ctacctgagg	agccctagtc	ttccgagccc	gcttcgcctt	caccttgccc	ttctgcggcg	480
cagcaccacc	cgctacttcc	ggctggattc	tcggcctgtg	ctgagacct		529

&lt;210&gt; 709

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g558 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 709

atgaccagaa	aaaattatac	ctcaactgact	gagttcgtcc	tattgggatt	agcagacacg	60
ctggagctac	agattatcct	ctttttgttt	tttcttgtga	tttatacact	tacagtactg	120
ggaaatctcg	ggatgatcct	cttaatcagg	atcgattccc	agcttcacac	acccatgtat	180
ttcttctctg	ctaacctgtc	ctttgtggac	gtttgtaact	caactacat	caccccaaag	240
atgctggcag	atttattatc	agagaagaaa	accatctctt	ttgctggctg	cttctctacag	300

atgtacttct	ttatctccct	ggcgacaacc	gaatgcatcc	tctttgggtt	aatggcctat	360
gacaggtagt	cgcccatatg	tcgcccgtg	ctttactcct	tgatcatgtc	caggaccgtc	420
tacctaaaaa	tggcagccgg	ggcttttgct	gcagggttgc	tgaacttcat	ggtcaacaca	480
agccatgtca	gcagcttgct	attctgtgac	tccaatgtca	tccatcactt	cttctgtgac	540
agccccccac	ttttcaagct	ctcttggtct	gacacaatcc	tgaagaaaag	cataagttct	600
attttggtg	gtgtgaatat	tgtggggact	ctgcttgtea	tcctctcttc	ctactcctac	660
gttctcttct	ccattttttc	tatgcattcg	ggggagggga	ggcacagagc	tttctccacg	720
tgtgcctctc	acctgacagc	cataattctg	ttctatgcca	cctgcatcta	tacttacctg	780
agacctagtt	ccagctactc	cctgaatcag	gacaaaagtg	cttctgtgtt	ctacacagtg	840
gtgattccca	tgttgaatcc	tctgatctac	agcctcagga	gtaagggaag	aaagaaggct	900
ttagcgaatg	taattagcag	gaaaaggacc	tcttccttte	tg		942

&lt;210&gt; 710

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g559 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 710

atgaccagaa	aaaattatac	ctcactgact	gagttcatcc	tattgggatt	agcagacacg	60
ctggagctac	agattatcct	ctttctgtta	tttcttgtga	tttacacact	taccgtactg	120
ggaaatatcg	ggatgatcct	cttaatcagg	atcgattccc	ggcttcacac	acccatgtat	180
ttcttctctg	ttaacctgtc	ctttgtggac	atttgttact	caaccacccat	caccccaaag	240
atgctggcag	atattattac	agagaagaaa	accatctctt	ttgctggctg	cttcctacag	300
atgtacttct	ttatcgccct	ggcgacaacc	gaatgcatcc	tctttgggtt	aatggcctat	360
gaccggtatg	tgaccatag	tcgcccgtg	ctttactcct	tgatcatgtc	caggacagtc	420
tgcttaaaaa	tggcagccgg	ggcttttgct	gcagggttgc	tgaactccat	ggtcaacact	480
agctatgtca	gcagcttgte	attctgtggc	tccaatgtca	tccatcactt	cttctgcaac	540
agtccccccac	tttttaagct	ttctgtttct	gacacacact	tgaaggaaaag	catattttcc	600
acttttctgt	gtgtgaataa	ggtcggggct	ctgcttgtea	tcctctcttc	ctattcctac	660
gttctcttct	ccattttttc	tatgcattca	ggggagggga	ggcacagagc	tttctccacg	720
tgtgcctctc	acctgacagc	cataatcctc	ttctacacca	cctccatcta	tacctacctg	780
agacctagtt	ccagctactc	cctgatcagg	acaaagtggg	ttctgtgttc	tacacagtgg	840
tgatccccc	attgaatcct	ctgatctaca	gcctcaggaa	taagggaagta	aagaaggctt	900
tagcgaatgt	aattagcagg	aaaaggatcc	cttcatttct	g		941

&lt;210&gt; 711

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g560 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 711

atgagtgggg	agaatgtcac	caaggtcagc	accttcatcc	tggtgggcct	ccccacggcc	60
ccagggtctg	agtacctgct	cttcctcttc	ttctgtctca	cctacctctt	tgctctgggtg	120
gagaacctgg	ccatcatcct	catcgtcttg	agcagcacct	ccctccacag	gccccatgtac	180
tactttctga	gtctccatgtc	tttctggag	atctggtacg	tgtctgacat	cacccccaag	240
atgctggagg	gcttctcct	ccagcagaaa	cgcatctctt	tcgtcgggtg	catgacgcag	300
ctctacttct	tcagctccct	gggtgacacc	gagtgtgtgc	ttctgcctcc	atggcctacg	360
accgctacgt	ggccatctgc	caccgctgc	gctaccacgt	ccttgtgacc	gccgggctgt	420
gtccagctg	gtgggcttct	cctttgtgag	tgcttctcca	tctccatgat	caaggctctgt	480
tttatctcca	gcgtcacgtt	ctgtggctcc	aacgtcttga	acccacttct	tctgtgacat	540
ttcccccatc	ctcaagctgg	cctgcacgga	cttctccact	gcagagctgg	tgatttcatc	600
ctggccttca	tcatcctggg	gtttccgctc	ctggccacca	tactgtcata	ttggcacatc	660
accctggctg	tcctgcgcgt	cccctcgccc	accgctgctg	ggagagcctt	ctctacctgc	720
gcctctcacc	tcaccgtggg	caccgtcttc	tatacagcct	tgcttttcat	gtatgtccgg	780
ccccaaagca	ttgattccca	gagctccaac	aagctcatct	ctgccgtgta	cactgtttgtc	840



acgccataa ttaacccttt gatttactgc ctgaggaaca aggaatttaa ggacgccttg 900  
 aaaaaggcct tgggcttggt tcaaacttca cactaagac 939

<210> 712  
 <211> 642  
 <212> DNA  
 <213> Unknown (H38g561 nucleotide)

<220>  
 <223> Synthetic construct

<400> 712  
 ctggctgacc tctgtttctc taccaacata gttcctcagg cactagtcca cctgctttcc 60  
 agaaagaagg tcattgtatt cacactgtgc gcagctcgac ttctctttct cctcattggg 120  
 ggggtgtacc agtgccctct tcttgagtg atgtcctatg atcgctatgt tgcaatctgc 180  
 aatcctctgc gttaccctaa catcatgacc tggaaagtgt gtgtccagct ggcaacagca 240  
 ccatggacca gtggtattct ggtgtctgtg gtagacacca ccttcacact gaggctaccc 300  
 taccgaggca gtaacagcat tgctcatttc tgggtgtgagg cccctgcact attgatctta 360  
 gcatccacag acacccatgc atcagagatg gccatttttc ttacgggggt tgtgattctc 420  
 ctcatacctg tttttctgat tctggtatcc tatggccgta tcatagtaac tgtggtcaag 480  
 atgaagtcaa ctgtggggag tctcaaggca ttttctacct gtggctccca cctcatgggtg 540  
 gtcatacttt tttatggatc agcaattatc acttacatga cacccaagtc ttccaaacag 600  
 caggaaaaat cgggtgtctgt tttctatcca atagtgtact cc 642

<210> 713  
 <211> 948  
 <212> DNA  
 <213> Unknown (H38g562 nucleotide)

<220>  
 <223> Synthetic construct

<400> 713  
 atgttggaga gtaattacac catgccaaact gagttcctat ttgttggatt cacagattat 60  
 ctacctctca gagtcacact gttcttggta ttcttcttgg tatatacatt aactatgggc 120  
 ggaaatatac tcttaataat tctagttaat attaatcaa gccttcaaact tcccatgtat 180  
 tattttctta gcaacttata tttcttagac atcagctggt ctacagcaat cactcctaaa 240  
 atgtcggcaa acttcttggc atccaggaaa agcatctctc cttatgggtg tgcactacaa 300  
 atgtttttct tcgcttcttt tgctgatgct gagtgcctta tcctggcagc aatggcttat 360  
 gaccgctatg cagccatctg caacccactg ctctatacta cactgatgtc taggagagtc 420  
 tgtgtctgct tcattgtgtt ggcatatttc agtgggaagta caacatcact ggtccatgtg 480  
 tgctcacat tcaggctgtc attttgtggc tccaatatcg tcaatcattt tttctgtgat 540  
 atcccacctc ttttggtttt atcatgtaca gacactcaga tcaaccagct tctgtctctt 600  
 gctttgtgca gttcatcca gaccagcact tttgtggtaa tttttatttc ttacttctgc 660  
 atcctcatca ctgtgttgag catcaagtcc tcagggtggca gaagcaaac attctccact 720  
 tgtgttctcc acctcatagc agtcacctta ttctatggag cgctcctggt tatgtactta 780  
 cagcccacca ctagctattc cctagacact gataaggtgg tggcagtggt ttatactggt 840  
 gtatttccca tgtttaatcc aataatttat agtttcagaa acaaggatgt gaaaaatgct 900  
 ctcaaaaagc tattagaaag aattggatat tcaaatgaat ggtattta 948

<210> 714  
 <211> 939  
 <212> DNA  
 <213> Unknown (H38g563 nucleotide)

<220>  
 <223> Synthetic construct

<400> 714  
 atgtcaaccc acagaaatgg aaatctctca gtggttcctt tgtgggagag catgctgaag 60  
 ggacttgagg gtggcctgga gaaccaggcc ctgctctttg ctgtgttccc aggtctatac 120

atggtgacca	tcccgggaaa	cctcaccatg	accatgggtca	tcatacctgga	cacgcacctg	180
cacttcccag	tgaacttctt	cctcaggagc	ctcccccttc	ctggaccttg	gccatgcctc	240
catcacccca	atgccctggt	taacttctct	tcctcggtcca	aggtcgtcac	ctttgcaggc	300
tgtgctgccc	ggttcttttt	ctccttgctg	tctaccactg	agactttcct	gctggccgtg	360
atggccctatg	actgcttcgt	ggccatctgt	agtctgggtg	ggtgcccagt	gaccacgtgc	420
ctctcgatct	gcatcatect	gggaccaggc	acctaactgca	gggtctgcct	cagctccatc	480
gtgcagaccg	gcctcatggt	ccagctccct	tctgcaggga	ccaaccacat	tgaccactct	540
gtgacatgcc	ccagctgctc	cggctggcct	gtgcatgcct	ggccctcaat	gagctgacca	600
agttcagcct	ttgtgggctc	atgatgggaa	cgccactctt	gtggctcctcg	tctccttttg	660
ctgtgtcaca	gtgaccatcc	tgaggacacc	ctccgcagcc	agtgcataaa	ggtcttcacc	720
tgtagctccc	acgtgatgac	cgtgtccctg	tttgatggga	ctgtgtttgt	cacatatgcc	780
cagccaggga	ctatggagtc	catggagcag	ggcaagggtg	tgtctgtctt	ctacagcctg	840
gtcatcccga	tgcttggccc	cttcactctac	agcctacgaa	acaaggacat	gaaggaggcc	900
ctgcgagggc	tgggccagag	acaagcactc	atgggaagg			939

&lt;210&gt; 715

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g564 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 715

atgtacttct	tccttggcaa	cctctccttt	tgtgatatact	gctactctac	tgtctttgct	60
cctaagatgc	tagtcaattt	cctatcaaaa	cataagtcca	gtacattttc	tggtgtgttt	120
ctacagagtt	tcctttttgc	agtatatgta	accacaaagg	acattctcct	gtccatgatg	180
gcttatgacc	attacgtggc	catagctaata	cccttgttgt	atacagtcac	tatggcccaa	240
aaagtttgta	ttcagatggt	ccttgccttc	tacttaggtg	ggctcattaa	ttccctgaca	300
cacacaatag	gtttgctcaa	attagacttc	tgtggtccta	atattgtgaa	tcattatttc	360
tgtgatgttc	ctcctcttct	gaggctttct	tgctctgatg	ctcatatcaa	tgaaatgctg	420
cccttgggtc	tctctgggct	cattgcaatg	ttcactttca	ttgtcattat	ggtgtcttat	480
atctgcatca	tcattggccat	ccagagaatc	catgcagctg	agggaaggta	caaagccttc	540
tcactttgtg	tctccacact	aaccacggtg	accttattct	atgggtctgt	ttcttttagt	600
tatatccagc	caagttctca	gtattccttg	gaacaggaga	aggctctggc	tgtgttttat	660
acactggtga	tcctcatgct	aaaccactt	atttatagcc	tgagaaataa	ggatgtaaaa	720
gatgcagcca	aaaggttgat	atgggtgggg	gaaaaa			756

&lt;210&gt; 716

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g565 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 716

atgagtgggg	agaatgtcac	cagggtcggc	accttcatcc	tggtgggctt	ccccacggcc	60
ccagggtgct	agtacctgct	cttcctcctc	ttcctgctca	cctacctctt	tgtcctgggtg	120
gagaacctgg	ccatcatcct	caccgtctgg	agcagcacct	ccctccacag	gcccatgtac	180
tactttctga	gtcccatgct	tttcttagag	atctggtacg	tgtctgacat	cacccccaag	240
atgctggagg	gcttctcctc	ccagcagaaa	cgcactctct	tcgtcgggtg	catgacgcag	300
ctctacttct	tcagctccct	ggtgtgcacc	gagtggtgct	ttctggcctc	catggcctac	360
gaccgctacg	tggccatctg	ccaccgctg	cgctaccacg	tccttgtgac	cccgggctgt	420
gcctccagct	ggtgggcttc	tcctttgtga	gtggcttcac	catctccatg	atcaaggctc	480
gttttatctc	cagcgtcacg	ttctgtggct	ccaacgtctt	gaaccacttc	ttctgtgaca	540
tttcccccat	cctcaagctg	gcctgcacgg	acttctccac	tgacagagctg	gtggatttca	600
ttctggcctt	catcatcctg	gtgtttccac	tcctggccac	catgctgtca	tatgcgcaca	660
tcaccctggc	tgtcctgcgc	atccctcctc	caccggctgc	tggagagcct	tcttcacctg	720
cgcctctcac	ctcaccgtgg	tcaccgtctt	ctatacagcc	ttgtctttca	tgtatgtccg	780
ccccaggcca	ttgattcccc	gagctccaac	aagctcatct	ctgtttttga	cacagttatc	840

acccccatct tgaacccctt gatatactgc ctgaggaata aggaatttaa gaatgccttg 900  
 aaaaacagtc ggcttgacga ctgcgccgta gaggggaggc tttctagtct tctg 954

<210> 717

<211> 960

<212> DNA

<213> Unknown (H38g566 nucleotide)

<220>

<223> Synthetic construct

<400> 717

atggctgatg ttaattttac attggttact gagtttatcc ttttggaact gacagatcgt 60  
 gctgaactga agatggctct cttcgtgttg ttcctgctga tctacacat ttccctggtg 120  
 ggaaatatag gaatgctctt tctaattctat gtaactccca aactccacac acccatgtat 180  
 tatttctca gctgtctgtc atttgttgat gcctgctatt catcagtttt tgcaccacaga 240  
 atgctgctga acttctttgt tgagcgggag acaatcttat tctctgcatg tattgtgcag 300  
 tattttttat tctgtctctc ccttaccact gagggcttct tgctggccac aatggcttac 360  
 gaccgttaca tggccattgt gaacccttta ctttatacag tagctatgac taaaatagtt 420  
 tgtattgtgc tcgcatttgg gtcatgtatg ggagggttaa tcaactcatt gacacataca 480  
 attggcttgg tgaaactgtc tttctgtggg ccaaagtca tcagtcactt cttctgtgat 540  
 cttcccccac tgttgaagct gtcatgttct gagacatcta tgaatgaatt gttgcttttg 600  
 atcttctctg gcattattgc cacgctcact tttttgactg tgggtgatctc ctacatcttc 660  
 attgttctg ctatcctgag gatccgctaa gcagcaggta gacgtaaagc cttctccacc 720  
 tgcacctctc acctgattac cgtgacctta ttctatggat cgataagctt tagttacatt 780  
 cagccaaact cccagtattc cctagaacaa gaaaagggtg tgtctgtatt ttataacctg 840  
 gtggttccta tgttaaacc attgatttac agcctaagga acaaggaagt gaaggaagct 900  
 gtgaaaagg ctatagaaat gaaacatttt ccttggtta ttcataattc catatccaaa 960

<210> 718

<211> 938

<212> DNA

<213> Unknown (H38g567 nucleotide)

<220>

<223> Synthetic construct

<400> 718

atgttgggga attactctag cgccactgaa tttttctct taggcttccc tggtcccaa 60  
 gaagtacgcc gtatcctttt tgtgaacttc ttcttctgt acgcagtgc agtgatggga 120  
 aacacggtca tcatcgtcac tgtctgtgt gataaacatc tgcagtcccc catgtatttt 180  
 ttcttgggac acctctgtgt cctggagatc ctgatcacat ccaccgctgc cccttttatg 240  
 ctgggggggt gctgcttcca agcaccacaga tcatgtcttt gacagcctgt gctgcacagc 300  
 tatatacctt tctttgggta cctcggagtt ggcattaatg ggagtgtggt ctgtggacca 360  
 ttatgtggct gtgtgttaacc ctttgaggta caacatcatt atgaacagca gcacatgtgt 420  
 ctggatggtc attgtatcat ggggtgtttg gttccttttt caaatctggc cagtttatgc 480  
 cacttttcag cttactttct gcaaatcaaa tgtgttagat catttttact gtgactgagg 540  
 acaattgtc aaggtatcct gtgaggacac tcttttcaca gagtttatc tttttcta 600  
 ggctgttttc attatcattg gttccttttg tccctacgat tgtctcctac acctacatca 660  
 tctccaccat cctcaagatc ccgttagcct ctggctggag gaaatccttt tccacttgtg 720  
 cctcccaact cacctgtgtt gtgatcggct acagcagctg cttgtttctc tacacgaaac 780  
 ccaagcaaac acaggcagcc aagtataacc ggatagcgtc actgctgggt ttagtgggtga 840  
 ccccttttct gaacccttct atcttcaccc tgaggaatga caaattcata caggcctttg 900  
 gagatggcat gaaacactgc tatcaactcc tcagaatt 938

<210> 719

<211> 942

<212> DNA

<213> Unknown (H38g568 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 719

atataaatgg	ctgacagaaa	tgtcactgtg	ataactgaat	tcatacctcct	ggggttgact	60
gataaccctg	aaatgaatgt	tgtcctttct	gtgctctttc	tattaatcta	tctcattact	120
gtcttgggca	acttttggat	tatcataata	attctggcta	gtgcccaact	ccattcaccc	180
atgtactttt	tccttagcca	gttggctttc	ttagatttct	gctattcttc	agtcttgatt	240
cctaaatgt	tggatgaatta	catagcagga	cagaaagtca	tctcttatca	cggttgcttc	300
cttcagtatt	cctttgtcag	cttgttcctg	actactgaat	gcttcctcct	ggctgccatg	360
gcatgtgatc	ggatctctgc	tgtttgccac	ccacttcact	acaaaggtct	catgactcct	420
actttctgaa	tctatttggg	gactgtttct	tacctgctgg	gctctgtaaa	ctccctcacc	480
cacctgagta	gcttactcag	tttgtctttc	tgtgggtcca	atgttatcaa	ccgttatctc	540
tgtgacattc	cattgctctt	ccaactctcc	tgttccaaca	cccaacacag	taagatttta	600
tttactgtcc	tttctggagc	aacatcagtg	actacctttt	tgatagtggg	tagttcctat	660
ctggtaatcc	tactcattgt	cctgaagata	cattccacca	ggggcagaaa	taaagccata	720
tccacatgtg	cctccacact	aatggtagtg	actctcttct	acagaacagt	gatatttact	780
tatctgggag	ccaaccctgg	atactcacag	gatagaccca	aaattctgcc	tgtggagtgc	840
acacttttgt	tgtcaatact	aaatcttcta	atatatagcg	tgagaaacag	agaagtcaaa	900
gaagccataa	aaataattat	taagagaaaa	atacttcttc	ag		942

&lt;210&gt; 720

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g569 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 720

atgttgatga	attactctag	tgccactgaa	ttttatctcc	ttggcttccc	tggtctgtaa	60
gaactacatc	atatcctttt	tgctatatcc	ttctttttct	acttggtgac	attaatggga	120
aacacagtc	tcatacatgat	tgtctgtgtg	gataaacgtc	tgcatgcccc	catgtatttc	180
ttcctcggcc	acctctctgc	cctggagatc	ctgggcacaa	ccataatcgt	ccccgtgatg	240
ctttggggat	tgctgtctcc	tggtgatgcag	acaatatatt	tgtctgcctg	tggtgtccag	300
ctcttcttgt	accttgctgt	ggggacaaca	gagttcgcat	tacttggagc	aatggctgtg	360
gaccgttatg	tggtctgtctg	taaccctctg	aggtacaaca	tcattatgaa	cagacacacc	420
tgcaactttg	tggttcttgt	gtcatgggtg	tttgggtttc	tttttcaaat	ctggccggtc	480
tatgtcatgt	ttcagcttac	ttactgcaaa	tcaaatgtgg	tgaacaattt	tttttgtgac	540
cgagggcaat	tgctcaaaact	atcctgcaat	aatactcttt	tcacggagtt	tatcctcttc	600
ttaatggctg	tttttgttct	ctttgggtct	ttgatcccta	caattgtctc	caacgcctac	660
atcatctcca	ccattctcaa	gatcccgtea	tcctctggcc	ggaggaaatc	cttctccact	720
tgtgcctccc	acttcacctg	tggtgtgatt	ggctacggca	gctgcttgtt	tctctacgtg	780
aaaccgaagc	aaacgcaggc	agctgattac	aattgggtag	tttccctgat	ggtttcagta	840
gtaactcctt	tcctcaatcc	tttcatcttc	accctccgga	atgataaagt	catagaggcc	900
cttcgggatg	gggtgaaacg	ctgctgtcaa	ctattcagga	at		942

&lt;210&gt; 721

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g570 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 721

atgatgggta	gaaggaatga	cacaaatgtg	gctgacttca	tccttacggg	actgtcagac	60
tctgaagagg	tccagatggc	tctgtttatg	ctattttctc	tcataacact	aattactatg	120
ctggggaatg	tggggatgct	attgataatc	cgctgggacc	tccagcttca	cactcccatg	180
tattttttcc	ttactcacct	gtcatttatt	gacctcagtt	actcaactgt	cgtcacacct	240
aaaacccttag	cgaacttact	gacttccaac	tatatcttct	tcacgggctg	ctttgccag	300
atgtttctgtt	ttgtcttctt	gggtactgct	gaatgttata	ttctctcttc	aatggcctat	360

gacgcgatg	cagcgatctg	cagtcctcta	cactacacag	ttattatgcc	caaaaggctc	420
tgccctcgctc	tcatacactgg	gccttatgtg	attggcttta	tggaactcctt	tgtcaatgtg	480
gtttccatga	gcagattgca	tttctgtgac	tcaaacataa	ttcatcactt	tttctgtgac	540
acttccccaa	tttttagctct	gtcctgcact	gacacagaca	acactgaaat	gctgatattc	600
attatcgctg	gttccaccct	gatgggtgcc	cttatcacaa	tatctgcata	ctatgtgtcc	660
attctctcta	ccatcctgaa	aattaattcc	acttcaggaa	agcagaaagc	tttctctact	720
tgcgctctctc	atctcttggg	agtcaccatc	ttctatggaa	ctatgatttt	tacttactta	780
aagccaagaa	agtcttattc	cttgggaaga	gatcaagtgg	ctcctgtgtt	ttatactatt	840
gtgattccca	tgctgaatcc	actcatttat	agtcttagaa	acagagaagt	gaaaaatgct	900
ctcattagag	tcatagcagag	aagacaggac	tccagg			936

&lt;210&gt; 722

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g571 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 722

atgtcatgat	gaattttctg	cctgccaaaa	ataatcatta	ctttattgca	gtaggagtgg	60
gatgctttta	atttagagac	acgggttttt	ctggaagagg	acttcccatg	tggaattcagc	120
ttgtggattg	tacgtcaatt	gtcttttttc	ttggaaataa	attaatttgc	tcatttataaa	180
aaatgatgca	ggaagcatat	gagtactttt	tctctgagca	acttggcttt	tttaagtttct	240
gttatgcttc	agtcattaca	tccaaaatgt	ttggaagtgt	cttgtacaaa	caaaaaaaat	300
taaccttcaa	tgacatagag	ctgctctctc	accttcatga	ccaccgagtg	cttgccttag	360
ctttcatggc	ctgtgatcaa	tacctgggtca	tttgtaatcc	tcctttgtat	atggtcacca	420
tgtccccccc	gcaaggagtc	tgcatcagc	ttatgcctgc	ctcctatagc	tatagcttcc	480
tgatgacact	ttcacattat	cctcagcctt	tgtctcccct	attgccccctc	tgtatcattg	540
atgttcaatg	gaagcctgtt	ccttatgtac	ttaatgtcca	gaaaattctc	ttgacacaga	600
caggatggcc	tctgtcttct	acacagtagt	cattcccatg	ttgagccctt	tgatctggag	660
cctcaggaac	aaggatgtga	aagatgcctt	gaggaaagtc	attgtcaaca	gaaaccaggc	720
attattttgt						730

&lt;210&gt; 723

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g572 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 723

atggctctctg	aaaatttcac	cagggtcact	gagtttatcc	tcacaggtgt	ctctagctgt	60
ccagagctcc	agattcccct	cttccctggc	ttcctagtgc	tctatgtgct	gaccatggca	120
gggaacctgg	gcatacatc	cctcaccagt	gttgactctc	gacttcaaac	ccccatgtac	180
tttttctctga	gacatctagc	tatcatcaat	cttggcaact	ctactgtcat	tgcccctaaa	240
atgctgatga	acttttttagt	aaagaagaaa	actacctcat	tctatgaatg	tgccacccaa	300
ctgggagggt	tcttgttctt	tattgtatcg	gaggtaatga	tgctggctgt	gatggcctat	360
gaccgctatg	tggccatttg	taaccctctg	ctctacatgg	tggtgggtgc	tcggcggctc	420
tgcctctctgc	tggtgtccct	cacgtacctc	tatggctttt	ctacagctat	tgtggtttca	480
ccttgatat	tctctgtgtc	ttattgctct	tctaataata	tcaatcattt	ttactgtgat	540
attgcacctc	tgtagcatt	atcttgctct	gatacttaca	taccagaaac	aatagtcttt	600
atatctgcag	caacaaattt	gtttttttcc	atgattacag	ttctagtatc	ttattttcaat	660
attgttttgt	ccattctaag	gatacgttca	ccagaaggaa	ggaaaaaagc	cttttccacc	720
tgcgcttcgc	atatgatagc	agtcacggtt	ttctatggga	caatgctatt	tatgtatttg	780
cagccccaaa	ccaaccactc	actggatact	gataagatgg	cttctgtgtt	ttacacattg	840
gtgattccta	tgctgaatcc	cttgatctac	agcctgagga	ataatgatgt	aaatgttgcc	900
ttaaagaaat	tcatggaaaa	tccatgttac	tccttt			936

&lt;210&gt; 724

<211> 481  
 <212> DNA  
 <213> Unknown (H38g573 nucleotide)

<220>  
 <223> Synthetic construct

<400> 724  
 atatgtggga gtcacagtgg tgttactgaa ttttgtctct taggcttccc tggctcccag 60  
 taagtatgcc atttgttacc ttcttccttt gtcagtgatt gtaataagaa attatgtaat 120  
 catcatagta tgtgttgaga aatgcctgct gtctctccta tatttattct atgggtgacct 180  
 ctctgtcatg gaaatcctta tcacatatac tgcgtgttccc ttgatgctca ggggttggtta 240  
 ctttccatga ttcaaacaat acctttaatg acatgtgctg tccaactcta tatgaacttt 300  
 tttgggggta cacaaaattt gcattactgg gagtgatgac tgtgaacctat tatgtggctc 360  
 tctgtaactc tttgaagtaa aacatcatta tgagcagaca cactgcatct ggctggtaat 420  
 tgtattattg attgggttcc tttctgaaat ctgggtcagtc tatgccacat ttcagctccc 480  
 t 481

<210> 725  
 <211> 971  
 <212> DNA  
 <213> Unknown (H38g574 nucleotide)

<220>  
 <223> Synthetic construct

<400> 725  
 cacacagagc cacggaatct cacaggtgtc tgagaattcc tctcctggg actctcagag 60  
 gatccagaac tgcagccggt cctcgctttg ctgtccctgt ccctgtccat gtatctggctc 120  
 acgggtgctga ggaacctcct cagtatcctg gctgtcagct ctgactcccc cctccacacc 180  
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcgggttcac ctgggccatg 240  
 gttcccaaga tgattgtgga catgcagtcg catagcagag tcatctctca tgagggtgc 300  
 ctgacacaga tgtttttctt ggctcctttt gcatgtatag aaggcatgat cctgactgtg 360  
 atggcctatg actgctttgt agccatctgt cgcctctga attaccctagt catcgtgaat 420  
 cctcacctct gtgtcttctt cattttgatg tctttttcc ttagcctgtt ggattcccag 480  
 ctgcacagtt ggattgtgtt acaattcaca atcatcaaga atgtggaaat ctctaatttt 540  
 gtctgtgacc cctctcaact tctcaaactt gcctgttctg acagcgtcat caatagcata 600  
 ttcacataat tccatagtag tatgtttgct tttcttccca tttcagcaat ccttttatct 660  
 tactataaaa tgcacacctc cattctcagg atttcatctt cagatgggaa gtataaagcc 720  
 ttctccacct gtgactctca cctagcagtt gtttgctgat tttatggaac agacattggg 780  
 atgtacctga cttcagctgt gtcaccacct cccaggaatg gtgtagtggc gtcaatgatg 840  
 tacgctgtgg tcacccccat gctgaacctt ttcattctaca gcctgagaaa cagggacata 900  
 caaagtgcct tgcggaggct gcgcagcaga acagtcgaat ctcatgatct gttccatcct 960  
 ttttcttgtg t 971

<210> 726  
 <211> 960  
 <212> DNA  
 <213> Unknown (H38g575 nucleotide)

<220>  
 <223> Synthetic construct

<400> 726  
 cacacaaagc cacggaatct cacaggtgtc tgagaattcc tctcctggg actctcagag 60  
 gatccagaac tgcagcccat cctggctggg ctgtccctgt ccatgtatct ggtcacggtg 120  
 ctgaggaacc tgctcatcat cctggctgtc agctctgact cccacctcca cactcccatg 180  
 tgcttcttcc tctccaacct gtgctgggct gacatcggtt tcacctcggc cacggttcct 240  
 aagatgattg tggacatgca tgcgcatagc agagtcatct cttatgaggg ctgcctgaca 300  
 aggatgtctt tcttggctct ttttgcagtg acagaagaca tgcttctgac tgtgatggcc 360  
 tatgactgct ttgtagccat ctgtcgccct ctgcactacc cagtcacgtg gaatcctcac 420

```

ctctgtgtct ttttcatttt ggtgtccttt ttccttagcc tgttggtatc ccagctgcac 480
agtttaggttg tattacaatt caccttcttc aataatgtgg aaatctctaa ttttgtctgt 540
gagccatctc aacttgtcaa ccttgccagt tctgacagcg tcgtcaatag catattcata 600
tatttcgata gtactatgtt tggttttctt cccatttttag gggtcctttt gtctcactat 660
aaaattgtcc cctccattct aaggatttca tcgtcagatg ggaagtataa agtcttcgct 720
acctgtggct ctcacctggc agttgtttgc tgatttgatg gaacaggcat tgacatgtac 780
ctgacttcag ctgtgtcacc accccacagg aatgggtgtgg tggcatcagt gatgtatget 840
gttttcaccc ccatgctgaa ccctttcatc tacagcctga gaaacaggga catacaaagt 900
gccctgcgga ggctgctcag cagaacagtc gaatctcatg atctgttcca tccctttttct 960

```

&lt;210&gt; 727

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g576 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 727

```

gtctccctca tcacctacct gatcacagtg atgagcaacc tgggcatgaa tattttgacc 60
aaactagact cccacctata cacacctgtt gtatatTTTT taatcaaaca catatttttc 120
attgattttt acaattgtat tgttatttac accaataaaa tgttaaattt tgttggtgat 180
cagaataaca ttctctatta tgcattgtgc acacatatga ctttcttatg ttcattatca 240
ctgaactttt aatcttggta agcatggcct atgattgcta tgtgggtgaa tccaaccctt 300
tgtttttacat tgttatcatg tgtctgtgac tgtaacatgt gctgatgagc attccatacc 360
tctgtaatac atttcaatct ctaattatca caatgacctt tttttgacct tctgtagctt 420
tatcatcagt catttctatt gttatgatgt tctcttcttc catatgctat gctcaaatgc 480
acaggaaaga gaattgttga tcacactgct tacagcattt aatttgatcc ctacctcctg 540
gtattgctag tgttaaacad tctgattttg ttagccatat gttgaatgca ttctgcaactg 600
ggcaggaaaa aagcttttct catgtgtggt tctcatctta caatgggtgt tatgttctat 660
ggatctctac tttttgatat ggataaatgg cctccttgtt ctacacttta atgacctca 720
ggtttaacct cttgatctac agcttttagc acttaggggt taaaaatgtc ttttatagag 780
tctttaagaa ttagtgcaaa ctttgt

```

&lt;210&gt; 728

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g577 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 728

```

atgggaggca agcagccctg ggtcacagaa ttcctcctgg tgggattcca gctctgtgca 60
gagatggaga tctttctctc ttgcactctc tcgcgatttt atgccttcag tctactgagg 120
aatggcatga acatgggact cacctatctg gatgacagag acgacagact acacaccctc 180
atatacattt tctcttcaca cctggccatc aatgacatgt actatgcttc caacaatgtt 240
ccaaagaggc aggtgaacca aatgaaccag aaaaaaaaaa actttgttct atggataaag 300
cagatatttt tgtatttggc ttttgtcac acagagtgc taatttaggc aatgatgtcc 360
tgtaatagat atgtggcaat ctgc

```

&lt;210&gt; 729

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g578 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 729

```

atgggccaac acaatctaac agtgctaact gaattcattc tgatggaact cacaaggcgg 60

```

```

cctgagctgc agattcccct ttttggagtc ttctctgca tctacctaata cacagtgggtg 120
ggcaacctaa ctatgatcat tttgacaaa ctggactccc acttacatac acctatgtac 180
ttttctatca gacatttggc ttctgttgat ctgggtaatt ctactgtcat ttgtcccaag 240
gtgctggcaa attttgttgt ggatcgaaat actatttcct attatgcatg tgctgcacag 300
ctggcattct tccttatgtt cattatcagt gaatttttca tcctgtcagc catggcctat 360
gaccgctatg tggccatttg taaccctctg ctctattatg ttattatgtc tcagcgactg 420
tgtcatgtac tgggtgggcat tcaatatctc tacagcacat ttcaggctct gatgttctact 480
attaagattt ttacattgac cttctgtggc tctaattgtca tcagtcattt ttactgtgat 540
gatgttccct tgctacctat gctttgtcga aatgcacagg aaatagaatt gttgagcata 600
ctattttctg tatttaattt gatctcctcc tttctgatag tcttagtgtc ctacatgttg 660
atthttgttag ctatatgtca aatgcattct gcagagggca ggaaaaaggc tttctccaca 720
tgtggttccc atttgacagt ggtgggtgtg ttctatgggt ctctactctt catgtacatg 780
cagcccaatt ccactcactt ctttgatact gataaaatgg cttctgtgtt ttacacttta 840
gtaatcccca tgcttaaccc tttgatttac agcttaagaa acgaagaggt gaaaaatgcc 900
ttctataagc tctttgagaa t 921

```

&lt;210&gt; 730

&lt;211&gt; 654

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g579 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 730

```

ttgcctgaca tcagttttcac ctccaccaca gtccccaaga tgattgtgga catccaatct 60
cacagcagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgtcattttt 120
ggaggcatgg aagagaggca tgctcctgag tgtgatggcc tatgactggg ttgtagccat 180
ctgtcaccct ctatatcatt cagccatcat gaaccctgtt ttctgtggct tcctagtttt 240
gttgtctttt tttttctcag tcttttagat gccagctgc acaacttgat tgccttaca 300
gtgacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaactcccc 360
catcttgcat gttgtgacac cttcaccatt aacataatca tgtatttccc tgccgccata 420
tttggttttc tcccatctc ggggacctt ttctctact ctaaaattgt ttctccatt 480
ctgagggttt catcgtcagg tgggaggtat aaagccctct ccacctgtgg gtctcacgtg 540
tcagttgttt gctgagtta tggacaggc gttggagggt acctcagttc ggatgtgtca 600
ttttcccca gaaagggtgc agtggcctca gtgatgtacg cggttgtcac cccc 654

```

&lt;210&gt; 731

&lt;211&gt; 683

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g580 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 731

```

atgtacttct tcttctccaa cctgtccttg cctgacgacg gtttcacctc caccacggtc 60
cccaaagatg attgtggaca tccagtctca cagcagagtc acctcctatg caggctgcct 120
gactcagatg tctctctttg ccatttttgg aggcattgaa gagagacatg ctctgtagt 180
tgatggccta tgaccggttt gtagccatct gtcacctct atgtcattca gccatcacga 240
acctgtgttt ctgtggcttt ctagtgttgt tgtctttttt ttttctcagt ctttttagacg 300
cccagctgca caacttgatt gccttaca aaagcctgct caaggatgtg gaaattccta 360
atttctctg tgaccttct caattcccc gtcttgcatg ttgtggcacc ttcaccaata 420
acataatcat gtatttccct gcagccatat ttggttttct tcccatctcg gggacctttt 480
tctcttacga taaaattgtt ttctccattc tgagggtttc atcatcagggt gggaagcata 540
aggccttctc caccagggg tctcacctgt cagttgtttg ctgattttat ggaacaggca 600
ttggaggcta cctcagttca gatgtgtcat cttccccgag aaaggctgca gtggcctcag 660
tgatgtacac ggtggccatc ccc 683

```

&lt;210&gt; 732

&lt;211&gt; 582



&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g581 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 732

tactttttcc	tctccaacct	ctccttcttg	gacctctgtt	tcaccataag	ttgtgtcccc	60
gggatgctgg	tcaacctctg	ggagccaaag	aagaccatca	tcttactggg	ctgctctgtc	120
cagttcttca	tcttctctgt	cctggggacc	actgagtga	tcctcctgac	ggtgatggcc	180
tttgaccgct	acatggctat	ctgccagccc	ctccactatg	ccaccatcgt	ccaccctctg	240
ctgtgctggc	agctggcctc	tgtggcctgg	gtcatgagtc	tggtagagtc	agtgggtccag	300
acaccatcca	ccctccactt	gcctttctgc	cccgatcggc	aggtggatga	ttttgtctgt	360
gaggtcccag	ctctaattcg	actctcctgt	gaagacacct	cctacaatga	aatccagttg	420
gctgttgcca	gtgtcttcat	cttggctgtg	cctctcagcc	tcacccctgt	ctcttatgga	480
gccattgcct	gggcagtgtc	aaggactaac	tctgcaaaag	ggcagaggaa	agcttttggg	540
acctgctcct	cccctctcac	tgtggtcacc	ctcttctaca	gc		582

&lt;210&gt; 733

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g582 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 733

atggtcagtt	ccaatcagac	ctccccctgtg	ctggggttcc	ttctcctggg	gctctctgcc	60
catccaaagc	tggagaagac	attcttctgtg	ctcatcctgc	tgatgtacct	ggtgatccta	120
ctgggcaatg	gggtcctcat	cctggtgacc	atccttgact	cccgcctgga	cacaccatg	180
tacttcttcc	tggggaacct	ctccttctctg	gacatctgct	atacaacctc	ctcatccttg	240
acagcttcct	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagta	cagatgttcc	300
tctcccttgc	catggggagcc	acagagtgtg	ttctcctgag	catgatggcg	tttgatcgct	360
acgtggccat	ctgcaacccc	ctttgggtacc	ctgaagtcac	gaacaaagct	acttatgtgc	420
ccatggctgc	tggctcctgg	gtagctggaa	gcctcactgc	catggtgcag	acacccttg	480
cattgaggct	gcccttctgt	ggagacaaca	tcacatca	cttcacctgt	gagattctgg	540
ctgtcctgaa	gttggcctgt	gctgatattc	ctgtcaatgt	gatcagtatg	ggagtggcca	600
atgtgatctt	cctggggggtc	cctgttctgt	tcattctctt	ctcctatgtc	ttcatcattg	660
ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	acctgctctg	720
cccacctcac	tgctgtgac	gtcttctacg	ggaccatcct	cttcatgtac	gggaagccca	780
agtctaagga	ccactggga	gcagacaaac	aggaccttgc	agacaaactc	atttcccttt	840
tctatggggt	ggtgaccccc	atgctcaacc	ccatcatcta	cagcctgagg	aacaagggaag	900
tgaaggctgc	tgtgaggaac	ctggtatttc	agaaacgctt	cctgcagtga	tggtggagg	959

&lt;210&gt; 734

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g583 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 734

atggtaagtg	ccaatcagac	agcctctgtg	accgagttta	ttctcctggg	cctctctgcc	60
cacccaaagc	tggagaaaac	gttctttgtg	ctcatcctgc	tgatgtacct	ggtgatccta	120
ctgggcaatg	gggtcctcat	cctgatgact	gtgtccaact	cccacctgca	catgccatg	180
tacttcttcc	tggggaacct	ctccttctctg	gacatctgct	atacaacata	ctcagtcctc	240
ctcatccttg	acagcttctt	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagtg	300
cagatgttcc	tctcctttgc	catggggagcc	acagagtgtg	ttctcctgag	catgatggcg	360
tttgatcgct	acgtggccat	ctgcaacccc	cttaggtacc	ctgtgggtcat	gagcaaggct	420
gcctacatgc	ccatggctgt	cggctcctgg	gtagctggaa	gcactgcttc	catggtgcag	480

acatcccttg	caatgagget	gcccttctgt	ggagacaaca	tcatcaatca	cttcacctgt	540
gagattcttg	ctgtccagaa	gttggcctgt	gctgatatct	ctgtcaatgt	gatcagtatg	600
ggagtgacca	atgtgatctt	cctgggggtc	ccggttctgt	tcatctcttt	ctcctatgtc	660
ttcatcattg	ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	720
acctgctctg	cccacctcac	agtcgtgggtc	atcttctatg	ggaccatcct	cttcagtgtat	780
gggaagccca	agtctaagga	cccgtggggg	gcagacaagc	aagactttgc	agacaaactc	840
atttcccttt	tctatgggtt	ggtgaccccc	atgctcaacc	ccatcatcta	cagcctgagg	900
aacaaggatg	taaaggctgc	tgtgagggtc	ttgatatttc	agaaatgctt	tgcc	954

&lt;210&gt; 735

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g584 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 735

atgaacaggt	ccaatgaggc	ctcccctgtg	ttgggggttcg	ttctcctggg	cctctctgcc	60
cacccatagc	tggagaagac	attctttgtg	ttcatcctgc	tgggtgtacct	ggtgatcctg	120
ctgggcaacg	gggtcctcat	cctggtgacc	atccttgact	ccgcctgca	cacacccatg	180
tactttctcc	tggggaacct	ctccttctctg	gacatctgct	atacaacctc	ctcatccttg	240
acagcttcct	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagta	cagatgttcc	300
tctcctttgc	catgggagcc	acagagtgtg	ttctcctgag	catgatggct	tttgatcact	360
acctggacat	gtgcaacccc	cttaggtacc	ctgtggtcac	gagcaaggct	gcctacatgc	420
ccatggctgt	tggctcctgg	gcagctggta	tcaccaacte	tgtagtacag	atatccctag	480
caatgtgact	gcccttctgt	ggggacaatg	tcataaatca	cttcacctgt	gagatcctgg	540
cagttctaaa	gttggcctgt	gctgacatct	gcatcaacgt	gatcagcatg	gttgtgacca	600
acatgatctt	ccttgcaactc	ccagtcctgt	ttatttttgt	ctcatatgtc	ttcatcattg	660
ccaccatcct	gagaatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	acctgctctg	720
cccacctcac	tgctgtgac	gtcttctatg	ggatgatcct	cttcagtgtat	gggaagccca	780
agtctaagga	cccaatggga	gcagacaaac	aggaccttgc	agacaaactc	atctccattt	840
tctatggagt	ggtgaccccc	attctcaacc	ccatcatcta	cagcccagg	aacaaagatt	900
tgaagctgc	tatgaggaac	ctgggtggctc	aaaaacacct	aacagagtga	ctatcacaga	960
tc						962

&lt;210&gt; 736

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g585 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 736

agactaaatg	tcatcagtca	cctgcccttc	tatggggaca	tcatcaacca	cttgacctgt	60
gaggtcctgg	ctgtcctgaa	gttggcctgt	gctgacatct	ctatcaacat	gatcaggcaa	120
aaggccttct	ccacctgtc	tgcccacctc	acagttgtgg	tcatcttcta	caggaccatc	180
ctcttcacgc	atgggaagcc	caagtcgaag	gacccactgg	gggcagacaa	gcaggatttt	240
gcagacaaac	tcatctccct	ctcctatgga	gtggtcaccc	ccatgctgaa	caccatcatc	300
tacagcctga	ggaaaaaggg	tgtgaaggct	gctgtgaaga	acctggtatt	tcagaaaccc	360
ctaactgaat	gacag					375

&lt;210&gt; 737

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g586 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 737

tttggtgaca	tgggtttaac	gtcctccaca	gttaccaaga	tgctggtgaa	tatacagact	60
cggcatcaca	ccatcaccta	tacgggttgc	ctcacgcaaa	tgtatttctt	tctgatgttt	120
ggtgatctag	acagcttctt	cctggctgcc	atggcgtatg	accgctatgt	ggccatctgc	180
cacccctct	gctactccac	ggtcagtagg	ccccaaagtct	gtgccctaata	gcttgcatgt	240
tgctgggtcc	tcaccaatat	cggtgccctg	actcacacgt	tcctcatggc	tcggttgctc	300
ttctgtgtga	ctggggaaat	tgctcacttt	ttctgtgaca	tcactcctgt	cctgaagctg	360
tcatgttctg	acaccacat	caacgagatg	atgggtttttg	tcttgggagg	caccgtactc	420
atcgtccct	ttttatgcat	tgtcacctcc	tacatccaca	ttgtgccagc	tatcctgagg	480
gtccgaaccc	gtggtgggg	gggcaaggcc	ttttccacct	gcagttccca	cctctgcgtt	540
gtttgtgtgt	tctatgggac	cctcttcagt	gcctacctgt	gtcctccctc	cattgcctct	600
gaagagaagg	acattgcagc	agctgcaatg	tacaccatag	tgactccc		648

&lt;210&gt; 738

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g587 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 738

atggaaaaag	ccaatgagac	ctcccctgtg	atgggggttcg	ttctcctgag	gctctctgcc	60
cacccagagc	tggaaaagac	attcttctgt	ctcatcctgc	tgatgtacct	cgtgatcctg	120
ctgggcaatg	gggtctctcat	cctgggtgacc	atccttgact	cccgcctgca	cacgcccattg	180
tacttcttcc	tagggaaacct	ctccttccctg	gacatctgct	tcactacctc	ctcagtccca	240
ctggctcctg	acagcttttt	gactccccag	gaaaccatct	ccttctcagc	ctgtgctgtg	300
cagatggcac	tctcctttgc	catggcagga	acagagtgtc	tgctcctgag	catgatggca	360
tttgatcgct	atgtggccat	ctgcaacccc	cttaggtact	ccgtgatcat	gagcaaggct	420
gcctacatgc	ccatggctgc	cagctcctgg	gctattgggtg	gtgctgcttc	cgtgggtacac	480
acatccttgg	caattcagct	gcccttctgt	ggagacaatg	tcatcaacca	cttcacctgt	540
gagattctgg	ctgttctaaa	gttggcctgt	gctgacattt	ccatcaatgt	gatcagcatg	600
gaggtgacga	atgtgatctt	cctaggagtc	ccgggttctgt	tcatctcttt	ctcctatgtc	660
ttcatcatca	ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggtcttctcc	720
acctgctctg	cccacctcac	cgtgggtgatc	gtcttctacg	ggaccttatt	cttcatgtat	780
gggaagccta	agtctaagga	ctccatggga	gcagacaaag	aggatctttc	agacaaactc	840
atcccccttt	tctatgggg	ggtgaccccg	atgctcaacc	ccatcatcta	tagcctgagg	900
aacaaggatg	tgaaggctgc	tgtgaggaga	ctgctgagac	caaaaggctt	cactcag	957

&lt;210&gt; 739

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g588 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 739

ctgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatagcc	tatgagcgg	ttgtagccat	180
ctgtcaccct	ctatatcatt	cagccatcat	gaacccatgt	ttctgtggct	ttctagtttt	240
gttgtctttt	tttttctcag	tcttttagac	gccagctgc	acaacttgat	tgctttacaa	300
aggacctgct	tcaaggatgt	ggaaattcct	aatttcttct	gtgaccttc	tcaactcccc	360
atcttgcata	ttgtggcacc	ttcaccaata	acataatcat	gtatttccct	gccgccaat	420
ttgggtttct	tcccatctcg	gggaccttt	tctcttacaa	taaaattggt	ttctccattc	480
taagggtttc	atcatcaggt	gggaagtata	aggccttctc	cacctgtggg	tctcacctgt	540
cagttgtttg	ctgattttat	ggaacaggca	ttggaggcta	cctcggttca	gatgtgtcat	600
cttccccgag	aaaggctgca	gtggcctcag	tgatgtacac	ggtgggtcatc	ccc	653

&lt;210&gt; 740

<211> 648  
 <212> DNA  
 <213> Unknown (H38g589 nucleotide)

<220>  
 <223> Synthetic construct

<400> 740  
 tttgtggatg tctgcttctc ctctaccact gtccctaaag ttctggccaa ccatatactt 60  
 gggagtcagg ccatttcctt ctctgggtgt ctcaccacgc tgtattttct cgctgtgtgt 120  
 ggtaacatgg acaatttcct gctgggtgtg atgtcctatg accgatttgt ggccatatgc 180  
 caccctttac actacacaac aaagatgacc cgacagctct gtgtcctgct tgttgtgggg 240  
 tcatgggttg tagccaacat gaattgtctg ttgcacatac tgctcatggc tcgactctcc 300  
 ttctgtgcag acaacatgat cccccacttc ttctgtgatg gaactcccct cctgaaactc 360  
 tcctgtctcag acacacatct caatgagctg atgattctta cagagggagc tgtggtcatg 420  
 gtcaccccat ttgtctgcat cctcatctcc tacatccaca tcacctgtgc tgtcctcaga 480  
 gtctcatccc ccaggggagg atggaaatcc ttctccacct gtggctccca cctggctgtg 540  
 gtctgcctct tctatggcac cgtcatcgtc gtgtatttca acccatcatc ctctcactta 600  
 gctgggaggg acatggcagc tgcagtgtg tatccagtgg tgacccca 648

<210> 741  
 <211> 988  
 <212> DNA  
 <213> Unknown (H38g590 nucleotide)

<220>  
 <223> Synthetic construct

<400> 741  
 atggcagaag aaaataagat tctgggtgact cactttgtcc tcacaggact cacagatcat 60  
 ccagggctgc aggcgccctt gttcctgggtg ttcttgggtca tctacctcat caccctgggtg 120  
 ggcaaccttg gcctgatggc tctcatctgg aaggaccccc accttcacac ccccatatac 180  
 ttatttcttg gcagtttagc ctttgcagat gcatgcactt catcctctgt aacttctaag 240  
 atgcttatca atttttttat caaagaatca tatgctatcc atggctaagt gtgccaccca 300  
 gttttacttt tttggttcca atgcaaccac agaatgcttc ctgctggtag tgatggccta 360  
 tgaccgctat gtagccatat gcaatccctt gctttatcca gtggtgatgt ccaatagcct 420  
 ctgtactcag tttataggta tttcatattt tattggtttt ctgcattcag cgattcatgt 480  
 gggtttggta tttagattaa ctttctgcag gtccaatatt atacattatt tctactgtga 540  
 aattttacag ctgttcaaaa tttcttgac caatcctaca gttaatatac ttctgatttt 600  
 catcttttca gcatttatac aagtcttcac ttttatgact cttatcgtct cttactccta 660  
 tattctctct gccatcctga aaaagaagtc tgagaagggt agaagcaaag ccttctctac 720  
 ttgcagtgcc catctgctct ctgtctcttt gttctacggc accctcttct tcatgtatgt 780  
 gagttctagg tctggatcag ctgcagatca ggccaaaatg tattctttat ttacacaat 840  
 aataattcct ttactaaatc cttttattta cagcctaagg aacaaagagg ttatagatgc 900  
 cctgagaaga atcatgaaga aataaatagt tgtcagacaa cattcaaacc atttcttctt 960  
 tatattctgc tgaagaaaac cccaagtc 988

<210> 742  
 <211> 636  
 <212> DNA  
 <213> Unknown (H38g591 nucleotide)

<220>  
 <223> Synthetic construct

<400> 742  
 tgtcactccc agggtcacgg ctagcagggc taggttactt agagggtagg aggctaagtt 60  
 cctcgtaaca tgcttgtgct gctcagatgt tcttttttgt agccttggcc acagtggaaa 120  
 atatcgctgt tgacatcaat ggcctatgac cactatatag cagtgtgcaa acccctacac 180  
 tacactacca ccacgatagc cagtgtatgt gctcatctgg tcataggctc ctatgtctgt 240  
 ggctttctaa atgcctccct ccgcattgtg gacatattca gtctctcttt ctgtaagtcc 300

aatcttgtcc atcacctttt ctgtgatgtt ccaccagtca tggetgtgtc ttgctctggt	360
aaacacatta gcaagaagat tctgggtttt atgtcaagct tcaatgtctt tttggctctt	420
ctagttatct tgacctccta cctgttcata ttcatcacca tcttgaagat gcaactcagct	480
cagggaact taaaagcttt gtccacctgt gcctctcacc tcattgcagt ctccatcttc	540
tatggaacta ctatctttat gtacttacag cctagctcca gccattccat ggacacagat	600
gaaatggcat ccttgttcta tgetgtgttc atctcc	636

&lt;210&gt; 743

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g592 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 743

atgggggaca accaatcacg ggtcacagaa ttcatcctgg ttggattcca gctcagtgtg	60
gagatggaag tgctcctctt ctggatcttc tccctgttat atctcttcag cctgctgggg	120
aatgggggtca tctttgggct catctgcctg gactctaagc ttcacacccc catgtacttc	180
ttcctctcac acctggccgt cattgacatg tcctatgctt ccaacaatgt tccaagatg	240
ctggcaaac tagtgaacca gaaaagaact atctcgttca tctcttgc ataatgcagact	300
ttttgtatt tggcttttgc tgttacagtg tgcttgattt tgggtggtgat gtcctatgac	360
agatttgtgg ccatctgcca tccctgcat tacactgtca tcatgagctg gagagtgtgc	420
actgtcctgg ctgtggcttc ctgggtgttc agcttcctcc tggctctggt ccatttagtt	480
ctcattctga ggctgccctt ctgtgggccc caggaggtga accacttctt cggtgaaatc	540
ctgtctgtcc tcaagttggc ctgtgctgac acctggctca accaggtggt catctttgca	600
gcctgcatgt tcatcctggt agggtgactc tgcctgggtc tggctctcta cttgcacatc	660
ctggcgccca tcttgaggat ccagtctggg gagggccgca gaaaggcctt ctctacctgc	720
tcctccacc tctgcgtggt ggggcttttc ttggcagcg ccattgtcat gtacatggcc	780
cccaagtcaa gccattctca agaacggagg aagatccttt cctgtttta cagccttttc	840
aaccgatcc tgaacccct catctacagc cttaggaatg cagaggtgaa aggggctcta	900
aagagagtcc tttggaaca gagatcaatt gaagaatcat tt	942

&lt;210&gt; 744

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g593 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 744

ttctctgacc tctgcttctc ttccgtgacc attcccaagt tgttacagaa catgcagaac	60
caggacccat ccatcccta tgccgactgc ctgacccaaa tgtacttctt cctgttattt	120
ggagacctgg agagcttctt ccttgtggcc atggcctatg accgctatgt ggccatctgc	180
ttccccctgc actacaccgc catcatgagc cccatgctct gtctcgccct ggtggcgctg	240
tcctgggtgc tgaccacctt ccatgccatg ttacacactt tactcatggc caggttgtgt	300
ttttgtgcag acaatgtgat cccccacttt ttctgtgata tgtctgctct gctgaagctg	360
gccttctctg aactcagat taatgaatgg gtgatattta tcatgggagg gctcattctt	420
gtcatcccat tctactcat ccttgggtcc tatgcaagaa ttgtctctc catcctcaag	480
gtcccttctt ctaagggtat ctgcaaggcc ttctctactt gtggctccca cctgtctgtg	540
gtgtcactgt tctatggaac cgttattggt ctctacttat gctcatcagc taatagttct	600
actctaaagg acactgtcat ggctatgatg tacactgtgg tgacccc	648

&lt;210&gt; 745

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g594 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 745

atggatggag	agaatcactc	agtgggtatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaacacatcc	tcattgtgtt	ttctgtgacc	actgacctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcgt	tgggtggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcttttcat	ttctggctgt	tgctgggacc	cttgggtgtca	gtcactccct	gttccaactg	480
gcatttcttg	ttaatttagc	cttctgtggc	cctaattgtgt	tggacagctt	ctactgtgac	540
cttcctcggc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggtcact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacgtcttc	660
atcctgttta	ctgtttggaa	acattcctca	gggtgttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacacgg	780
ccacacctta	attcacagat	ggacaagtgt	ctggctatgt	ttgatgcagt	tctcactcct	840
tttctgaaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagagg	atctca			936

&lt;210&gt; 746

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g595 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 746

atgaactcag	agaacctcac	ccggggccg	gttgccctg	ctgaattcgt	cctcctgggc	60
atcacaaatc	gctgggacct	gcgtgtggcc	ctcttcctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcattggatgc	ccgggtccac	180
acacctatgt	acttcttctc	ggccaacctc	tccctgtctg	atgcctgcta	ttcctccgcc	240
atcgccccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacacagcc	300
tgtgccctcc	agatgtttgt	ctttgcaggt	ctggctgata	ctgagtgttc	aatgcaatta	360
atgccaaaag	tgaacaaaaa	tgtat				384

&lt;210&gt; 747

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g596 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 747

atgaccattg	tcttgctttc	agctctggat	tcccggctgc	acacaccaat	gtatttcttt	60
ttggcaaac	tctcattcct	ggacatgtgt	ttcaccacag	gttccatccc	tcagatgttc	120
tacaaccttt	gggtccaga	taagaccatc	agctatgtgg	gttgtgccat	ccagctgtac	180
tttgcctcgg	ccctgggagg	ggtggagtgt	gtcctcctgg	ctgtcatggc	atatgaccgc	240
tatgctgcag	tctgcaaac	cctgcactac	accatcatca	tgcacccacg	tctctgtgga	300
cagctggctt	cagtggcatg	gctgagtggc	tttggaatt	ctctcataat	ggcaccaccg	360
acattgatgc	taccccgctg	tgggcacaga	cgagtggacc	actttctctg	tgagatgcca	420
gcactaattg	gtatggcctg	tgtagacacc	atgatgcttg	aggcactggc	ttttgccctg	480
gcaatcttta	tcactcctgg	accactcatc	ctcattctca	tttcttatgg	ttacgttgga	540
ggaacagtgc	ttaggatcaa	gtcagctgct	gggcgaaaga	aagccttcaa	cacttgcagc	600
tcgcatctaa	ttgttgtctc	tctcttctat	ggtacaatca	tatacatgta	cctccagcca	660
gcaaatactt	attcccagga	ccagggcaag	tttcttacct	ttttctacac	aattgtcact	720
cccagtgtta	acccctgat	ctatacacta	agaaacaaag	atgttaaaga	ggccatgaag	780
aagtgctag	ggaaggggag	tgcaaaata				810

&lt;210&gt; 748

<211> 342  
 <212> DNA  
 <213> Unknown (H38g597 nucleotide)

<220>  
 <223> Synthetic construct

<400> 748  
 atttgctttc ctctccacta tcccatccgt ataagcaaaa gagtgtgtgt gatgatgata 60  
 acaggatctt ggatgataag ctctatcaac tcttgtgctc acacagtata tgcactctgt 120  
 atcccatatt gcaagtccag agccatcaat cattttttct gtgatgttcc agctatgttg 180  
 acgctagcct gcacagacac ttgggtctat gagagcacag tgtttttgag cagcaccatc 240  
 tttcttgtgc ttcttttcac tggattgca tgttcctatg gccgggttct ccttgctgtc 300  
 taccgcatgc actctgcaga agggaggaag aaggcctatt ca 342

<210> 749  
 <211> 635  
 <212> DNA  
 <213> Unknown (H38g598 nucleotide)

<220>  
 <223> Synthetic construct

<400> 749  
 tttgtggaca ttgcctgttc ctcagccaca gcaccaaga tgattgtaga ctctgtttct 60  
 gagaaaaaga ctatttccta ctggggctgt ataactcaga tgtttacctt ccactttttt 120  
 ggttgtgctg acatttttgt ttgactgtc atggcttttg atcgctatgc tgctatctgc 180  
 caaccctcc gttacactgt catcatgagt gctaagtctt atactgtgct ggcactactg 240  
 tcctggttgg gggccctggg tcattccttt gtccagaccc tcctgacctt ccagctgccc 300  
 ttctgtaatg ctcaggttat agaccattac ttttgtgatg tccaccagt cctaaaactt 360  
 gccgtgctg atacaactct ggtaagtatg ttggtggtg ccaacagtgg tctcatctcc 420  
 ctgggtgtt tcctcattct ttggccctcc tacacagtca ttctgtttag tcttcaaaaa 480  
 cagtctgcag agagctgaca caaagtcttc tctacctgtg gatctcatct gactatagta 540  
 actttcttct ttgttccgtg tacctttatt tatctccatc cactactttc ccattggata 600  
 aagctgtgtc tgtgttctat accaccatca ccca 635

<210> 750  
 <211> 633  
 <212> DNA  
 <213> Unknown (H38g599 nucleotide)

<220>  
 <223> Synthetic construct

<400> 750  
 tttgttgatt tctgttatcc caccacaatt acacccaaac tgctggagaa cttggttgcg 60  
 gaagatagaa ctatctcctt cacaggatgc accatgcagt tattctttgt ctgcataattt 120  
 gtagtaacag aaacatgcat gctggcagt atggcctatg accgatatgt ggcggtgtgt 180  
 accctcttct ctacacagtt gcaatgtacc agaggctttg ctccttggtta gtggctacat 240  
 catactgctg ggggatagtc tgttccctga cacttaccta gtttctactg gagttatcct 300  
 tcagaggaaa taatatcatt aataactttg tctgtgagca cgctgccatt gttgctgtgt 360  
 cttgtctctga cccctgtgtg agccagtaga tcactttagt ttctgccaca ttcaatgaaa 420  
 taagcagcct gcttccatg ctttcatttt tatcactgtc atgaagacgg cttccactgg 480  
 ggggcgcaag aaagcgttct ccacgtctgc ctccactga cggccattac cattttccat 540  
 gggactattc ttttctcta ctgtgttct aacgccaaaa gttcgtggct catggtcaag 600  
 gtggcctctg gcttttacac agtggctcatg ccc 633

<210> 751  
 <211> 646  
 <212> DNA  
 <213> Unknown (H38g600 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 751

tttgtagaca	tctgtgttac	ctccaccaca	gtcccaaaga	cactgtcaaa	catccggaca	60
cagagtaaag	tcatcaccta	tgcagggtgc	atcaccacaga	tgtacttttt	tgtactcttt	120
atagtgttg	acagcttact	cttgaccgtg	atggcctatg	accagtttgt	ggccatctgt	180
cacccctgc	actacacgg	catcgtgaac	cctcggtct	gtggactgct	ggttctggcg	240
tcttgatca	tgagtgcct	gaattccttg	atagaaagct	taatgggtgt	gccactgctc	300
ttttgtacag	acttgaaaat	ccccacttt	ttctgtgaac	ttaatcagat	aatccgcagt	360
gcctgttctg	acacctttct	taatgacatg	gtgatgtatt	tgtagctgt	gcttctaggt	420
aggggatgtt	tactgggat	cctgtactct	tactttaaga	cagtttctc	catacgtgca	480
atctcatcag	ctcaggggaa	gtacaaggca	ttttccacct	gtgcatcgca	cctctcagtt	540
gtctccttat	tttattgtat	gggccttggg	gtgtacctta	gtgctgctgc	aaccacaaac	600
tcactctcaa	gtgcaacagc	ctctgatgta	cactgtggtc	accccc		646

&lt;210&gt; 752

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g601 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 752

atttgctttc	ctctccacta	tcccatccgt	atgagaaaaa	gagtgtgtgc	actgatgata	60
acaggatctt	ggatgatagg	ctccatcaac	tcttgtgctc	acacggtata	tgcactccgt	120
atcccatatt	gcaagtccag	agccatcaat	cattttttct	gtgatgttcc	agctatgttg	180
accctagcct	gcacggatac	ctgggtctat	gagtgcacgg	tgtttttgag	caccaccatt	240
ttctttgtgt	ttcccttcat	ttgtattgca	tgttcctatg	gccggattct	ccttgctgtc	300
taccacatgc	actctgcaga	agggaggaag	aaggcctatt	cg		342

&lt;210&gt; 753

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g602 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 753

cttgtcgtg	tctctatgc	cacaagtgtg	gtccctcagc	tgctggcaca	ttttcttgca	60
gaacataaag	ccatcccat	ccagagctgt	gcagccag	tattttctc	cctggccttg	120
gggtggattg	agtttgttct	cctggcggtg	atgggctatg	accgctatgt	ggctgtgtgt	180
gatgcctgc	gatactcggc	catcatgcat	ggagggtgt	gtgctaggtt	ggccatcaca	240
tcttggtca	gtggcttcat	cagctctcct	gtgcagactg	ctatcacctt	tcagctgccc	300
atgtgcagaa	acaagtttat	tgatcacata	tcctgtgaac	tcctagctgt	ggtcaggctg	360
gctcgtgtgg	acacctctc	caatgaggtc	accatcatgg	tgtctagcat	tgttcttctg	420
atgacacctt	tctgctgggt	tcttttgtcc	tacatccaga	tcactctccac	catcctaaag	480
atccagtcca	gagaagggaag	aaagaaagct	ttccacacgt	gtgcctctca	cctcacagtgt	540
gttgccctgt	gctatgggtg	ggccattttc	acttacatcc	agccccactc	cagtcctct	600
gtccttcagg	agaagttgtt	ctctgtcttt	tatgccattt	taacacca		648

&lt;210&gt; 754

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g603 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



<400> 754  
 tttgtggaca ttgcctgttc ctcagccaca gcacccaaga tgattgaaga ctttgtttct 60  
 gagaaaaaga ctatttccta ctggggctgt ataactcaga tgtttacctt ccactttttt 120  
 ggttgtgctg agatttttgt cttgactgtc atggcttttg atcgctatgc tgctatctgc 180  
 caacccctcc gttacactgt catcatgagt gctaatagctt atactgtgct ggcactactg 240  
 tcctgggttg gggccctggg tcatttcctt gtccagaccg tcctgacctt ccagctgccc 300  
 ttctgtaatg ctcagggttat agaccattac ttttgtgatg tccacccagt cctaaaactt 360  
 gctgtgctg atacaactct ggtaaatatg ttgggtggtg ccaacagtggt tctcatctcc 420  
 ctgggggtgt tcctcattct tttggcctcc tacacagtca ttctgtttag tcttcaaaaa 480  
 cagtctgcag agagctgaca caaagttctc tctacctgtg gatctcatct gactatagta 540  
 actttcttct ttgttccgtg tatctttatt tatctccatc cactacttcc ccattggata 600  
 aagctgtgtc tgtgttctat accaccatca cccca 635

<210> 755

<211> 342

<212> DNA

<213> Unknown (H38g604 nucleotide)

<220>

<223> Synthetic construct

<400> 755  
 atatgcaaac ctttacttta tccagccatt atgaccaatg gactgtgcat ccggctatta 60  
 atcttgtcat atgtagggtg tcttcttcat gctttaatcc atgaaggatt tttattcaga 120  
 ctaaccttct gtaactccaa catagtacat cacatttact gtgacattat ccattgtct 180  
 aagatttctt gtactgattc ttctattaat tttctaattg tttttatttt ctcaggttca 240  
 attcaggtat tcagcattgt gactattctt gtatcttata catttggtct cttcgcaatc 300  
 taaaaagga aatctgataa aggtgtaagg aaagcctttt cc 342

<210> 756

<211> 333

<212> DNA

<213> Unknown (H38g605 nucleotide)

<220>

<223> Synthetic construct

<400> 756  
 atttgtaacc ctctgagata ccccatcatc atgagcaggg acgtctgtgt gcagatggcc 60  
 gccatctcct gggtagacagg ctgtctgact gctctgctgg taactagttg tgccctgcag 120  
 atccccctct gtgggaatgt catcgaccat ttcacatgtg aaatccttgc agtgctaaaa 180  
 ctagcttgtg tgagttccct gctcgtggac atgggttatgc tgggtggtcag tattctcctg 240  
 ctgcccaccc caatgctttt gatttgcac tcgtatggct tcatecttcc tacaattctg 300  
 aggatcggct caacagaggg aagaaacaaa gct 333

<210> 757

<211> 665

<212> DNA

<213> Unknown (H38g606 nucleotide)

<220>

<223> Synthetic construct

<400> 757  
 ttgcctgaca tcggttttcac ctccaccacg gtccccaaga tgattgtgga catccagtct 60  
 cacagsagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgccatttkt 120  
 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatggccggg ttgtagccat 180  
 ctgtcaccct ctatatcgtt cagecatctt gaacccatgt ttctgtggct tcctagattt 240  
 gttgtcttcg ttttgttttg ttttgtttt ctcagtcttt tagactccca gctgcacaac 300  
 ttgattgcct tacaatgac cggcttcaag gatgtggaat tcctaatttc ttctgggaac 360

cttctcaact	ccccatcttg	catgttgtga	caccttcacc	aggaacatca	acctgtattt	420
ccctgctgcc	gtatttggtt	ttcttcccat	cttggggacc	ttttctctta	ctgtaaaatt	480
gtttcctcca	ttctgaggtt	ttcatcatca	ggtgggaagt	ataaaccttc	tccacctgtg	540
ggtctcacct	gccagttggt	tgttgatttt	gtggaacagg	tgttgagggt	taccttggtt	600
cagatgtgtc	atcttcccca	agaaagagtg	cagtgccttc	agtgatgtac	cgggtgtgtc	660
cctcc						665

&lt;210&gt; 758

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g607 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 758

ttttagaca	tctgtgttac	ctccaccaca	gtcccaaaga	caactgtcaa	catccggaca	60
cagagtaaag	tcataccta	tgcagattgc	atcaccaga	tgtacttttt	tgtactcttt	120
atagtgttgg	acagcttact	cttgaccgtg	atggcctatg	accagtttgt	ggccatctgt	180
cacccctctg	actacacggt	catcgtgaac	cctcggctct	gtggactgct	ggttctggcg	240
tcttgatca	tgagtgcctt	gaattccttg	atagaaagct	taatggtgtt	gccactgtct	300
ttttgtacag	acttgaaaat	ccccacttt	ttctgtgaac	ttaatcagat	aatccgcagt	360
gcctgttctg	acacctttct	taatgacatg	gtgatgtatt	tgtcagctgt	gcttctaggt	420
aggggatgtt	tcactgggat	cctgtactct	tactttaaga	cagtttcctc	catacgtgca	480
atctcatcag	ctcaggggaa	gtacaaggca	ttttccacct	gtgcacgca	cctctcagtt	540
gtctccttat	tttattgtat	gagccttggg	gtgtacctta	gtgctgctgc	aaccacaac	600
tcactctcaa	gtgcaacagc	ctctgatgta	caactgtgtc	accccc		646

&lt;210&gt; 759

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g608 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 759

atggcaatta	ggaaccattc	caccctccac	aaaccatgt	actttttttt	agctaataatg	60
tccttttctg	agatttggtg	tgtcactgtc	actattccca	agatgcttgc	tggctttggt	120
ggatccaaac	aggatcatgg	acagctaata	tcctttgagg	gatgcatgac	acagctttac	180
tttttctctg	gcttgggctg	caactgagtg	gtccttctcg	ctgttatggc	caatgatcgc	240
tatatggcca	tctgctatct	tctccacaac	ccagtcattg	tcagtggccg	gctgtgtgtg	300
cagatggctg	ctggctcttg	ggctggaggt	tttggcatct	ccatgggtcaa	agtttttctt	360
atttcgggcc	tctctaacgg	tggtcccaac	atcatcaacc	actttttctg	tgatgtctct	420
ccattgtcca	acctctcatg	caactgatatg	tccacagcag	agcttacaga	tttcatcctg	480
gccattttta	ttcttctagg	gccactctct	gtcactgggg	cctcctatgt	ggccattact	540
ggtgctgtga	tgcacattcc	ttcggctgct	ggacggtata	aggccttttc	cacctgtgcc	600
tctcatttca	atgttgtgat	aattttttat	gcagccagta	tcttcattta	tgctcggcca	660
aaggcacttt	cagcttttga	caccaacaag	ttggtctctg	tactgtatgc	tgctcattgta	720
ccattgtcca	atcccatcat	ttactgctg	cgcaatcaag	aggtcaagag	agccctatgc	780
tgtattttgc	acctgtacca	gcaccaggat	cctgacccca	agaaaggtag	caga	834

&lt;210&gt; 760

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g609 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 760

atggaattta	cagatagaaa	ctacacgttg	gtcactgagt	ttattctatt	aggttttcca	60
actcgccctg	aactgcagat	tgtcctgttc	ctcatgtttc	tgacattgta	tgctataatt	120
ctgatagggg	acattggatt	gatgctgttg	atcaggattg	atcctcacct	tcaaaccccc	180
atgtattttt	tccttagcaa	cctatcattt	gtagaccttt	gctatttttc	agacattggt	240
cccaaatgc	tggccaattt	cctctcggag	aacaaatcta	tttctatta	tgggtgtgcc	300
ctgcagtttt	attttttctg	tacttttgca	gatacagaat	ccttcacct	ggccgccatg	360
gcctatgac	gctatgtcgc	catctgtaac	cctttattgt	acacagttgt	gatgtctagg	420
ggcctctgta	tgcggttgat	tgtcttgta	taccttgagg	gcaacatgag	ttccctgggt	480
cacacatcct	ttgcctttat	tctgaaatat	tgtgacaaaa	atgttattaa	tcattttttc	540
tgtgacctcc	ctccccctgt	taaactatcc	tgcactgaca	caacaattaa	tgagtggctc	600
ctctccacat	acggcagctc	agtggaaatc	atttgtttta	tcacatcat	catctcctac	660
tttttcatte	ttctctcagt	cttaaagatc	cgctctttca	gtgggaggaa	gaagaccttt	720
tctcagtcgc	cctctcacct	gacttcagtg	acgatctacc	aagggaactct	cctctttatt	780
tactcacggc	ccagctacct	gtattctcca	aacactgata	aaattatctc	agtgttctac	840
accattttca	ttccagtgct	gaatccgttg	atttatagtt	tgagaaataa	agatgtaaag	900
gatgcagctg	agaaagtctt	aagatcaaa	gtagattctt	ca		942

&lt;210&gt; 761

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g610 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 761

atggataacc	aaagctccac	accgggcttc	ctccttctgg	gcttctctga	acacccaggg	60
ctgggaagga	ctctcttcgt	ggatgtcatc	acttctacc	tcctaaccct	agtgggcaac	120
acactcatca	tctgtctgtc	tgcgctggac	accaagctcc	actctccaat	gtactttttc	180
ctctccaacc	tctccttctt	ggacctctgt	ttcaccacga	gttgtgttcc	ccaaatgctg	240
gccaaacctt	ggggcccaaa	gaagaccatc	agcttctctg	actgctctgt	ccagatcttc	300
atcttctctg	ccctggggac	aactgagtgc	atcctcatga	aagtgatggc	ttttgatcgc	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccaccccg	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggtcattggg	ctagtggggg	cagtgggtcca	gacaccatcc	480
accctgcacc	tgccttctg	ccccgatcgg	caggtggatg	attttgtctg	tgagggtccca	540
gctctaattc	gactctcctg	tgaagacacc	tcctacaatg	agatccagg	ggctgttgcc	600
agtgtcttca	tcttggttgt	gcctctcagc	ctcatccttg	tctcttacgg	agccattacc	660
tgggcagtgc	tgaggattaa	ctccgccaca	gcatggagaa	aggccttttg	gacctgtccc	720
tcccattctca	ctgtggtcac	cctcttctac	agctcagtc	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcact	840
ccttcactta	accctctcgt	atacacctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaa	agactccagg	gaaagctgga	gagctgct		948

&lt;210&gt; 762

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g611 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 762

atgaaaagag	agaactttac	tctcatcact	gactttgttt	tccaaggttt	ctctagcttc	60
catgagcagc	agatcacctt	ttttggcgtg	ttccttgca	tatacatctt	aaccttagca	120
ggcaatatca	tcattgtgac	catcatccga	attgatcttc	atcttcacac	acctatgtac	180
ttcttctctga	gcatgctgtc	cacttcagag	actgtatata	cattgggtcat	tctcccaaga	240
atgctctcca	gcctcgtagg	tatgagccag	cccatgtcat	tggcaggggtg	tgccacacag	300
atgttctttt	ttgtaacctt	tggcatcact	aactgcttcc	tgctcacagc	aatgggatat	360
gaccgctatg	tggccatctg	caacccctg	agatacatgg	ttattatgaa	caagaggctg	420
cgtatccaac	ttgtcctggg	ggcctgcagc	attgggctga	ttgtagcaat	aacgcaagtg	480
acatctgtat	tcaggttacc	cttctgtgct	agaaaggtgc	cccacttctt	ctgtgacatc	540

```

cgccctgtga tgaagctctc ctgcattgac accactgtca atgaaatcct gactttgatt    600
atcagtgtgc tgggtgctgt tgtacctatg ggtctggttt tcatttctta tgttctcatt    660
atctctacaa tcctcaagat tgcttcagtt gagggccgga agaaggcttt tgccacctgt    720
gcatcccacc tcaactgtgtt cattgtccac tacagctgtg cctccattgc ctacctcaag    780
cccaagtcag agaacaccag agaacatgac cagctgatct cggtgacctt cactgtcatc    840
actcccctac tgaaccctgt ggtatacacc ctgagaaata aagagggtcaa agatgctctg    900
tgcagggctg ttgggtggga gttttcc

```

&lt;210&gt; 763

&lt;211&gt; 650

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g612 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 763

```

tgggctgaca tcggtttcac ctgggccacg gtcaccaaga tgattgtgga catgcagtcg    60
cataggagag ccattctctca tgcgggctgt ctgacgcaga tgcctttctt gttcctttgt    120
gcatgtgtag aaggcatgct cctgactgtg atggcctatg actgctttgt agacatctgt    180
cgccctctgc actaccagtc catcggaat cctcacttct gtgtcttctt cgtgggggtg    240
tcctttctcc ttagcctgtg ggattcccag ctgcacagtt ggattgtgtt acaatatcac    300
catcttcaag aatgtggaaa tctctaattt tgtctgtgac ccctctcaac ttctcaaact    360
tgcctgttct gacggcgtca tcaatagcat attcatatat ttgatagta ctatgtttgg    420
tttccttccc atttcaggga tcctatggtc ttactataaa atcgtcccct ccattctaag    480
gatttcacgc tcagatggga agtataaagc cttctccacc tgtggctcct caccaggcag    540
ttgtttgctg attttataga acaggcattg gcattgacct gacttcagct gtgtcaccac    600
ccccaggaa tggtgtggtg gcattcattga tatacgtctt tgtcactccc    650

```

&lt;210&gt; 764

&lt;211&gt; 641

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g613 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 764

```

ttcactgacc tcttctttgt caccaacaca atccccaaga tgctggtgaa cctccagtc    60
cagaacaaag ccattctcta cacagggtgt ctgacacagc tctacttcct ggtctccttg    120
gtggcccttg acaacctcaa cctggccgtg atggcgtatg atcgctatgt ggccatctgc    180
cgtcccctcc actatgtcac agccatgac cctgggctct gtatcttctt cctctccttg    240
tggtgggtgt tctctgccct ctatggcctc atccatatcc tcctcatgac cagggtgacct    300
tctgtgggtc tcaaaagatc cactacctct tctgtgagat gtacttcctg ctaaggctgg    360
catgttccaa catccacgtc aaccacacag tactggttgc cagggtctgc ttcattctcc    420
tcattcccct aggtctcatg atcacatcca acgcccgcac tgtcagagcc atcctccaaa    480
taccctcagc cactgggaag tacaaagcct tctccacctg tgcttcccat ttggctgtgg    540
tctccctctt ctatgggact ctgggtatgg tgtacctgca gccctccaa acctactcca    600
tgaaggactc agtagccaca gtgatgcatg cgggtggtgac g

```

&lt;210&gt; 765

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g614 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 765

```

tttgttgatt tctgttatc caccacaatt acacccaaac tgctggagaa cttggtgtg    60
gaagatagaa ctatctcctt cacaggatgc accatgcagt tattctttgt ctgcatattt    120

```

gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtgggtaca	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgcat	tgttgctgtg	360
tcttgctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcagttaa	420
ataagcagcc	tgcttcctat	gctttcattt	ttatcactgt	catgaagacg	ccttccactg	480
gggggcgcaa	gaaagcggtc	tccacgtctg	cctcccactt	gacggccatt	accattttcc	540
atgggactat	ccttttcctc	tactgtgttc	ctaactccaa	aagttcgtgg	ctcatggtca	600
aggtggcctc	tgtcttttac	acagtgggtca	ttccc			635

&lt;210&gt; 766

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g615 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 766

ttagttgatt	tctgttattc	caccacaatt	acacccaagc	tgctgaggaa	cttggttgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	accatgcagt	tattctttgt	ctgcatattt	120
gtagtaacag	aaacattcgt	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtgggtaca	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgcat	tgttgctgtg	360
tcttgctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
ataagcagcc	tgcttcctat	gctttcattt	ttatcactgt	catgaggacg	ccttccactg	480
gggggcgcaa	gaaagcggtc	tccacgtctg	cctcccactt	gacggccatt	accattttcc	540
atgggactat	ccttttcctc	tactgtgttc	ctaactccaa	gagttcgtgg	ctcatggtca	600
aggtggcctc	tgtcttttac	acagtgggtca	ttccc			635

&lt;210&gt; 767

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g616 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 767

atgtccattt	ccaacatcac	agtctacatg	ccctctgtgt	tgacactagt	agggatccca	60
ggcctagaat	ctgtgcagtg	ctggattggg	attccattct	gtgccattta	tctcattgct	120
atgattggaa	attccttgct	tctgagcatc	atcaaatctg	agcgagctct	ccatgagccc	180
ttgtacattt	tcttaggcat	gctaggagcc	acagacattg	cacttgctag	cagcattatg	240
ccaaagatgc	ttggaatatt	ctggtttaat	gtgectgaaa	tctattttga	ttcctgcttg	300
cttcaaatgt	ggttcatcca	cacattgcag	ggtatagagt	caggcatcct	tgtggccatg	360
gccctggacc	gttatgtggc	catctgttat	gcactaagac	atgccaacat	cttcacccac	420
cagcttggtca	ttcagatagg	aactatggtc	gtactcaggg	ctgctattct	tgtagcccca	480
tgccctagtag	tgataaagt	ccggtttcaa	ttttatcaca	caacagtcac	ctcccactcc	540
tactgtgagc	atatggccat	tgtgaaacta	gcagcagcaa	atgttcaagt	caacaaaatc	600
tatggtttgt	ttgtggcctt	cactgtagca	ggatttgacc	tcacattcat	cacattgtcc	660
tacatccaga	tatttatcac	agtttttcgt	ttgcccaga	aggaggctag	gtttaaagca	720
ttcaataacct	gcattgtcca	catctgtgtc	ttcctccagt	tctacctcct	tgcccttctc	780
tccttcttca	cacataggtt	tgggtctcac	atccccctt	atatccatat	tctcttttct	840
agcatttact	tgctgggtccc	tccatttctc	aatccacttg	tctatgggtgc	aaagaccaca	900
cagattcgca	ttcatgtggt	aaaaatgttc	tgttca			936

&lt;210&gt; 768

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g617 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 768

atgtggcaga	agaatcagac	ctctctggca	gacttcatcc	ttgaggggct	cttcgatgac	60
tcccttacc	accttttcc	tttctccttg	accatgggtg	tcttccttat	tgcggtgagt	120
ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttcctgctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaat	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaaccag	300
cacttccctc	atttgtgtct	agggtgtgct	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcattccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggctgtcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcacttccc	tttctgtggg	cctcggaaag	tctaccactt	ctactgtgag	540
ttcccagctg	ttgtgaagtt	ggtatgtggc	gacatcactg	tgtatgagac	cacagtgtac	600
atcagcagca	ttctcctcct	cctccccatc	ttcctgattt	ctacatccta	tgtcttcac	660
cttcaaagtg	tcattcagat	gcgctcatct	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacgggtgg	ttctctttgg	tttgggtgct	gcactcttct	ctacatgaga	780
cccaggctcc	agtgcaactc	attgcagaac	aaagttgggt	ctgtgttcta	cagcatcatt	840
acgccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tgttatcacc	cagtgcattc	aacgactgca	attg	954

&lt;210&gt; 769

&lt;211&gt; 881

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g618 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 769

gccacgtaca	attccagcaa	tactgtgggt	acagagtttg	tgtttctgag	cttcccagag	60
ctgcaccatc	ttcaagggtc	gctatttgg	cactcctcat	catctatgtg	gtgaccatcc	120
tagaggacct	ggctgtcgtg	gggaccatca	gagccagcca	ccacctgcac	atatccacac	180
acctcttcc	ggccaaactc	tcgggtgctg	agactctgta	cacctcggtc	accgtcccaa	240
agctgttggc	cggactccca	gcacgagcga	cgaccatcta	tctccttctc	ggggcacctc	300
acctggctgc	tcctcttcc	ctcactcagc	tcctctgagt	gcgtcctccc	ggccaacatg	360
gactgtgact	ggcaccag	catctgccac	ctgctgcact	acccagccca	tcattggactc	420
catgcagctg	gctctgcctg	cacctggcca	tcagcgccta	gctcagcagc	ttcccagcct	480
cctttgtgtc	caaggctctc	aactccagcc	tgaggctccg	cagccccgat	gtcctcaacc	540
acttctgtga	tatccacccc	ccgctagggc	tctcttgctc	cagcaccact	accatagaaa	600
tgcggtactca	ggcagccccc	gtgatccttg	cggtctccct	gcaggcaacc	acgggtctcct	660
acacccacat	cctggccaga	tcgctgagga	ttccagaaa	gcccagcagc	taaaggcctt	720
ccccacctat	gcctcccacc	tgggtggg	gctcctctaa	cctcatcaag	ctggtgttca	780
ggggtctact	tggttgggat	ccctctgctc	aaacccatca	tctactgcct	gggaactgca	840
acatcaggga	ggcctgggcc	aaactcctcc	aggcccttcc	c		881

&lt;210&gt; 770

&lt;211&gt; 880

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g619 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 770

gccacataca	attccagcaa	tactgtgggt	acagagtttg	tctttctgag	cttcccagag	60
ctgcgccatc	ttcaagggtc	gctatttgg	cactcctcat	catctatgtg	gtgaccatcc	120
tagaggacct	ggctgtcgtg	gggaccatca	gagccagcca	ccacctgcac	atatccacac	180
acctcttcc	ggccaaactc	tcgggtgctg	agacctgta	cacctcggtc	accgtcccaa	240
agctgttggc	cggactccca	gcacgagcga	cgaccatcta	tctccttctc	ggggcacctc	300

```

acctggctgc tctcttccct ctactcagc tctctgagt gcatcctccc ggccaacatg 360
gactgtgact ggcacccggt catctgccac ctgtctgact acccagccca tcatggactc 420
catgcagctg gctctgcttg cacctggcca tcagcgccca gctcagcagc ttcccagcct 480
cctttgtgtc cagggtcttc aactccagcc tgaggctccg cagccccgat gtcctcaacc 540
acttctgtga tatccacccc ccgctagggc tctcttgctc cagcaccact accatagaaa 600
tgcggaactca ggcagcccag gtgatccttg cggtctccct gcaggcaacc acggtctcct 660
acaccacat cctggccaga tcgctgagga ttccagaaag gcccagcagc taaaggcctt 720
ccccacctat gcctcccacc tggggtggcg gctcctctaa cctcatcaag ctgggtgtcag 780
gggtctactt gggtgggatc cctctgtcga aacctatcat ctactgcctg ggaactgcaa 840
catcagggag gccctggcca aactcctcca ggcccttccc 880

```

&lt;210&gt; 771

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g620 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 771

```

ctcctaattg cagcagacaa ccacacagcg tagaggcggt tgtcctgcag ggtttctctg 60
aagaccttcc actccagggc tgctgcttgg ctttttccct cctttacctg atggcacttg 120
taggaaacat cctcatggtc atggccatca gtctgaatcc aggcctccac acgccagtgt 180
acttctttct caccaacctg gcccttttag acatcgtctg cacatccatg gacaacagca 240
gagtgggtggc tgtgctgtac acagtggta gccccaccct gaaccctca cctactccct 300
gcggaacaag gacttatcag tagcactgag gagagtgttt tcttgcatca ggtaaaagga 360
agggaagttt ctagtgtgaa atgttccagg tgtaacaaa ctaatttcaa catatgactt 420
tgagaatctc atgcaagcag caaggaacaa gaaagtaatt aatgccacat atttataaat 480
aatgtgctcc cgcacggggc tgccatcatt caatgtggaa ctcc 524

```

&lt;210&gt; 772

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g621 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 772

```

atggaaagga ccaacgattc cacgtcgaca gaatttttcc tggtagggct ttctgcccac 60
ccaaagctcc agacagtttt ctctgttcta attttgtgga tgtacctgat gatcctgctt 120
ggaaatggag tcttatctc agttatcatc ttgtattctc acctgcacac ccccatgtat 180
ttcttctctt gtaatcttcc ctctctcgac gtttgctaca caagttctc tgteccacta 240
attcttgcca gctttctggc agtaaagaaa aaggtttccct tctctgggtg tatggtgcaa 300
atgtttattt cttttgccat gggggccacg gagtgcata tcttaggcac gatggcactg 360
gaccgctatg tggccatctg ctaccactg agataccctg tcatcatgag caagggtgcc 420
tatgtggcca tggcagctgg gtctgggtc actgggcttg tggactcagt agtgcagaca 480
gcttttgcaa tgcagttacc attctgtgct aataatgtca ttaaactttt tgtctgtgaa 540
attctggcta tcttgaaact ggcctgtgct gatatttcaa tcaatgtgat tagtatgaca 600
gggtcgaatc tgattgttct ggttattcca ttgttagtaa ttccatctc ttacatattt 660
attgttgcca ctattctgag gattccttcc actgaaggaa aacataaggc cttctccacc 720
tgctcagccc acctgacagt ggtgattata ttctatggaa ccatcttctt catgtacgca 780
aagcctgagt ctaaagcctc tgttgattca ggtaatgaag acatcattga ggccctcatc 840
tcccttttct atggagtgat gactcccatg cttaatctc tcatctatag tctgcgaaac 900
aaggatgtaa aggctgctgt caaaaacata ctgtgtagga aaaacttttc t 951

```

&lt;210&gt; 773

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g622 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 773

atggaatggg	aaaaccaaac	cattctggtg	gaattttttc	tgaagggaca	ttctgttcac	60
ccaaggcttg	agttactctt	ttttgtgcta	atcttcataa	tgtatgtggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcatc	ttggaccctc	accttcacac	ccctatgtac	180
ttctttctgg	ggaacctctc	cttcttggac	atctgttaca	ccaccacctc	tattccctcc	240
acactagtga	gcttcctttc	agaaagaaaag	accatttcct	tttctggctg	tgcagtgcag	300
atgttccttg	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcat	gatggccttt	360
gaccgctatg	tggctatctg	caaccctctg	agatatccca	tcacatgag	caagaatgcc	420
tatgtacca	tggctgttgg	gtcctgggtt	gcagggattg	tcaactctgc	agtacaaaact	480
acatttgtag	tacaattgcc	tttctgcagg	aagaatgtca	tcaatcattt	ctcatgtgaa	540
attctagctg	tcataagtt	ggcctgtgct	gacatctcag	gcaatgagtt	cctcatgctt	600
gtggccacaa	tattgttcac	attgatgcc	ctgctcttga	tagttatctc	ttactcatta	660
atcattttcca	gcacctctca	gattcactcc	tctgagggga	gaagcaaagc	tttctctacc	720
tgtcagccc	atctgactgt	ggtcataata	ttctatggga	ccatcctctt	catgtatatg	780
aagcccaagt	ctaaagagac	acttaattca	gatgacttgg	atgctaccga	caaaattata	840
tccatgttct	atggggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaaac	900
aaggatgtga	aagaggcagt	aaaacaccta	ccgaacagaa	ggttctttag	caag	954

&lt;210&gt; 774

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g623 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 774

ttctctcttt	aggccaacta	cagcgagag	gagcgctttc	tcctgctggg	tttctccgac	60
tggccttccc	tgcagccggt	cctcttccgc	cttgtcctcc	tgtgctacct	cctgaccttg	120
acgggcaact	cgcgctgggt	gctgctggcg	ggtcgaccgc	cgccctgcaca	cgcccatgta	180
ctacttcttc	tccacctggc	cttggtagac	gcgggcttca	ctactagcgt	gggtccgccc	240
ctgctggcca	acctggcgga	ccagcgctct	cgtgcgcgca	gccactgcac	ggcccagctg	300
tgcgcacgc	tggctctggg	ttccgcccga	tgcgtccatc	tggcggtgat	ggctctgggc	360
cgcgcggtc						369

&lt;210&gt; 775

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g624 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 775

atgagacaga	ataacaatat	tacagaattt	gtcctcctgg	gcttttctca	ggatcctggt	60
gtgcaaaaag	cattatttgt	catgttttta	ctcacatact	tggtgacagt	gggtggggaac	120
ctgctcattg	tgggtggatat	tattgccagc	ccttccttgg	gttccccaat	gtatttcttc	180
cttgccctgcc	tgtcatttat	agatgctgca	tattccacta	ccatttctcc	caagttaatt	240
gtaggcttat	tctgtgataa	aaagactatt	tccttccaag	gttgcatggg	ccagctattt	300
atagaccatt	tcttgggtgg	ggctgaggtc	ttccttctgg	tgggtgatggc	ctgtgatcgc	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgcttc	420
cttctgttgg	tgggtggccat	gattggaggt	tttgtacatt	ctgcgtttca	aattgttgtg	480
tacagtctcc	ctttctgtgg	tccaatgtc	attgttcatt	tcagttgtga	catgcaccca	540
ttactggaac	tggcatgcac	tgacacctac	tttataggcc	tcactgttgt	tgtcaatagt	600
ggagcaatct	gtatggatcat	tttcaacctt	ctgttaatct	cctatggagt	catcctaagc	660
tcccttaaaa	cttacagtca	ggaaaagagg	ggtaaagcct	tgtctacctg	cagctccggc	720
agtaccgttg	ttgtcctctt	ttttgtacct	tgtattttca	tatatgttag	acctgtttca	780
aactttccta	ctgataagtt	catgactgtg	ttttatacca	ttatcacaca	catgctgagt	840



cctttaatat atacgttgag aaattcagag atgagaaatg ctatagaaaa actcttgggt 900  
 aaaaagttaa ctatatattat tataggagga gtgtccgtcc tcatg 945

<210> 776

<211> 352

<212> DNA

<213> Unknown (H38g625 nucleotide)

<220>

<223> Synthetic construct

<400> 776

cgctgtgcgc cccgcctgct ggaccacttc atctgtgagc tgccggcggt gctcaagctg 60  
 gcctgcggag ggcacggaga cactaccgag aaccagatgt tcgccgcccg cgtgggtcatc 120  
 ctgctgtctg cgtttgccgt catcctggcc tcctacggtg ccgtggcccg agactgtctg 180  
 ttgcatgcgg ttcagcggag gccggcagag aggcggtggg cacgtgtggg tcccacctga 240  
 cagecgtctg cctgttctac ggctcggcca tctacaccta cctgcagccc gcgcagcata 300  
 caaccaggca cggggcaagt tcgtatcgct cttctacacc gtggtcacac ct 352

<210> 777

<211> 937

<212> DNA

<213> Unknown (H38g626 nucleotide)

<220>

<223> Synthetic construct

<400> 777

ggactgagta ataatgttac agaatttgtc ctcttgggca acactcagtg tcctgatgtg 60  
 caaaatgcat tatttgtcat ggttttactc acatacgttg tgagtatggc gggaaacttg 120  
 cttgctgtgg tggctattat ttccagccct tcctttggct ccccaatgta cttcttcctc 180  
 acagcctgtt atttatatat gctgcattat ccaataccat ttctcccaa ttgattatag 240  
 gcttactcca tgataaaaag actattttct tcacagcatg catggggcag ctatttatag 300  
 accacttatt tgggtgtgct gaggtcttcc tacttgtggg gatgtcctac gatttctatg 360  
 tggccatctc taagccactg cactatttga ccatcatgaa tcaacagggt tgtatccttc 420  
 tgttggtggt ggctgtgact ggaggttttg tgagttgtgt gtttcaaatt gttgtgtgtg 480  
 acactctctc gttctgtgyc caaatgtcac tgaccacttt gtctgtgaca tgtaccatt 540  
 attggaactg gtttgcactg atacctactt tataggtctc actgttgttg ccaatgggtc 600  
 agcaatctgt atggtcgtct tcacccttct actaatctcc tatggagtca tcctaaacaa 660  
 ctttaaaact tatagtcagg aaggaggct taaagccctg tctgcctgca tctcctacat 720  
 aacagtcact gtctgtttc ttgttcctg tattttcctt ttcgttagac ctgtttcgaa 780  
 ctttctatt gataaattca tgactgtgtt ttatacagtt atcatacaca tgttgaatcc 840  
 attaataac acactgagaa atttagagat gagaattgct gtaaaatcca atgtaaaaaa 900  
 actctggcat taaaaactta actatagtta gaatgag 937

<210> 778

<211> 970

<212> DNA

<213> Unknown (H38g627 nucleotide)

<220>

<223> Synthetic construct

<400> 778

atgagactga gtagcgatgt tacagcattt gtctctctag gccttactca ggatcctgat 60  
 gtgtaaaaatg cattatttgt cgtacattta ctcacataca ttatgactat ggtggggaac 120  
 ctgcccattg tgggtactat tattgccacc cccaccttag gctcccaggt gtacttcttc 180  
 attgtctgct tgtcatttat agatgtttgt tattccacca ccattcctcc caaattgatt 240  
 gtaagctatc tccatgataa aaagactatt tccttccgag cttgcatggg tcagcccttt 300  
 tatagaccac ttagttggtg gtgctgaggc cttcattctg ttggtgatgg cctataatcg 360  
 ctatgtagcc atctgtaagc cactgcacta tttcaccatc atgaattgac aggtttgcat 420

```

ccttctgttg gtggtggctg tcaactgctg ttttgtgcat tctgtgtttc aaatttttagt 480
tgcgtagagt ctctttttct gtggtcccaa tatcattgac cactttttct gtgacatgta 540
cccattattg gaactggcac acactgacac ctactttata ggcctcactg ttgttgccaa 600
tggtggagga atctgtatgg tcttgttcat ccttctacta atctcctgtg gggtcacct 660
aatctccctt aaaacttata gtcaggaagg gaggcataaa gccctgtcta cctgcagctc 720
ccacattacc gtggttgctc tgtttttgt tccctgtatt ttctgtatg ttagacctgt 780
ttcaaacttt cctattaata aattcattac tgtgttttat acagttatca caccatgtt 840
gaatccatta atatacacat tgagaaactg agagatgaaa aatgctatag gaaacctctg 900
gtgtaaatat taactctaga tagaataaga ggttacattt tcatgtaggt acagggtaat 960
gcaggtaaag 970

```

&lt;210&gt; 779

&lt;211&gt; 704

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g628 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 779

```

cccatgtact tgttcctcgg caatttgtcc ttcattgac tctgttattc atttgtcttt 60
acccccaaaa tgctgatgag ctttatttca gagaggaaca tcatctcctt tccaggatgc 120
ataactcagc tcttttttct ctgctttttt gtccactctg agtgctatgt gctgacagcc 180
atggcctatg atcgctatgt ggccatctgc aaacccttc tgtacatggt caccacgtcc 240
ctcagatctg ttctctactg atgcttggtt catatgtgat ggggtttgct ggggccatgg 300
tccacacaga gtgtatgatg aagctcatct tttgtgactc caacgtcatc aaccataaca 360
tgtgtgacat cttcccaactg ctccagctct cctgcagcag cacctaggcc aatgagctgg 420
tgatgtctgt tattgttagc acagttgtta tagtatcaag cctcattatc ttaatctctt 480
atgctttgat tcttttcaat atccttcaca tgtcctcagc cgaggggttg ttcaaagcca 540
tcggtacctg tggctccac ataataactg ttggcctatt ctatgaattt gggctgatca 600
ctcatgttaa gttatcatct gattggtata tgggtcaggg gaagtttctc tcagtgtttt 660
atacaaatgt ggttcccatg ctgaaccctc tcatctactg tctg 704

```

&lt;210&gt; 780

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g629 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 780

```

atgaggcaga ataacaatat tacagaattt gtcctcctgg gcttctctca gtatcctgat 60
gtgcaaaatg cattatttgt catgttttta ctcatatata ttgtgactat ggtggggaac 120
ctgctcattg tgggtgtctat tattgccagt cccttttttg gctccccagt gtacttcttc 180
cttgccctgcc tgtcatttat agatgctgtg tattccacca ccatttctcc tgtattgatt 240
gtagacttac tctgtgataa aaagactatt tccttccag cttgcatggg tcagctattt 300
atagagcact tgtttggtga tactgacgtc ttcttcttg tgggtgatggc ctatgatcgc 360
tacgtggcca cctgtaagcc actgcgctat ttgaccatca tgaattgaca ggtttgcac 420
cttctgttgg tgggtggctgt gactggagg tttctgcatt ctgtgtttca aatttttagt 480
gtgtacagtc tccctttctg tggccccaat gtcatttacc actttttctg taacatatac 540
cctttattgg acctggaatg cactgacacc tacttcgtag gcctcgctgt ggttttcaat 600
ggtggagcaa tctgtatggc catcttcacc ctctactaa tctcctatgg ggtcatccta 660
aactccctta aaacttatag tccggaaggg aggcataaag ctccgtttat ctgcagctcc 720
cactttatca tgggtatctt gttttttgtt ccctgtatgt tcttatatgt tagaccggt 780
tcaaacttcc ctattgataa attcctgact gtgttttatt cagttatcac acccaagtgt 840
aatcctttta tatacatgtt gagaaattca gagatgagaa atgctataga aaatctcttg 900
ggataccaaa gtgggaagac agga 924

```

&lt;210&gt; 781

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g630 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 781

```

cccatgtact tgttccctgc caacttgtcc ttgcctgaca tcggtttcac ctccagcatg      60
gtccccaaga tgattgtgga catctaactc cacagcagac tcatctccta ggcaggctgc      120
ctgactccca tgtctctctt tgccattttt ggaggcatgg aagagagaca tgctcctgag      180
tgtgatccct atgaccggtt tgtagccatc tgtcaccctc tatatcattc agccatcatg      240
aaccgctggt tctgtggcct tctagttttg ttgtcttttt tttctcagtc tcttttagac      300
gcccagggtgc acaacttgat tgccttaca atgacctgct tcaaggatgt ggaaattcct      360
aatttcttct gggaaccttc tcaactcccc catcttgcac gttgcgacac cttcaccaat      420
aacataatca tgtattcccc tctgtccata tttgggtttt tcccatctc ggggaccctt      480
ttctcttact ataagattgt ttctccatt cggagggttt catcatcagg tgggaagtat      540
aaggcctgct ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaacaggc      600
ttttgggggt acctcagttc agatgtgtca tcttccccgg gaaaggctgc agtggcctca      660
gtgatgtaca cggtggtcac ccccatgctg      690

```

&lt;210&gt; 782

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g632 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 782

```

tctttcctgg agattggcct caacctagtc attgtgcca aaatgctggg gacctgctt      60
gcccaggaca caaccatctc cttccttggc tgtgccactc agatgtattt cttcttcttc      120
tttggggtag ctgaatgctt cctcctggct accatggcat atgaccgcta tgtggccatc      180
tgcagtccct tgcactaccc agtcatcatg aaccaaagga cacgggcca actggctgct      240
gcttctggtt tcccaggctt tctgtagct actgtgcaga ccacatggct cttcagtttt      300
ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccgcc tgtgctgaag      360
ctggtctgtg cagacacagc actgtttgag atctacgcca tcgtcggaac cattctggtg      420
gtcatgatcc cctgcttgcct gatcttgtgt tcttatactc gcattgctgc tgctatcctc      480
aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgctctc acacctcctt      540
gttgtctctc ttttctatat atcattaagc ctcacgtact tccggcctaa atcaaataat      600
tcacctgagg gcaagaagct gctatcattg tcgtacactg ttatgactcc catgctgaac      660
ccctttcatc tactgtcctg g      681

```

&lt;210&gt; 783

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g633 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 783

```

atggtcacag agttcctcct actgggattt ctccctgggc caaggattca gatgctcctc      60
tttgggctct tctccctggt ctatgtcttc accctgctgg ggaatgggac catcctgggg      120
ctcatctcac tggactccag actccacacc cccatgtact tcttctctc acacctggcg      180
gtcgtcgaca tcgcctacgc ctgcaacacg gtgcccggga tgcgtgtgaa cctcctgcat      240
ccagccaagc ccatctcctt tgcgggcccgc atgatgcaga cttttctgtt ttccattttt      300
gctgtcacag aatgtctcct cctgggtggt atgtcctatg atctgtacgt ggccatctgc      360
caccacctcc gatattcat catcatgacc tggaaagtct gcactactct ggccatcact      420
tctgggacat tgggtccct cctggctatg gtccatgtga gcctcatcct aagactgccc      480
ttttgtgggc ctggtgaaat caaccactty ytctgtgaaa tctkkctgt cctcaggctg      540
ggctgtgctg atacctggct caaccagggt gtcac      576

```

<210> 784  
 <211> 924  
 <212> DNA  
 <213> Unknown (H38g634 nucleotide)

<220>  
 <223> Synthetic construct

<400> 784  
 tatgcagacc cacagaatct aacagatgtc tcwatattcc tcstcctaga actctcagag 60  
 gatccagaac tgcagccagt ccttgctggg ctgttcctgt ccatgtgcct ggtcacgggtg 120  
 ctggggaacc tgetcatcat cctggccatc agccctgact cccacctcca ccccccatg 180  
 tactttcttc tctccaacct gtcttgctc gacatcggtt tcacctccac cacggteccc 240  
 aagatgattg tggacatcca gtctcacagc agagtcattc cctatgcagg ctgcctgact 300  
 cagatgtctc tctttgccat ttttgaggc atggaagaga gacatgctcc tgagtgtgat 360  
 ggcctatgac tggttttagt ccatctgtca cccgctatat cattcaccat catgaaccgg 420  
 tgtttctgtg cctttctagt tttgttgtc tttttttct cagtcttta gactcccagc 480  
 tgcacaactt gattgcctta caagtaccc gcttcaagga tgtggaaatt cctaatttct 540  
 tctgtgaccc ttctcaactc ccccatcttg catgttgtga caccttcacc aataacataa 600  
 tcatgtattt cctgtctgcc atatttggtt ttcttcccat ctgggggacc cttttctctt 660  
 actataaaat tgtttctcc attctgaggg ttcatcatc aggtgggaag tataaagcct 720  
 tctccacctg tgggtctcac ctgtcagttg tttgctgatt ttatggaaga ggtgttgag 780  
 ggtacctcag ttcagatgtg tcatcttccc ccagaaaggg tgcagtggcc tgcagtgatg 840  
 tacacgggtg tcacctccat gctcaacccc tttatctaca gcctgagaaa cagggatatt 900  
 aaaagtgtct tgcggcgcc gcaa 924

<210> 785  
 <211> 714  
 <212> DNA  
 <213> Unknown (H38g635 nucleotide)

<220>  
 <223> Synthetic construct

<400> 785  
 atgtacttgt tcttgaggaa tctgtccttg cctgacatcg gtttcacctc caccattgtc 60  
 cccaagatga ttgtggacat ccagtctcac agcagagtga tctcctatgc aggcgcctg 120  
 actcagatgt ctctctttgc catttttgga ggcattggaag acaacatgct cctgagtgtg 180  
 atggcctatg accggtttgt agccatctgt caccctctat atcattcagc catcatgaat 240  
 ccgtgtttct gtggcttctt acttttgggt tcttttttt tttttctcag tcttttagac 300  
 acccagctgc acaacttgat tgctttacaa atgacctgct tcaaggatgt ggaaattcct 360  
 aatttcttct gtgaccttc tcaactcccc catcttgcac gttgtgacac ctccaccaat 420  
 aacatcatcg tgtatttccc tgcgtgcata tttgttttcc ttcccatctc ggggacctt 480  
 ttctctttta aactgtttgt ttctccatt ctgagggttt catcatcagg cgggaagtat 540  
 aaaaccttct ccacctgtg gtctcacctg tcagtatttt gcttatttta tggaaagggt 600  
 gttggagggt acctcagttc agatgtgtca tcttccctga gaaaggctgc agtggcctca 660  
 gtgatgtaca agatggtcac ccccatgctg aaccttcca tttacacct gcgg 714

<210> 786  
 <211> 962  
 <212> DNA  
 <213> Unknown (H38g636 nucleotide)

<220>  
 <223> Synthetic construct

<400> 786  
 ttcaaacggt ccataacatt cacacctaca acattcactc tcgttggcat cccgggactg 60  
 gaggcagaac attatgtgga tatccatccc cttctgcctg atatacacca tcatctttcc 120  
 gggaaatggc atcattcttc acatcatccg aattgactct tccttgacc aacctatgta 180

ctattttctg gccatgccgg cctttgttga acttggtgtc tctgcttcca ccatgcccac	240
tgtgttaagc atattcctct ttggcattaa cgatgtcagt tttggtgggt gcctgtcca	300
gatgttttct atgcactctt tcactcttat ggagtcagggt gtccttcttg caatgtcagt	360
ggaccgcttt gtggccatct acagcccact gcgctacaca accattctga caattgcctg	420
catttctggg atgggtgccg ccattgcctt gcgcagtgtg atgcttatgc tcccactgct	480
ctttctcctg aggcgtctgc ctttctgtgg ccacaatacc ctcacacact cttattgcct	540
ccactcagat ctgatcaaat tgccctgtgg agacacacgc cccaatagca tcctggctct	600
atthgtcatt accttcacat ttggactgga cttattgttc attgtgggtt cttatgtgct	660
gattcttcat acagtactgg aaatagcttc tggagcaggg cgtggcaggc actcaacaca	720
tgtgtgtgcg acatatgtgc tgtgcttgtg tactatgtgc ccatgatcag cctctcctga	780
tgcaccgctt tggacggcat ttacctccac ttttccagac tgtcacggcc aatgcttacc	840
tcttctttcc tcctgtggtc aaccctattg tctatagtat caaaatcaaa gaaattcgca	900
acagcgttgt tcttacacta tccaggaaga ggggtgagtt ctaatggaga ccgaagatac	960
cc	962

&lt;210&gt; 787

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g637 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 787

acctcagagg atccagaacg gcagctgggc cttgctggac tgttctctgc catgtgcctg	60
gtcatgggtg tggggaacct gctcatcctc cggccatgag cctgactcc cacctccaca	120
cctccatgta cttcttctc tccaacctgt cttgcctga catcggtttc acctccacca	180
cgggtcccca gatgactgtg gacatccagt ctgcagcag agtcatctcc tatgcaggct	240
gcctgactca gaagtctctc tttgccattt ttggaggcac ggaagagaga catgctcctg	300
agtgtgatgg cctatgaccg gttttagacc atctgtcacc ctctatatca ttcagccatc	360
atgaacctgt gtttctgtgg ctctcctagt ttgctgtctt tttttttct cagtctttta	420
gactcccagc tgtacaactt gattgcctta ctaatgacct gcttcaagga ggtggacatt	480
cctaatttct tctgtgacct ttctcaactc ccccatcttg ccgttgtgac accttcatca	540
ataacataat catgtatttc cctactgcc aatttgggtt tcttcccac tcggggaccc	600
ttttctctta ctataaaatt gtttctcca ttctgagggt ttcatcatca ggtgggaagt	660
ataaagcctt ctccacctgt ggggtctacc tgtcagttgt ttgctgattt tatggaagag	720
gtgttggagg gtacctcagt tcagatgtgt catcttcccc cagaaagggt gcagtggctg	780
cagtgtatga cacggtggtc acctccatgc tcaaccctt tatctacagc ctgggaaaca	840
gggatattaa aagtgtcttg cggcgccgc aa	872

&lt;210&gt; 788

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g638 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 788

ctagtggact tttgttactc ttcagctgtc actcccacag tcatagctgg gctcgttata	60
ggagacaagg tcatctctta caatgcatgt gctgctcaaa tgttcttttt tgcagccttt	120
gccactgtgg aaaatttctt cttggcctca atggcctatg accgctatga tgcagtgtgc	180
aaacccttac attacaccac caccatgaca acaagtgtgt gtgcatgtct ggctataatc	240
tgttatgtct gtggtttctt gaatgcctcc atacacattg gggaaacatt gtctctcttt	300
ctgtatgtcc aatgaagtcc attgcttttt ctgtgatgtt ccaccagtca tggctctgtc	360
ttgctgtgat agacatgtga atgagctagt tctattttat gtagccagtt tcaatatctt	420
ttctgccatc ctagttatct tgatctccta cctattcata ttatcacca tcctaaagat	480
gcactcagct tcaggatacc agaaggcttt gtccacctgt gcctcccacc tcaatgcagt	540
catcatcttc tatgggacta ttatcttcat gtacttacag ccagctctg gtcactccat	600
ggacacagac aaactggcat ctgtgttcta tactatgatc atcccc	646

<210> 789  
 <211> 648  
 <212> DNA  
 <213> Unknown (H38g639 nucleotide)

<220>  
 <223> Synthetic construct

<400> 789  
 tttgtggaca tctgcttctc ctgcaccacc gtccccaaga tgctggccaa tcacatactc 60  
 gagactcaga ccattctcct ctgtggctgt ctacacacaga tgtatttcgt tttcatgttc 120  
 gtggacacgg acaatttcct cctagctgtg atggcctatg accactttgt cgccgtgtgc 180  
 caccctttac attacacagc aaagatgacc catcagctct gtgccctgct gggtgtgtga 240  
 ttatgggtgg ttgccaacct gaatgtcctt ctgcacaccc tgctgatggc tccactctca 300  
 ttctgtgcag acaatgccat cactcacttc ttctgcgatg tgactcccct actgaaactc 360  
 tcctgtctcag acacacacct caatgaggtc ataatcctta gtgagggtgc cctgggtcatg 420  
 atcaccccat ttctttgcaa cctggcgtct tatatgcaca tcacctgcac tggcctgaag 480  
 ggcccatcca caaaggaag gtggaaagcc ttctccacct gtggctctca cctggctgtg 540  
 ggtctcctct tctacagcac catcactgct gtgtatttta accctctgtc ctccactca 600  
 gctgcgaaag acactatggc tactgtgttg tatacagtag tgactccc 648

<210> 790  
 <211> 471  
 <212> DNA  
 <213> Unknown (H38g640 nucleotide)

<220>  
 <223> Synthetic construct

<400> 790  
 atctgcagcc ccttgcgtga caatgtcacc atgtcctacc accactgctt ctggctcaca 60  
 gtgggagttt acatttttagg catccttgga tctacaattc acaccggctt tatgttgaga 120  
 ctctttttgt gcaagactaa tgtgattaac cattattttt gtgatctctt ccctctcttg 180  
 gggctctcct gctccagcac ctacatcaat gaattactgg ttctggctct gagtgcattt 240  
 aacatcctga cgctgcctt aaccatcctt gcttcttaca tctttatcat tgccagcacc 300  
 ctccgcattc gctccactga gggcaggctc aaagccttca gcacttgagc ctcccacatc 360  
 ttggctgttg ctggtttctt tgggtctgca gcattcatgt acctgcagcc atcatctgtc 420  
 agtcccatgg accaggggaa agtgcctctt gtgttttata ctattgttgt g 471

<210> 791  
 <211> 975  
 <212> DNA  
 <213> Unknown (H38g641 nucleotide)

<220>  
 <223> Synthetic construct

<400> 791  
 atgaagactt tgtgttcctt tcttcagatc agcagaaata tgcatacaaga aaaccaaacc 60  
 accatcactg aattcattct cctgggactc tccaaccagg ctgaacatca aaacctcctc 120  
 tttgtgcttt tcctgagtat gtatgtggct actgtggttg ggaacgggct catcattgtg 180  
 gctatcagct tggatatata ccttcacacc ccatgtatc tcttccttgc ctacctatcc 240  
 ttgtgctgata tttcctccat ttccaactca gtccccaata tgctgggtgaa tattcaaacc 300  
 aacagccaat ccattctctta tgagagctgc atcacacaga tgtacttttc tattgtgttt 360  
 gtcgtcactg acaatttgct tttggggacc atggccttcg accactttgt ggcgatctgc 420  
 caccctctga actatacaac tttcatgcgg gccagggttc gcactttgct cacagtcatc 480  
 tcgtgggttc tcagtaatat tattgtctct acacacaccc ttctgtcatc tcaattgtct 540  
 ttctgtgacc acaacactct cccacacttc ttctgtgact tggccctctt gctcaaatctg 600  
 tctgtttcag atacaatgat caatgagctt gtgtgtttta ttgtgggttt atcagttatc 660  
 atcttccctt ttgtactcat cttcttctcc tatgtctgca tcatcagagc tgtcctggga 720  
 gtatcatcca cacagggaaa gtggaaagcc ttctccactt gtggctctca cctgacaatt 780

gcattactgt	tctacggaac	cactgtaggc	gtgtactttt	tccccctcctc	cactcaccct	840
gaggacactg	ataagattgg	tgctgtccta	ttcactgtgg	tgacacccat	gatgaacccc	900
ttcatctaca	gcttgaggaa	taaggatatg	aaaggtgccc	tgagaaagct	catcaataga	960
aaaatttctt	ccctt					975

&lt;210&gt; 792

&lt;211&gt; 943

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g642 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 792

atgagaccta	ataacagcat	tacagaattt	gtcctcctgg	gattctctca	ggatcctgg	60
atgcaaaaag	aattatttgt	catgttttta	ttcacatacg	ttgtgactgt	gttggggaac	120
cagctcattg	tggtgactat	cattgccagc	ccttccttgg	gtccccaat	gtacttcttc	180
cttgccctgcc	tgctatttat	agatgctgca	tatttcaactg	tcatttctcc	caaattgatt	240
gtggactttac	tctgtgataa	aaagactatt	tccttccaaa	cgttcatggg	ccaactattt	300
atagaccact	tctttgggtg	tgagaggcc	ttccttctgg	tggtgatggc	ctatgatcgc	360
tatgttgcca	tctgtaagac	attgcactat	ttgaccatca	tgactcgaca	ggtttgatc	420
cttgcatcgc	tgggtggctgc	gacaggcgg	tttgtgcatt	ctgtgtttca	aattgttggt	480
gtgtacagtc	tccttttctg	tggcgccaat	gtcattgatc	atttcagttg	tgacatgtat	540
ccattattgg	aactggcatg	aactgacacc	tactttatag	gcctcactgt	tgttttcagt	600
ggtggagcac	tctgtatgg	catcttcacc	cttctaataa	tttctctatg	ggtcaccta	660
aactccctta	aaacttacac	tcaggaagg	agcataaagc	cctgtctacc	tgagctccc	720
acatcactgt	gattgttctc	tttttattcc	ctgtatttcc	atatatgtga	gacctgttcc	780
aaacttttct	attgacacat	tcatgactgt	cttttataca	gttatcacac	ccaagttaa	840
tcctttaata	tacactttca	gaaattcaga	gatgagaaat	gttatagaaa	aactcttgg	900
gaaaaaggta	actatattta	gaataacagg	gtccatcctc	atg		943

&lt;210&gt; 793

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g643 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 793

atgagacaga	ataaaaaataa	tacagaattt	gtcctcttgg	gcttctctca	ggatcctgat	60
gtgcaaatgc	attatttgtc	atgttttact	cacataattg	gtgacaacag	tggggaacct	120
gtcatttgtg	gtgactatta	ttgccagccc	ttccttgggc	tcctccagtgt	atttctgact	180
tgctgtctcg	tcatgtatag	atgctgcata	ttccactacc	atttctccca	aactgattgt	240
agagttactc	attgataaaa	agactatttc	cttccgagct	tgcatgggcc	agctatttat	300
agaacacttg	tttgggtgta	ctgagatctt	cattctgatg	atgatggcct	gtgatcgcta	360
tgtggacatc	tgtaagccac	tgactatttt	gaccatcatg	aattgacagg	tttgcacct	420
tctgttgggtg	ttggctgtga	caggagggtt	tgtacattct	atgtttcaaa	ctgttgttgt	480
gtacaatctc	cctttctctg	gccccaatgt	cattgacatt	gaccactttg	tctgtgacat	540
gtacccatta	ttggaactgg	cgttcactga	tacctacttt	ataggcctca	ctgttgttgt	600
caatggtgga	gcaatgtgta	tggtcatctt	caccattcta	ctaatacct	acggaatcat	660
cctaaactct	cttaaaactt	atagtcagga	agggagggtg	aaagccctgt	ctacctgcag	720
ccccacata	accgtggttg	tcctcttttt	tggtccctgt	attttcatat	atgttagacc	780
tgtttcaacc	tttctatttg	ataaattcat	gactgtgttt	tatacagtta	tcacacccat	840
gttgaatcct	ttaatatata	cgttgagaaa	ttcagagatg	agaaactcta	tagaaaatct	900
cttgtgtaaa	aaagctatct	gtagttagaa	taagagtgtc	cc		942

&lt;210&gt; 794

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g644 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 794

gagtaaatga	gacagaataa	cagtagtaca	gaatttggtc	tccctgggctt	ttctcaggat	60
cctgatgtgc	aaaatgcgct	atttgatcatg	tttttactga	catacattgt	gacaatgggtg	120
gggaacctac	tcattgtggt	gactattatt	gccagccctt	ccttgggctc	cccaatgtac	180
tttttccttg	cccacctgtc	atttatagat	gctgtgtatt	ccaccaccat	ttctcctgta	240
ttgattgtag	acttactctg	tgacaaaaag	acgatttcct	tctgagcttg	catgggacaa	300
ctgtttatag	accacttatt	tggtgggttct	gaggtcttcc	ttctgggtgt	gatggcctgt	360
gacgcgtgtg	tgcccatctg	taagccactg	cactatttga	ccatcatgaa	tcgacagggt	420
tgcatctctc	tcttggtgtt	ggctgtgact	ggagggtttt	tgcatcctgt	atttcaagtt	480
gttggtgtgt	acagtctccc	tttctgtggc	cccaatgtca	ttgaccactt	tttctgtgac	540
atataccctt	tatttggaac	tgcatgcac	tgacacctac	tttataggcc	tcactgtgggt	600
tttcaatggt	ggagcaatgc	gtatgggtcat	cctcaccctt	ctactagtct	tctatggagt	660
catcctaaac	tcccttaaaa	cttacagtca	ggaagggagg	cataaagccc	tgtctacctg	720
cagctcccat	gttaccgtgg	ttatcttgtt	ttttgcttcc	tgtattttca	tatatgttag	780
acctgtttca	aattttctgt	tgataaatte	atgactgtgt	tttatacggg	tatcacaccc	840
atgttgaaac	cttttatatg	catgttgaga	aattcagaga	tgagaaatgc	tatagaaaaa	900
ctcctgtgta	aaatgaactg	tagttagaat	aagagtgttc	cttcc		945

&lt;210&gt; 795

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g645 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 795

atgggactga	gtaacaatgt	tacagaactt	ttcctcctgg	gcctcactca	ggatctcgat	60
gtgcaaaatg	cattatttgt	catgttttta	ctaacataca	ttgtgactat	ggtgggggaa	120
ctgctcattg	tggtgactat	tattgccacc	ccatccttgg	gtcctccaat	gtactttttc	180
cttgccctgcc	tgtcatttat	agatgctgtg	tattccacca	ccatttatcc	caaattgggt	240
gtagactaac	tccataatta	aaagactatt	ttgttcccaa	cttgcatggg	ccagccactt	300
acagaccact	tatttggtgg	tggtgaggtc	tttttttctg	ttgggtgatg	cctgtgatcg	360
ctatgtggcc	atctgtaagc	cactgcacta	ttttaccatc	atgaatcgac	agggttttcat	420
ccttctgttg	gtagtggctg	tgactggagt	tttgtgcgtt	ctgtgttcca	aattgttgtt	480
gtgtacagtc	tccctttctg	tgccccaat	gtcattgacc	actttttctg	taacatgtac	540
ccattaatgg	aaatggcatg	aactgacacc	tactttatag	gcctcactgt	ggttttcaag	600
gttgaagcaa	tctgtgtggt	catcttcacc	cttctactaa	tctcctctgg	cgtcactccta	660
atctccctta	aaacttacag	tcaggaaggg	aggcataaag	ccctgtttac	ctgcagctcc	720
cgcattactg	tagttgtcct	cttttttgtt	ccctgtattt	tcatgtatgt	tagacctgtt	780
tttaacttcc	ccattgataa	atattattatt	gtgttttata	cagttatcac	acccatgctg	840
aatcctttta	tatacatgtt	gagaaattca	tagacgagaa	atgctataga	aaacccttag	900
tgtaaaaaat	taactgtaga	tagaataaga	gtgtacatc			939

&lt;210&gt; 796

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g646 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 796

atgagacctt	ataacagtat	tacagaattt	gtcctcctgg	gcttttcaca	ggatcctgat	60
atgcaaaaca	cattatttgt	catgttttta	ctcacataca	ttgtgacagt	ggtgggggaa	120
ctactcgttg	cgggtgactat	tattgtcagc	ccttccttga	gtcctccaat	gtaattcttc	180
cttgcttgcc	tgtcattaat	agatgctgta	ttatccacca	ccatttctcc	catattgatt	240



gtagacctac	tctgtgacaa	aaagactatt	tccttcccag	cttgcattggg	ccagctatatt	300
acagaccact	tggttggtgg	aactgagatc	ttccttctgg	tggtgatggc	ctatgatcgc	360
tacgtggcca	tctgtaagcc	actgcactat	ttaccatca	tgaatcgaca	ggtttccatc	420
cttctgttgg	tggtggccat	gactggaggt	ttccttcatt	ctgtgtttca	aattgctggt	480
ctgtacagtc	tccctttctg	tggtcccaat	gtcattgacc	actttttctg	tgacatgtac	540
ccattattgg	aactggcgtg	cactgacacc	tactctatag	gcctcactgt	agttttcagt	600
gggtggagcaa	tgtgtatggg	catcttcgcc	cttctactaa	tctcctatgg	agtcagccta	660
aactccctta	aaacttatag	tcaggaaggg	aggcgtaaag	ccctgtctac	ctgcagctcg	720
cacatcaccg	tggttgctct	cttttttggt	ccctgtatgt	tcatgtatgt	tagacctgtc	780
tcaaaccttc	ctattgataa	attcgttact	gtgttttata	cagttaatcac	acccatgctg	840
aatccttttt	tatacacgtt	gagaaattca	gagatgataa	atgctataaa	acacctgttg	900
tgtaagaagc	taactatagt	tagaataaga	gtgtccctcc	tcatg		945

&lt;210&gt; 797

&lt;211&gt; 967

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g647 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 797

atgggatcta	gtaacaatgt	tacagaatgt	gtcctcctgg	ccctcactca	ggctcctgat	60
gtgcaaaaag	tattatgtgt	aatgttttta	ttcacatata	ttgtgactat	gggtggcaac	120
ctgctcactg	tggtgaccat	ttttgccctc	cctcttttgg	ctccccagtg	taactcttcc	180
ttgcctgcct	gtcattgatg	gatgccgtat	attccacttc	attttctcct	aaactgatga	240
tagacttact	ctgcgataaa	aaagactggt	tccttcccgg	cttgcattgg	ccagctatatt	300
gcggaaccac	tatttggtgg	tggtgaggtc	tttcttttctg	tggtggatggc	ctatgatcac	360
tatgtggcca	tctctaagcc	actgcactat	ttgatcatcg	tgaatcgact	ggtttgcatc	420
cttctgttgg	tggtggccgt	gactggagga	ttttgaattc	tatgtttctt	tttttttaaa	480
tttatttatt	tttttatgtg	aattctatgt	ttcaaattgt	cgttgtgtac	agtcctccct	540
tctgtggctc	caatgtcatt	gaccacattg	tctgtgacat	gtaccatta	ctggaactgg	600
catgcgctga	cacctacttt	atagggtca	ctgtgattgc	caatgggtgga	gcaatctgta	660
tggtcatctt	ctgccttcta	ctaaccctct	atggagtcac	cctaaacttc	cttaaaactt	720
atagtcaaga	agggaggcat	agaaccctgt	ctacctgcag	ctcccacatt	actgtggttg	780
tcctcttttt	tggtccctgt	attttcatgt	atgttagacc	tgtttcaaac	ttccctattg	840
ataaatcat	tactgagttt	tatacagtta	tcaccccaa	gttgaatcca	ttaatccaac	900
cactgagaaa	ttgagaaatg	agaattacta	tgaagaaact	ctggtgttaa	acctgaacta	960
tagttag						967

&lt;210&gt; 798

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g648 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 798

atgaaaaata	agaacaatgt	gactgaatgt	atcctcttag	ggctcacaca	gaaccctgag	60
gggcaaaaag	ttttatgtgt	cacattctta	ctaacttaca	tggtgacgat	aatgggcaac	120
ctgcttatca	tagtgaccat	catggccagc	cagtccttgg	gttcccccat	gtactttttt	180
ctggcttctt	tatcatcatt	agataccgtc	tattctactg	catttgctcc	caaaatgatt	240
gttgacttgc	tctctgagaa	aaagaccatt	tcctttcagg	gttgatggc	tcaacttttt	300
atggatcatt	tatttgctgg	tgctgaagtc	attcttctgg	tggtaatggc	ctatgatcga	360
tacatggcca	tctgtaagcc	tcttcatgaa	ttgatcacca	tgaatcgctg	agtcctgtgt	420
cttatgtctg	tggtggcctg	gattggaggg	tttcttcaact	cattgggttca	atttctcttt	480
atttatcagc	tccctttctg	tggtaccaat	gtcattgaca	acttcctgtg	tgatttgat	540
cccttattga	aacttgcttg	caccaatacc	tatgtcactg	ggctttctat	gatagcta	600
ggaggagcga	tttggtctgt	caccttcttc	actatcctgc	tttcttatgg	ggatcatatta	660
cactctctta	agactcagag	tttggaaggg	aaacgaaaag	ctttctacac	ctgtgcatcc	720

cacgtcactg	tggtcatttt	attctttgtc	ccctgtatct	tcttgtatgc	aaggcccaat	780
tctacttttc	ccattgataa	atccatgact	gtagtcttaa	cttttataac	tcccatgctg	840
aaccactaa	tctataccct	gaagaatgca	gaaatgaaaa	gtgccatgag	gaaactttgg	900
agtaaaaaag	taagcttagc	tgggaaatgg				930

&lt;210&gt; 799

&lt;211&gt; 825

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g649 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 799

atgggtgggaa	acctcctcat	ttgggtgact	actattggca	gcccctcctt	gggctcccta	60
atgtacttct	tccttgccta	cttgtcactt	atggatgcca	tatattccac	tgccatgtca	120
cccaaattga	tgatagactt	actctgtgat	aaaatcgcta	tttccttgtc	agcttgcattg	180
ggtcagctct	tcatagaaca	cttacttggg	gggtgcagagg	tcttcctttt	gggtggatg	240
gcctatgac	gctatgtggc	tatctctaag	ccgctgcact	atttgaacat	catgaatcga	300
ctggtttgca	tccttctgtt	gggtggggcc	atgattggag	gttttgtgca	ctctgtggtt	360
caaattgtct	ttctgtacag	tctaccaatc	tgtggcccca	atgttattga	ccactctgtc	420
tgtgacatgt	accattgtt	ggaactgtt	tgccttgaca	cctactttat	aggactcact	480
gtggttgcca	atgggtggaat	aatttgtatg	gtcatcttta	cctttctgct	aatctcctgt	540
ggagtcaccc	taaacttcct	taaaacttac	agtcaggaag	agaggcataa	agccctgcct	600
acctgcatct	cccacatcat	tgtgggtgcc	ctcgtttttg	ttccctgtat	ttttatgtat	660
gttagaccgc	tttccaactt	tccctttgat	aaattaatga	ctgtgtttta	ttcaattatc	720
acactcatgt	tgaatccttt	aataactcgc	ttgagacaat	cagagatgaa	aaatgctatg	780
aaaaatctct	gggtgtgaaa	gttaagtata	gttagaaaaa	gagta		825

&lt;210&gt; 800

&lt;211&gt; 654

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g650 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 800

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagac	tcattctcta	ggcaggctgc	ctgactccca	tgtctctctt	tgccatcttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatccct	atgaccggtt	tgtagccatc	180
tgtcaccctc	tatatcattc	agccatcatg	aaccggtgtt	tctgtggctt	tctagttttg	240
ttgtcttttt	tttctcagtc	tcttttagac	gcccagggtg	acaacttgat	tgctttacaa	300
atgacctgct	tcaaggatgt	ggaaattcct	aatttcttct	gggaaccttc	tcaactcccc	360
catcttgcac	gttgcgacac	cttcaccaat	aacataatca	tgtattcccc	tgctgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ataagattgt	ttcctccatt	480
ctgagggttt	cttcatcagg	tgggaagtat	aaagccctct	ccacctgtgg	gtctcgctg	540
tcagttgttt	gctgagttta	tggaaacagg	gttggagagt	acctcggttc	agatgtgtca	600
tcttccccga	gaaagggtgc	agtggcctca	gtgatgtaca	cggtggtcac	cccc	654

&lt;210&gt; 801

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g651 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 801

tcaatggccc	tcattgtcat	ctgcaccacc	ggacccaaga	ggccttcaac	tacctgtctg	60
gcagcaagtc	ccatttctat	ggctgttgtg	ccacacaaat	tttcttctat	acatcactgc	120

ttggctctga	gtgctttctt	ttggctgtta	tggcttatga	ccgctacact	gccatttgcc	180
accctctaag	atacaccaat	ctcatgagcc	ctaaaatttg	tggacttatg	actgcctttt	240
cctggatcct	gggctctacg	gatggaatta	ttgatgttgt	agcaacattt	tccttctcct	300
actgtgggtc	tcgggaaata	gcccacttct	tctgtgactt	ccccctccct	actaatcctc	360
tcatgcagtg	acacatcaat	atttgaaaag	attcttttca	tctgctgtat	agtaatgatt	420
gttttccctg	ttgcaatcat	cattgcttcc	tatgctcgag	ttatcctggc	tgtcattcac	480
atgggatctg	gagagggtcg	tgcgaaagct	tttactactt	gttcctctca	cctcttggtg	540
gtgggaatgt	actatggagc	agctttgttc	atgtacatac	ggccacacac	tgatcgctcc	600
ccaacacagg	acaagatggt	gtctgtattc	tacaccatcc	tcactccc		648

&lt;210&gt; 802

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g652 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 802

tttgtggaca	ttgcctgttc	ctcagccaca	gcacccaaga	tgattgaaga	ctttgtttct	60
gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttgtgctg	agatttttgt	tttgactgtc	atggcttttg	atcgctatgc	tgctatctgc	180
caaccctcc	gttacctgt	catcatgagt	gctaattgctt	atactgtgct	ggcatcactg	240
tcctgggttg	gggcccctgg	tcattccctt	gttcagaccc	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaacattac	ttttgtgatg	tccaccagct	cctaaaactt	360
gcctgtgctg	atacaactct	ggtaaatatg	ttgggtggtg	ccaacagtgg	tctcatctcc	420
ctggggtgtt	tcctcattct	tttggcctcc	tacacagtca	ttctgtttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactactttc	ccattggata	600
aagctgtgtc	tgtgttctat	accaccatca	ccccca			635

&lt;210&gt; 803

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g653 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 803

ttgcctgaca	tgggtttcac	ctccacacgg	tccccaagat	gattgtggac	atccagtcctc	60
acagcagagt	catctcctat	gcaggctgcc	tgactcagat	gtctctcttt	gccatttttt	120
gaggcagga	agagagacat	gtcctgagt	gtgatggcct	acgaccagtt	tgtagccatc	180
tgtaaccctc	catatcggtc	agccatcttg	aaccctgtgt	tctgtggctt	cctagatttg	240
ttgtccttgt	ttttttttct	tttttttttt	tctcagctct	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	tcttctggga	360
accttctcaa	ctcccccatc	ttgcatgttg	tgacatcttc	accaggaaca	tcaacctgta	420
tttccctgct	gccatatttg	gttttcttcc	catctcgggg	acctttttct	cttactctaa	480
aattgtttcc	tccattctga	gggtttcatc	gtcagggtgg	aggtataaag	ccctctccac	540
ctgtgggtct	cacgtgtcag	ttgtttgctg	agtttatgga	acaggcgttg	gagggtacct	600
cagttcggat	gtgtcatttt	ccccagaaa	gggtgcagtg	gcctcagtga	tgtacgcggt	660
tgtcaccccc						670

&lt;210&gt; 804

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g654 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

<400> 804  
 ctccctggatc tttgtttacac cacatgtaca gtcccacaaa tgctagtaaa tttatgcagc 60  
 atcaggaaaag taatcagtta tctgtggctgt gtagcccagc ttttcatatt tctggccttg 120  
 ggggctactg aatatcttct cctggccgctc atgtcctttg ataggtttgt agctatttgt 180  
 cggcctctcc attactcagt tatcatgcac cagagactct gcctccagtt ggcagctgca 240  
 tccagggtta ctgggttttag taactcagtg tggttgtcta cctgactct ccagctgcca 300  
 ctctgtgacc cctatgtgat agaccacttt ctctgtgaag tccctgcaact gctcaagtta 360  
 tcttgtgttg agacaacagc aaatgaggct gaactattcc ttgtcagtga gctcttccat 420  
 ctaatacccc tgacactcat ccttatatca tatgctttta ttgtccgagc agtattgagg 480  
 atacagtctg ctgaagggtcg acaaaaagca tttgggacat gtgggttccca tctaattgtg 540  
 gtgtctcttt ttaatagtag agccgtctct gtgtacctgc aaccaccttc gccagctcc 600  
 aaggaccaag gaaagatggt ttctctcttc tatggaatca ttgcaccc 648

<210> 805  
 <211> 655  
 <212> DNA  
 <213> Unknown (H38g655 nucleotide)

<220>  
 <223> Synthetic construct

<400> 805  
 ttgcctgaca tgggtttcac ctccaccatt gtcccacaaga tgattgtgga catccagtct 60  
 cacagcagag tgatctccta tgcaggccgc ctgactcaga tgtctctctt tgccattttt 120  
 ggaggcatgg aagacagaca tgtccttgag tgtgatggcc tatgaccggg tctagccat 180  
 ctgtcaccct ctatatcatt cagccatcat gaatccgtgt ttctgtggct tctactttt 240  
 gttgtctttt ttttttctca gtcttttaga cgcccagctg cacaacttga ttgccttaca 300  
 aatgacctgc ttcaaggatg tggaaattcc taatttcttc tgtgaccctt ctcaactccc 360  
 ccatcttgca tgttgtgaca ccttcaccaa taacataatc atgtattttt ctgctgccat 420  
 atttggtttt ctteccatct cggggaccct tttctcttac gataaaattg tttcctccat 480  
 tctgagggtt tcatcatcag gtgggaagta taaagccttc tccacctatg ggtctcacct 540  
 gtcagatggt tcttgatttt atggaacagg cggtggaggg tacctcagtt cagatgtgtc 600  
 atcttccccg agaaagactg cagtggcctc agtgatgtac acagtgggtca ccccc 655

<210> 806  
 <211> 662  
 <212> DNA  
 <213> Unknown (H38g656 nucleotide)

<220>  
 <223> Synthetic construct

<400> 806  
 tttcctgaca tgggtttcac ctccaccaca gtcccacaaga tgattgtgga catccagtct 60  
 cacagcagag tcatctccta tgcaggctgc ccgactcaga tgtctctctt tgccattttt 120  
 ggagacacgg aagagagaca tgttcctgag tgtggtggcc tatgaccggg ttgtagccat 180  
 ctgtcaccct ctatatcgtt cagccatctt aaaccctgt ttctgtggct tcttagattc 240  
 gttgtccttg gttttttttt ttttctcagt ctttttagact cccagctgca caacttgatt 300  
 gccttataaa tgacctgctt caaggatgtg gaaattccta atttcttctg ggaaccttct 360  
 caactcccc atcttgcag ttgtgacatc ttcaccagga acatcaacct gtatttccct 420  
 gctgccatat ttgggtttct tcccatctcg gggacgctt tctcttgcta taaaattgtt 480  
 tctttcattc tgagggtttc atcatcagg gtggaagtata aaccttctcc gcctgtgggt 540  
 ctcatctgtc agttgtttac tgattttatg gaacaggctt tggagggtac ctgagttcag 600  
 atgtgtcatc ttccccgaga aagactgcag tggcctcagt gatgtacgca gtgggtcaccc 660  
 cc 662

<210> 807  
 <211> 647  
 <212> DNA  
 <213> Unknown (H38g657 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 807

gtgctggatg	tcggatgtat	cactgtcact	gttcctgcaa	tggtgggtcg	tctcttgccc	60
cacaagtcca	caatttccta	tgacgcctgc	ctctcccagc	tcttcttctt	ccaccttctg	120
gctgggatgg	actgcttctt	gctgaccgcc	atggcctatg	accgactcct	ggccatctgc	180
cagcccctca	cctacagcac	ccgcatgagt	cagacagtc	agaggatgtt	ggtggctgcg	240
tcctgggctt	gtgccttcac	caacgcactg	acccacactg	tggtccatgtc	cacgctcaac	300
ttctgtggcc	caaagtgggt	caatcacttc	tactgtgacc	tcccacagct	cttccagctc	360
tcctgtctta	gcacccaact	caatgagctg	ctgctctttg	tagcagcagc	cttcatggct	420
tggtcaccc	tggtcttcat	cagtgtgccc	tatgcccctg	tggttagctgc	tgtgctgcaa	480
atcgctccgc	tgagggcaga	aagaaggcct	tctccacatg	tggtctccac	ctcactgtgg	540
tggtcatctt	ctatgggaca	ggtgtcttca	gctacatgag	gctgggttca	gtggaatctt	600
cagacaagga	taaggggggt	ggggttttca	tgactgtgat	caacccc		647

&lt;210&gt; 808

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g658 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 808

tttgtggaca	tagcctgttc	ctcagccaca	gcacccaaga	tgattgaaga	ctttgtttct	60
gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggtgtgtctg	acatttttgt	tttgactgtc	atggcttttg	atcgctgtgc	tgctatctgc	180
caaccctcc	gttacactgt	catcatgagt	gctaattgctt	atactgtgct	ggcatcactg	240
tcctgggttg	gggcctggg	tcattccttt	gttcagaccc	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaccattac	ttttgtgatg	tccaccaggt	cctaaaactt	360
gcctgtgctg	atacaactct	ggtaaatatg	ttgggtgggtg	ccaacagtg	tctcatctcc	420
ctgggggtgt	tcctcattct	tttggcctcc	tacacagtca	ttctgtttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttcctgt	tatctttatt	tatctccatc	cactactttc	ccattggata	600
aagctgtgtc	tgtgtcttat	accaccatca	cccca			635

&lt;210&gt; 809

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g659 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 809

ttctctgacc	tctgcttctc	ttccgtgacc	attcccaagt	tgttacagaa	catgcagaac	60
caggacccat	ccatccccta	tgcggaactgc	ctgacccaaa	tgtacttctt	cctgttattt	120
ggagacctgg	agagcttctt	ccttctggcc	atggcctatg	accgctatgt	ggccatctgc	180
ttcccctgc	actacaccgc	catcatgagc	cccatgctct	gtctcgccct	ggtggcgctg	240
tcctgggtgc	tgaccacctt	ccatgccatg	ttacacactt	tactcatggc	caggttggtg	300
ttttgtgcag	acaatgtgat	ccccactttt	ttctgtgata	tgtctgctct	gctgaagctg	360
gccttctctg	acactcgagt	taatgaatgg	gtgatattta	tcatgggagg	gctcattctt	420
gtcatcccat	tcctactcat	ccttgggtcc	tatgcaagag	ttgtctcttc	catctcaag	480
gtcccttctt	ctaagggtat	ctgcaaggcc	ttctctactt	gtggctccca	cctgtctgtg	540
gtgtcactgt	tctatggaac	cgttattggt	ctctacttat	gctcatcagc	taatagtctt	600
actctaaagg	acactgtcat	ggctatgatg	tacactgtgg	tgaccccc		648

&lt;210&gt; 810

&lt;211&gt; 438

&lt;212&gt; DNA

<213> Unknown (H38g660 nucleotide)

<220>

<223> Synthetic construct

<400> 810

actttgcaga	atatcacctc	cactttccatc	attttctctgc	tcactgggtgt	tcctgggctg	60
gaagccttcc	acacctggat	ctccattccc	ttctgcttcc	tctctgtaac	tgctctcttg	120
ggaaacagcc	tgatcctctt	cgctaccatc	actcagccca	gcctccacga	accaatgtac	180
tatttctctt	ccatgctgtc	cgccactgac	ctcggcctgt	ccatatccac	tctggtcacc	240
atgctgagta	tattctgggt	caatgtgagg	gaaatcagct	ttaatgcctg	cttgtcccac	300
atgttcttta	ttaaattctt	cactgtcatg	gaatcctcag	tgctgttggc	catggctttt	360
gacgctttgg	tgccgtctct	atccccttag	tatgccatga	tttaactgac	tcagatagct	420
aaaatgagtg	cagtgtat					438

<210> 811

<211> 1002

<212> DNA

<213> Unknown (H38g661 nucleotide)

<220>

<223> Synthetic construct

<400> 811

gcaggtgtgg	aaaacgataa	tacaagttct	ttcgaaggct	tcatactggt	gggcttctct	60
gacgtccccc	acctagagct	gacgtctttt	gtgggtgtcc	tcatacttta	tctgctgact	120
cttcttggca	acatgacat	tgtcttgcct	tcagctctgg	attcccggct	gcacacacca	180
atgtatttct	ttttggcaaa	cctctcattc	ctggacatgt	gtttcaccac	aggttccatc	240
cctcagatgc	tctacaacct	ttgggggtcca	gataagacca	tcagctatgt	gggttgtgcc	300
atccagctgt	actttgtcct	ggccctggga	gggggtggag	gtgtcctcct	ggctgtcatg	360
gcatatgacc	gctatgctgc	agtctgcaaa	cccctgcact	acaccatcat	catgcaccca	420
cgtctctgtg	gacagctggc	ttcagtgcca	tggtctgagtg	gctttggcaa	ttctctcata	480
atggcaccac	agacattgat	gctaccccgc	tgtgggcaca	gacgagttga	ccactttctc	540
tgtgagatgc	cagcactaat	tggtatggcc	tgtgtagaca	ccatgatgct	tgaggcactg	600
gcttttgccc	tggcaatctt	tatcatcctg	gcaccactca	tcctcattct	catttcttat	660
ggttacgttg	gaggaacagt	gcttaggatc	aagtcagctg	ctgggcgaaa	gaaagccttc	720
aacacttgca	gctcgcactc	aattgttgct	tctctcttct	atgggtacaat	catatacatg	780
tacctccagc	cagcaaatac	ttattcccag	gaccagggca	agtttcttac	ccttttctac	840
acaattgtca	ctcccagtg	taaccccctg	atctatacac	taagaaacaa	agatgttaaa	900
gaggccatga	agaaggtgct	aggggaaggg	agtgcagaaa	tatagtaagg	gggtgattaaa	960
ctttgggatt	gtattttgac	ccatcttcta	tatatgttgt	ta		1002

<210> 812

<211> 827

<212> DNA

<213> Unknown (H38g662 nucleotide)

<220>

<223> Synthetic construct

<400> 812

ctctacctca	tcaagcatga	ccacagtctt	catgagccca	tgtactactt	cctcaccatg	60
ctggcaggca	cagacctcat	ggtgacattg	accacgatgc	ctactgtaat	gggcataccta	120
tgggtgaatc	acagggaaga	ttagcagtgt	gggctgcttc	ctacaggctt	actttattca	180
ctccctttct	gttgtggaat	caggttccct	cctggcaatg	gcatatgatc	gtctcattgc	240
catccgcaat	cctttgagat	atgctctcca	ttccaccaa	tactagagtc	atagcggttag	300
gagtgggatt	gttcctaagg	ggtttggtat	ccatcctgcc	tgtaattttg	cgtctttttc	360
catttccata	tggcaaatct	catgttatca	cacgttgctt	tctgcctcca	ccaagaaate	420
atgagactgg	cttgtgctga	cataacttcc	aataaacttt	accctgtaat	tttgatctct	480
ttaacaatct	ccctaaactc	tctgatcacc	ccctcctcct	atataccta	ccttaatact	540
gtcataggca	ttgcctctgg	tgaaaaaaaa	ccaaagccct	caatacctgt	atctcccaca	600

taagttgtgt	ccttatctcc	tatgttacgg	tgatgggttt	gacattcatt	tacaaatttg	660
ggaagaatgt	gccaaagggt	gtccacatta	tcataagtta	catctacttc	ctctttcccc	720
ctttaatgaa	ccctgtcatc	tacagcatca	aaaccaagca	aatacaatat	ggcattatcc	780
gcctttttatc	taaacaatagg	tttagtaggt	aaactcggat	ctggaaa		827

&lt;210&gt; 813

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g663 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 813

ttggccgaca	tcggttttcac	ctccaacacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgtgtgtttt	120
ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggg	ttgtagccat	180
ctgtcaccc	ctatattgtt	cagccatctt	taaccctgtg	ttctgtggct	tcctagattt	240
gttgtctttt	tttttttttt	ttctcagtct	ttcagactcc	cagctgcaca	acttgattgc	300
cttacaaatg	acctgcttca	aggatgtgga	aattcctaata	ttcttctggg	aaccttctca	360
actctcccat	cttgcattgt	gtgacacctt	caccagggaac	atcagtattt	ccctgctgcc	420
atatttggtt	ttcttcccat	ctcggggacc	cttttctctt	acgataaaat	tgttttctcc	480
attctgaggg	tttcatcatc	aggtgggaag	cataaggcct	tctccaccag	gggggtctac	540
ctgtcagttg	tttgcgtgatt	ttatggaaca	ggcattggag	gctacctcag	ttcagatgtg	600
tcattctccc	cgagaaaggc	tgcagtggcc	tcagtgatgt	acacgggtggc	catcccc	657

&lt;210&gt; 814

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g664 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 814

ttgcctgaca	tcggttttccc	ctccccacg	gtccccaaga	tggttggtgga	catccaatct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagacaca	tgctcctgaa	tgtgatggcc	tatgtccggg	ttgtagccat	180
ctgtcaccc	ctatattgtt	cagccatcat	gaaccctgtg	ttctgtggct	cttactttt	240
gttgtctttt	ttttttctcg	gtcttttaga	cgcccagctg	cacaacatga	ttgccttaca	300
aatgacctgc	atcaaggatg	tggaatttcc	taatttcttc	tgtgacctt	ctcaactccc	360
acaccttgcg	tggttggtgaca	ctttcaccaa	taacatagtc	atgtatttcc	ttgtgccaat	420
atttggtttt	cttcttatct	cacggatcat	tttctcttac	tataaaattg	tttctcccat	480
gctgagtggt	tcattcatcag	gtgggaagta	taaagccttc	tccatctgtg	ggctctccct	540
gtcagttggt	tgcttatttt	atggaaaagt	cgttgggggg	tacctgagtt	cagatgtgtc	600
atcttcccc	agaaagggtg	cagtggcctc	aatgatgtac	acggtgatca	cccc	655

&lt;210&gt; 815

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g665 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 815

ctagtggact	tttgttactc	ttcagctgtc	actcccacag	tcattgctgg	gtctgttata	60
ggagacaagg	tcattctctta	caatgcatgt	gctgctcaaa	tgctcttttt	tgacgctttt	120
gccactgtgg	aaaatttcc	cttggcctcg	atggcctatg	accgcatga	tgcatgtgtc	180
aaacccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tgttatgtct	gtggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300

```

ctgtatgtcc aatgaagtc attgcttttt ctgtgatgtt ccaccagtca tggctctgtc 360
ttgctgtgat agacatgtga atgggctagt tctcatttat gtagccagtt tcaatatctt 420
ttctgccatc ctagttatct tgatctccta cctattcata tttatcacca tcctaaggac 480
gcactcggct tcaggatacc agaaggcttt gtccacctgt gcctcccacc tcaactgcagt 540
catcatcttc tatgggacta ttatctccat gtacttacag cccagctctg gtcactccat 600
ggacacagac aaactggcat ctgtgtccta tactatgatc atcccc 646

```

&lt;210&gt; 816

&lt;211&gt; 649

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g666 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 816

```

ttgcctgaca tcggttttcac ctccaccatg gtccccaaga tgattgtgga atccaatctc 60
acagcagagt catctcctac gcaggctgcc tgactcagat gtctctcttt gccatttttg 120
gaggcatgga agagagacat gctcctgagt gtgatggcct atgaccggtt tgtagccatc 180
tgtcaccttc tatatcattc agccatcatg aaccctgttt tctgtggctt cctagttttg 240
ctgtcttttt tttctttctt tttctcagct gcacaacttg attgccttaa aaatgacctg 300
cttcaaggat gtggaaattc ctaatttctt ctgtgacct tctcaactcc cccatcttgc 360
atgttgtagc accttcacca ataagataat catgtatttc cctgctgcca tatttggttt 420
tcttcccatc tcagggaccc ttttctctta ctctaaaatt gtttctcca ttctgagggt 480
ttcatcatca ggtgggaagt ataaagcctt ctccacctgt gggctccacc tgtcagttgt 540
ttgctgagtt tatggaacag gcgttgagg ttacctcagt tcagatgatg tgcatcttc 600
ccccagaaag ggtgcagtgg cctcagtgat gtacacggtg gtcaccccc 649

```

&lt;210&gt; 817

&lt;211&gt; 651

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g667 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 817

```

atcattgata tttcgtatgc ttccaacaaa gtccccaaga tgctgacaaa ccttggtctg 60
aacaagagaa aaacaatctc ctttgtccca tgcacaatgc agaccttttt atacatggct 120
tttgctcaca ctgagtgtct catcttggtg atgatgtcct acgatcggta catggctatc 180
tgccaccctc tgcaatattc tgatcatcat agatggggag tgtgcacagt cctggctgtc 240
acttcttggg catgtggttc ccttctggcc ctgggtccatg tggttctcat cctgaggctg 300
cccttctgtg ggccccatga aatcaaccac ttcttctgtg aaatcctgtc tgtcctcaag 360
ttggcctgtg ctgacacctg gctcaaccag gtggtcatct ttgctgcttc agtggtcatc 420
ctggtggggc cgctctgcct ggtgctggtc tctactcgc gcatcctggc ggccatcttg 480
gggatccagt ctggggaggg ccgcagaaaag gccttctcca cctgctcctc ccaccttgc 540
atgggtgggac tcttctttgg cagcgccatt gtcatgtaca tggcccccaa gtcccgccac 600
cctgaggagc agcagaaggt cctttccctg ttttacagcc ttttcaaccc g 651

```

&lt;210&gt; 818

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g668 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 818

```

ctagtggact tttgttactc ttcagctgtc actccacag tcatagctgg gctcggtata 60
ggagacgagg tcatctctta cagtgcattg gctgctcaaa tgttcttttt tgcagccttt 120
gccactgtgg aaaatttcct cttggcctca atggcctatg accgctatga tgcagtgtgc 180

```



aaacccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tgttatgtct	gtgggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300
ctgaatgtcc	aatgaagtcc	attgcatttt	ctgtgatgtt	ccaccagtca	tggtctgttc	360
ttgtctgtat	agacatgtga	atgagctagt	tctcatttat	gtagccagtt	tcaatatctt	420
ttctgccatc	ctagtaatcc	tggctctccta	cctattcata	tttatcacca	tcctagagat	480
gcactcagct	tcaggatacc	agaaggcttt	gtccaactgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatcttcat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgttcta	tactatgatc	atcccc		646

&lt;210&gt; 819

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g669 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 819

atggctgtctg	agaattcctc	cttcgtgaca	cagtttatcc	tcgcaggctt	aactgaccaa	60
ccgggagctc	agatccccct	cttcttcctg	tttctaggct	tctacgtggt	cactgtgggtg	120
gggaacctgg	gcttgataac	cctgataagg	ctcaactctc	acttgcacac	ccctatgtac	180
ttcttctctc	ataacttgte	cttcatagat	ttctgtctatt	ccagtgttat	cactcccaaa	240
atgctgatga	gctttgtctt	aaagaagaac	agcatctcct	acgcagggtg	tatgactcag	300
ctcttcttct	ttcttttctt	tgttgtctct	gagtccttca	tcctgtcagc	aatggcgat	360
gaccgctatg	tggccatctg	taaccactg	ttgtacatgg	tcaccatgtc	tcccagggtg	420
tgttttctcc	ttttgttggg	tgtctatggg	atggggtttg	ctggggccat	ggcccacaca	480
gcgtgcatga	tgggtgtgac	cttctgtgcc	aataaccttg	tcaaccacta	catgtgtgac	540
atccttcccc	ttcttgagt	tgcttgacc	agcacctatg	tgaatgagct	tgtagtgttt	600
gttgttggg	gcattgatat	tgggtgtgcc	acagtcacca	tcttcatttc	ctatgtcttc	660
attctctcca	gcattctcca	cattgattcc	acggagggtg	ggcccaaagc	cttcagcacc	720
tgcagctccc	acataattgc	agtttctctg	ttctttgggt	caggagcatt	catgtacctc	780
aaaccctttt	ctcttttagc	tatgaaccag	ggcaagggtg	cttccttatt	ctataccact	840
gtggtgccca	tgtctaaccc	attaatttat	agcctgagga	ataaggacgt	caaagttgct	900
ctaagaaaa	tcttgaacaa	aatgcattc	tcc			933

&lt;210&gt; 820

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g670 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 820

atgactctga	gaaacagctc	ctcagtgact	gagtttatcc	ttgtgggatt	atcagaacag	60
ccagagctcc	agctccctct	tttcttctta	ttcttaggga	tctatgtgtt	cactgtgggtg	120
ggcaacttgg	gcttgatcac	cttaattggg	ataaatccta	gccttcacac	ccccatgtac	180
tttttctctc	tcaacttgte	ctttatagat	ctctgttatt	cctgtgtgtt	tacccccaaa	240
atgctgaatg	actttgtttc	agaaagtatc	atctcttatg	tgggatgtat	gactcagcta	300
tttttcttct	gtttctttgt	caattctgag	tgtatgtgt	tggatcaat	ggcctatgat	360
cgctatgtgg	ccatctgcaa	ccccctgtc	tacatgggtc	ccatgtcccc	aagggtctgc	420
ttctgtctga	tgtttgggtc	ctatgtggta	gggtttgctg	gggccatggc	ccacactgga	480
agcatgctgc	gactgacctt	ctgtgattcc	aacgtcattg	accattatct	gtgtgacgtt	540
ctccccctct	tgcagctctc	ctgcaccagc	acccatgtca	gtgagctggg	atttttcatt	600
gttgttggag	taatcaccat	gctatccagc	ataagcatcg	tcatctctta	cgctttgata	660
ctctccaaca	tcctctgtat	tccttctgca	gagggcagat	ccaaagcctt	tagcacatgg	720
ggctcccaca	taattgctgt	tgtctgtttt	tttgggtcag	ggacattcac	ctacttaaca	780
acatcttttc	ctggctctat	gaaccatggc	agatttgcct	cagtctttta	caccaatgtg	840
gttcccatgc	ttaacccttc	gatctacagt	ttgaggaata	aggatgataa	acttgcctctg	900
ggcaaaaccc	tgaagagagt	gctcttc				927

<210> 821  
 <211> 887  
 <212> DNA  
 <213> Unknown (H38g671 nucleotid )

<220>  
 <223> Synthetic construct

<400> 821  
 atgaaatgaa tggcagtgga aaataactct tcgggtgactg aatttatcct tgtgagatta 60  
 acaaaactccc gctgccccag tgttttatct ttaatgtggt ccctgtgggg agaatttgaa 120  
 cataatttta tgtccctaaa ttctcacctt cataccccca cacacttttt cctcttcacg 180  
 ctatccttca ttgatgtctg ctattcattt gtctgtacca caaaaattcc aatgggcttt 240  
 atctcagaga ggaacatcat ctctttgtg ggatggccaa cgtagctata tttcttttgc 300  
 atctttgtca aagaacctaa aaatggggtc attgtgggaa taatgttctc agccaagatg 360  
 cttgtagccg agagataatg gactagtcgt tgatgtgaaa ctagaaaatg cacatggccc 420  
 tagaaaggtc tgattttaga atgggataaa caggatctgc taaaaagaaa catttaatca 480  
 tattcttcta ttacagcgat tatttccaga gatagtgagg ctgcagagct ttgggacaag 540  
 gttccttagc gaagcaagac acactctcta gaattgcaca tgtactttaa aaagtctgtt 600  
 acatattata atatgttttt atatttggaa acagaaaaaa ataagttatt tatatcacia 660  
 atcatagaaa atggatcttt acaaaatctt catgttttgt gggttactca caagaaaaat 720  
 tttctccgct catttctact tctcaaatgg ttcaaggaaa aatgctcctt aaaggatata 780  
 tctgattctg gagaatgagc ttacctatgt gtgcaatttt tatctttgtc agaagatact 840  
 actaccttct gaaaaagttg aaaacactgc ttataagaa cagctat 887

<210> 822  
 <211> 939  
 <212> DNA  
 <213> Unknown (H38g672 nucleotide)

<220>  
 <223> Synthetic construct

<400> 822  
 atgctggcta gaaacaactc cttagtgact gaatttatct ttgctggatt aacagatcgt 60  
 ccagagttcc ggcaaccctt ctttttcctg tttctagtgg tctacattgt caccatggta 120  
 ggcaaccctg gcttgatcat tcttttcggt ctaaattctc acctccacac accaatgtac 180  
 tatttctctt tcaatctctc ctccattgat ctctgttact cctctgtttt cactcccaaa 240  
 atgctaataa actttgtatc aaaaaagaat attatctcct atgttgggtg catgactcag 300  
 ctgtttttct ttctcttttt tgtcatctct gaatgctaca tgttgacctc aatggcatat 360  
 gatcgctatg tggccatctg taatccattg ctgtataagg tcaccatgtc ccatcaggtc 420  
 tgttctatgc tcacttttgc tgcttacata atgggattgg ctggagccac ggcccacacc 480  
 ggggtgcatg ttagactcac ctctctgagt gctaatatca tcaaccatta cttgtgtgac 540  
 atactccccc tctccagct ttctgcacc agcacctatg tcaacgaggt ggttgttctc 600  
 attgttgggg gtattaatat catggtaccc agttgtacca tctcatttc ttatgttttc 660  
 attgtcacta gcattcttca tatcaaatcc actcaaggaa gatcaaaagc cttcagtact 720  
 tgtagctctc atgtcattgc tctgtctctg ttttttgggt cagcggcatt catgtatatt 780  
 aaatattctt ctggatctat ggagcaggga aaagtcttct ctgttttcta cactaatgtg 840  
 gtgcccatgc tcaatcctct catctacagt ttgaggaaca aggatgtcaa agttgcactg 900  
 aggaaagctc tgattaaaat tcagagaaga aatatattc 939

<210> 823  
 <211> 1071  
 <212> DNA  
 <213> Unknown (H38g673 nucleotide)

<220>  
 <223> Synthetic construct

<400> 823  
 atgaattggg taaataagag tgtccacag gagttcatct tgtagtttt ctcagatcaa 60

```

ccatggctag agattccacc ctttgtgatg tttctgtttt cctatatctt gacaatcttt 120
ggcaatctga caataattct tgtgtcacat gtggatttca aactccacac ccctatgtac 180
ttttttctta gcaatctctc actcctggac ctttgtctata ccacaagtac agttccacaa 240
atgtgggttaa acatattgcaa caccaggaaa gtaatcagtt atgggtggctg tgtggccag 300
cttttcattt tcttggcctt gggttccaca gaatgtcttc tcttggccgt catgtgcttt 360
gataggtttg tagctatttg tcggcctctc cattactcaa ttatcatgca ccagaggctc 420
tgcttccagt tggcagctgc atcctggatt agtggcttta gcaattcagt attacagtcc 480
acctggacac ttaagatgcc actgtgtggt cacaaagaag tggatcactt cttctgtgaa 540
gtccctgctc tgctcaagtt gtccctgtgt gacacaacag caaatgaggc tgaactattc 600
ttcatcagtg tgctattcct tctaataccc gtgacactca tctttatate gtatgctttt 660
attgtccaa gctgtttgag aatccagctc gctgaaggtc aacgaaaggc atttgggaca 720
tgtggctccc atctaattgt ggtgtcactt ttttatggta cagctatctc catgtacctg 780
caaccacctt caccagctc caaagaccgg ggaaagatgg tttctctctt ctgtggaatc 840
attgcacca tgctgaatcc ctttatatat acacttagga acaaagaggt aaaggaagcc 900
tttaaaaggt tggttgcaa gagtcttctt aatcaagaaa taagaaatat gcaaatgata 960
agctttgcta aagacacagt gcttacttac cttactaact tctccgcaag ttgtcctatt 1020
tttgtcatta ctatagaaaa ctattgtaat ctccctcaaa gaaaatttcc t 1071

```

&lt;210&gt; 824

&lt;211&gt; 991

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g674 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 824

```

atggctcctg gaaatggctt tttcatgact aaaatcattt tgctggagtt aacagatcag 60
ccagatctcc aactccctct gttcttcctg tttctagtgt atggctcactg cgttgggaaa 120
tttggcttgg taactctcgt tgtgtcfaat tcacaccttc atacccccat gtactttttc 180
ctctttaact tgtccttcat agatctctgt tattctctctg tgtttacacc ccaaagtctg 240
atgaacttca taacacagaa ggatattatc tcccacatgg ggtgcatgtc ccagcttttc 300
ttttttcttt attttttttt ggtatttctg aatgctatgt gctcacctca atggcctatg 360
atcagcatgt caccatgac accatgtagc catctgtaac ccacttttgt ataattattgc 420
catgtccccc aaagtgtact ctcaccttat gcttggttta tacttgctag ctttttctag 480
tgccatggcc cacactggat gcatgctgag actgaccttc tgtgatgcaa acaccatcca 540
tccctatttg tgtgacatcc tccctctgct ccagctctct tgcaccggca cctacatcaa 600
tgagctgggt gtttccactg cagcagtcac tttttccac tgtcaccata tttatctctt 660
gtgggtgcag ctccctacac atcctccaca tcaactccaa ggagggcagg tccaaagcct 720
tgaacacctg cagttccaac ctaattgctg tttctcttag tttggatcgt gtgcatttat 780
gtgtctcaaa ccatctctctg ctgggtccat ggatgagggg aagatttctt ctgtctttta 840
caccaataca gtcctcttga tgaaccctt aatctacagt ttgatgaata aaatgttcaa 900
ctttctctga gaaaaaaacc ctagtaggaa aaaattttga ctagaaatag tatctttctg 960
tgcatgtatt ttaggacag ggagcttctg t 991

```

&lt;210&gt; 825

&lt;211&gt; 997

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g675 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 825

```

atggctcctg gaaatggctc tttgatgaat gaattcattc tgggtggggtt aacagactag 60
ccagatcttt aactccctct gttcttcatg tttcttgtaa tgatgttgt cactgtgata 120
agaaactttg tcttggtaat tctaactatg cgaaattcac gtcttcacac tcccaagtac 180
tttttcttt ctaaatgtgt cttcacagac ctctgttatt cttctgtgtt tatactccaa 240
cttccgagga atgtattttc agaggagaat gttatctcct acatgggttg catgatctag 300
cttttctttt tctttttctg tttttttttt tttttaattt atttctgaat gttatatgct 360
gacgtcaatg gcctatgatt gctgtgtggc catctgttac ccacttcttt atcacattgc 420

```

catgtccct	aaagtgtgtt	tcagccttat	gcttgggtcc	tacttccctat	ccttttctgg	480
ggccatggcc	cacactggat	gcatgctgag	gctgacctgt	gatgcaaaca	ccatcaatca	540
ttacttccgt	gacatcctcc	ctgtgttcca	gctctcctgc	accagcacct	acatcaatga	600
actgggtgggt	ttcattgtgg	caggcatcaa	taccattgtg	cccactgtca	ccgtctttat	660
ctcttatggg	gacatcctct	ccaggatcct	ccacatcagt	tccaatgagg	gaagggtccaa	720
agccttcagc	acttgcagtt	cccacataat	tgtgttttct	ctgttctttg	gattaagtgc	780
atztatgtat	ctcaaaccat	cttctgctgg	gtctatggat	gagggaaaat	tctcttctgt	840
tttttatatg	aacgggcttc	ccatgatgag	ctccttaatc	tacagcttaa	ggaggaaaaga	900
tgtaaatttt	gccatgggaa	aatctctgag	taggagaatg	tttttgccat	aaacaacatt	960
tctctgtgta	tgtagttaca	ggatggggat	tctctgt			997

&lt;210&gt; 826

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g676 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 826

atggacagtc	taaaccaaac	aagagtgact	gaatttgtct	tcttgggact	cactgataac	60
cgggtgctgg	aaatgctgtt	tttcatggca	ttctcagcca	tttatatgct	aacgctttca	120
gggaacattc	tcacatcat	tgccacagtc	tttactccaa	gtctccatac	ccccatgtat	180
ttcttctga	gcaatctgtc	ctttattgac	atctgccact	catctgtcac	tgtgcctaag	240
atgttgagg	gtttgctttt	agaaagaaag	accatttcct	ttgacaactg	catcacacag	300
ctcttcttcc	tacatctctt	tgcctgtgcc	gagatcttcc	tgtgatcat	tgtggcgtat	360
gacgttacg	tggctatctg	cactccactc	cactacccca	atgtgatgaa	catgagagtc	420
tgtatacagc	ttgtctttgc	tctctggttg	gggggtactg	ttcactcact	agggcagacc	480
ttcttgacta	ttcgtctacc	ttactgtggc	cccaacatta	ttgacagcta	cttctgtgat	540
gtgcctcttg	ttatcaagct	ggcctgcaca	gatacatacc	tcacaggaat	actgattgtg	600
accaatagt	gaaccatctc	cctctcctgt	ttcttggccg	tggtcacctc	ctatatggtc	660
atcctgggtt	ctcttcgaaa	acactcagct	gaaggcgcc	agaaagccct	gtctacctgc	720
tcggcccaact	tcattggtgt	tgcctcttcc	tttgggccat	gtatcttcat	ctatactcgg	780
ccagacacca	gcttctccat	tgacaagggt	gtgtctgtct	tctacacagt	ggtcacccct	840
ttgctgaatc	ccttcattta	caccttgagg	aatgaggagg	taaaaagtgc	catgaagcag	900
ctcaggcaga	gacaagtttt	tttcacgaaa	tcatataca			939

&lt;210&gt; 827

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g677 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 827

atggctcctg	gaaatatttc	tactgtggct	gaattaattc	tgggtggggt	aaaagaccag	60
acagatctcc	aaccgcccct	gttcttcctg	tttctagtaa	tgggtgtggg	tgctgggtag	120
gggaatttgg	gcttggtaac	tctgattgtg	ttcagttcac	actttcatgc	acccatgtac	180
ttttttcttt	ttagtttagc	ttttatagac	cacttttatt	cttctgtgtt	tattccaaaa	240
atgctgatga	acttcataac	agagaagaat	attatttccct	atgcgggttg	catgtcagct	300
tttttttctt	tctttttttt	tttttttttg	ttatttctga	atgctatggt	ttgacgtcaa	360
tggctctctga	tcactagtgg	ccatggccat	ctgtaaccgg	cttctgtata	acattgccat	420
gtccccataa	gtgtgttcca	gccatagct	tggttccctac	ttctggccct	tttctggggc	480
catggcccat	accaggtgca	tgtgaaact	gacctcctgt	gaggcaaaca	ccatcaacca	540
ctacttctgt	gacacccttc	atctgtccca	gctctcttgc	accagcacct	acgtcagtga	600
gttgatgggt	ttcattgcag	caggcatcat	tttactgtg	cccagtatca	ccatctttat	660
ctcttatttt	tttacctctc	cattatccta	tcagcttcac	tgagggtctg	tcaaaatttt	720
tcagcacctg	cagtttccac	aaaattgcca	tttctctgtt	ctttggatta	ggtgcacat	780
tgtgtcttaa	attatctcca	actgggacta	taaatgaagg	taaaatatct	tctgtctttc	840
acattgatgt	agttcccatg	ataaactcct	caatttacag	cttaagaaac	aatgatgtta	900

aacttgcctg gagaaaaatc ctaagttgga gaaaatttcc atttgaaact atctctctcc 960  
atgcatatag ttacaggaca aggagattct gt 992

<210> 828

<211> 966

<212> DNA

<213> Unknown (H38g678 nucleotide)

<220>

<223> Synthetic construct

<400> 828

atgagtgtcg tagaagccaa taacatttct gggcctgtga gtgaatttat cctcctgggc	60
ttcccctgcc tgctgcagg agaccaagat cctcctcttt gtggtcttct ccctcatcta	120
ccttctgacc ctcatgggta acacatccat catctgcgct gtgtgggtcaa gccagaaact	180
ccacacacct atgtacatcc tcttggctaa tttctcttct ctggagatct gctgcattag	240
ttctgatgtc ccaaaatgtt ggccaatctc atctcccata tcaagagcat ctctatgct	300
ggctgcctgc tccagttctt ctacttctcc atgtgtgctg cagaaggcta ctttctgtct	360
gtgatgtcct ttgatcggtt ccttaccatc tgtcgacctt tgcattatcc cacagtcattg	420
atcaccacc tgtgtgtctg attagtggcc ttctgcaggg caggtgggtt tctatccata	480
ctgatgcctg cagtgtctat gtcccagtg cctttctgtg gccctaacat cactgaccat	540
tttttctgta acctgggacc attgctggca ctgtcctgtg cccagttcc caaaactact	600
ctgacttgtg ctacagtaag ctctctcatc atcttcatca ccttctctta cattcttggg	660
tcccatatct tagttttgcg agctgttctg tgggtcccag ctggctcagg caggaacaaa	720
gctttctcta catgtgcttc ccatttcttg gttgttctt tcttctatgg ctcatgcatg	780
gtgatgtatg tgagtccagg ctccaggagc cgccctggga cacagaaatt tgtgacattg	840
ttttactgca cagcaacccc attctttaat cccctgacct acagtctctg gaacaaagat	900
atgacagatg cccttaaaaa agtgctggga gtgccatcaa aagaaatata ttggaacaca	960
ctgaaa	966

<210> 829

<211> 1003

<212> DNA

<213> Unknown (H38g679 nucleotide)

<220>

<223> Synthetic construct

<400> 829

atggaagagg ccactctact caatcaaact tctttagtga catattttcg gcttagaggt	60
ttatctgtaa atcataaggc acggatagct atgttttcca tgttcctcat tttttatgtc	120
ctgacactga ttgggaatgt tctcattgtc ataactatta tctatgacca ccggctccat	180
actcccatgt atttcttctt cagcaacctg tcctttattg atgtctgcca ctccactgtc	240
actgtcccca agatgtctgag agacgtgtgg tcagaggaaa agctcatctc ttttgatgcc	300
tgtgtgacct agatgttctt cctgcacctc ttgacctgca cagagatctt cctcctcacc	360
gtcatggcct atgatcggtg tgtggccatc tgtaaacccc tgcagtacat gatagtgatg	420
aactggaagg tatgtgtgct gctggctgtg gccctctgga caggagggac catccactcc	480
atagccctca cctcccttac catcaagctg ccctactgtg gtccctgatga gattgacaac	540
ttcttctgtg atgtacctca ggtgatcaag ctggcctgca ttgacacacc cacgtccttg	600
agatcctcat tgtctccaac agtggattga tctccgtggg ctgttttgtg gtcctgggtg	660
tgtcctacgc agtcatcctg gtgagtctga ggcagcagat ctccaagggc aagtggaagg	720
ccctgtccac ctgtgcagcc catctcactg tagttacact gttcctggga cactgcactc	780
tcactgtatc ccgcccattc accagcctcc cagagacaaa ggcagtatct gtgtttttca	840
ctgcagtcac cccctgtctg aaccccatca tctataccct taggaatgaa gaaatgaaga	900
gtgccttaaa caagttagtg gggagaaaag agagaaaaga agaaaaatga aaatgtctac	960
gtccttagga tacgtggtgc tccaaattaa agaagcgct tgc	1003

<210> 830

<211> 478

<212> DNA

<213> Unknown (H38g680 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 830

acggggactg gatgatggct gtgtcatgcc atgatacctaa ctcccctcac ttccagttac	60
cttactgtgg cctaacaagg tgggctatac ttctgtgata tcctgcagtg tacctctagc	120
ctgtaaggac acatccttag cccagagggg aggtttttaca aatgttgggc ttttgtctct	180
catttgcttt tttctcatcc ttgtttccta tacttgcatt gggatttcca tatcaaaaat	240
ccgtcagca gagggcaggc agcgggcctt ctccacctgc agcgctcacc tcaactgcaat	300
cctttgtgct tatgggccag tcatcgttat ctatctacaa cccaatccca gtgccttgct	360
tggttccata attcagatat tgaataatct ggtaacccca atgttgaatc cactaatcta	420
tagccttagg aataaggatg taaaatcaga tcagccctga ggaatgtatt tcccaaga	478

&lt;210&gt; 831

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g681 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 831

ttactatttt taatgttctt tattacttcc ttgggtcata aattccatct gatatacttt	60
cccttcagtc aacaaaccac ctaacaaaaa tactttataa tttttgaagt atgactctgc	120
tgataacata cactcacagc attaatattat tgtaaattgt ccttgttcta gggtagagac	180
ctattttagt ggtataccct ttagtcccag agtattgttc ttatttctag ggcgtgggtcc	240
ttctgggttt tcattagaaa gcctaagttt ttaccgaacc tctttcactt ggcagcactt	300
gcatttaaaa ttctattgcc ctagttagagg gtaactgcta aaatcttttc tctcagccat	360
ctggctgctg ttttctactt actttcttag agtcttgtct	400

&lt;210&gt; 832

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g682 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 832

atggctactt caaaccattc ttcaggggct gagtttatcc tggcaggctt gacacaacgc	60
ccagaacttc aactgccact ctctctctctg ttctttggaa tatatgtggg cacagtgggtg	120
gggaacctgg gcatgatctt ctttaattgct ctctgtctc aactttaccc tccagtgtat	180
tattttctca gtcatgttgc tttcattgat ctctgtact cctctgtcat tacccttaag	240
atgctgggtga actttgttcc agaggagaac attatctcct ttctggaatg cattactcaa	300
ctttatttct tccttatttt tgtaattgca gaaggctacc ttctgacagc catggaatat	360
gaccgttatg ttgctatctg tcgcccactg ctttacaata ttgtcatgtc ccacaggggc	420
tgttccataa tgatggctgt ggtatactca ctgggttttc tgtggggccac agtccatact	480
acccgcatgt cagtgttgtc attctgtagg tctcatacgg tcagtcatta tttttgtgat	540
attctccccct tattgactct gtcttgtctc agcaccaca tcaatgagat tctgtgttgc	600
attattggag gagttaatac cttagcaact acactggcgg tccttatctc ttatgctttc	660
attttctcta gtatccttgg tattcatctc actgaggggc aatccaaagc ctttggcact	720
tgtagctccc atctcttggc tgtgggcac ttttttgggt ctataacatt catgtatttc	780
aagccccctt ccagcactac tatggaaaaa gagaagggtg ctctctgtgt ctacatcaca	840
ataatcccca tgctgaatcc tctaattctat agcctgagga acaaggatgt gaaaaatgca	900
ctgaagaaga tgactagggg aaggcagtc tcc	933

&lt;210&gt; 833

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g683 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 833

atgggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagtttttag	tcagacatca	tctccacacc	180
cctatgtact	tctcctgggt	gaacttgctc	tgtctggaga	tctgggtatac	ctctaaccatc	240
atcccaaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcacaggct	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcactct	tcttgcattg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atcccactct	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattggc	780
acataccttg	tgccctcagc	caactcatcc	caactcttgt	gcaaaggggc	ctctctgtct	840
tacatcatcc	tgacacccat	gtttaacccc	atcattttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggt	tttgctt		948

&lt;210&gt; 834

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g684 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 834

ccagtggagc	ccttggagac	tactaatatc	actggatttg	tgaatgagtt	catcctcttg	60
ggcttcccc	gccgtggga	gatccagatc	ctcctttttg	tggctctctc	tctcatctac	120
cttctgacct	tcctaggtaa	cacatccatc	atctgtgctg	tgtgggtcaag	ccagaaactc	180
cacacaccta	tgtacatcct	actggccaat	ttctccttcc	tggagatctg	ctgtgtcagt	240
tctgacgtgc	ccataatggc	agccaatctc	atctcccaga	cacagagcat	ctcctgtgct	300
ggctgcctgc	tcgggttcta	cttcttctcc	atgtgtgctg	cagagtgtct	atttctgtca	360
gtgatgtctt	ttgatagggt	tctgcccatt	tgtagacctt	tgactatcc	caccttaatg	420
acccatcacg	tttgtgtcga	tttttgtgat	cttctgctgg	gtgggtggct	gtctctgggt	480
attgacccct	ttgacactaa	tatctcaggt	gctcttttgt	ggtccaaaca	ctatcgacca	540
ttttttctgt	gatctggcac	ctttgctggc	actgtcttgt	gctccaatac	ctggaattac	600
tctgacttgt	ggtatcatta	gcgctctcat	catctttctt	accttcttgt	atataccttg	660
gacttatttc	tgtgttctaa	gcacagtgtc	acaggtgcct	tcaggcttag	gaaggcataa	720
ggctttctca	acttgtggct	gtcaccttgc	tgtagtgtct	ctcttctatg	gttctcttat	780
gggtgatgtat	gttagccag	gttctgggga	ctatcatggg	ataaagaaat	ttgcgacctt	840
gttctatact	ttgtcaactc	cattctttta	tcctctgata	tacagtctcc	ggaacaagga	900
tatgaaagag	gcactaaaga	aatttctgag	gaatcgccac	actgtc		946

&lt;210&gt; 835

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g685 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 835

cttatagcta	caggaaactg	gacaagaata	agtaagtta	tcctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctggtcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	accccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatcttct	ctggagattg	gcttcaacct	agtcattgcy	240

cccaacatgc	tgtggaccct	gcttgcccag	gacacaacca	tctccttcct	tggctgtgcc	300
acttagatgt	atttcgtctt	cttctttggt	gtggctgaat	gcctcctcct	ggctaccatg	360
gcatatgacc	gctatgtggc	catctgcagt	ccttgacta	cccagtcac	atgaaccaa	420
ggactcttgc	caaactggct	gtacctcct	ggttcccagg	ctttcctgta	gctactgtgc	480
agaccacatg	gctcttcagt	ttccattct	gtggcaccac	caaggtgaac	cacttcttct	540
gtgacagccc	acctgtgctg	aggctggct	gtgcagacac	agcactctt	gagatctacg	600
ccatcgctcg	aaccattctg	gtggctcatg	tcccctgctt	gctgatcttg	tgttcctata	660
ctcacattgc	tgtgccatc	ctcaagatcc	catcagctaa	agggaagaat	aaagcctttt	720
ctacatgttc	ctcacacctc	cttggtgtct	ctcttttcta	tatatcatta	agcctcacct	780
acttcgggcc	taaatcaaat	aattcacctg	agggcaagaa	gctgctatca	ttgtcctaca	840
ctgttatgac	tcccatgttg	aaccccata	tctacagcct	gagaaataac	gaggtgaaga	900
atgcctcag	caggacggtc	tctaaggccc	tagccctcag	aaactg		946

&lt;210&gt; 836

&lt;211&gt; 973

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g686 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 836

atggctgtgg	aaaatgactc	ttcagtgaca	agagtttatt	cttttgggat	taacagacca	60
gcctgagatc	taattgcccc	tgtttttcct	gttcttgggt	aactatatga	ccaccatggt	120
gggcaacttg	agtttaatta	atctaatttg	cctgaattca	caccttcaca	ctcccatgta	180
ttttttcctt	ttcaatctgt	ccttcattga	tctctgttat	tcatttgtct	ttaccccaa	240
aatgctgatg	agctttatct	cagagaggaa	catcatctcc	tttccaggat	gcgtaactca	300
gctctttttc	ttctgctttt	ttgtccactc	tgagtgtctat	gtgctgacag	ccatggccta	360
tgatcgctat	gtggccatct	gcaaaccctt	tctgtacatg	gtcaccacgt	cccctcagat	420
ctgttctcta	ctgatgcttg	gttcataatg	gatgggggtt	gctggggcca	tggtccacac	480
agagtgtatg	atgaagctca	tcttttgtga	ctccaacgtc	atcaaccatt	acatgtgtga	540
catcttccca	ctgtccagc	tctcctgcag	cagcacctag	gccaatgagc	tggtgatgtc	600
tgttattgta	ggcacagttg	ttatagtatc	aagcctcatt	atcttaattc	cttatgcttt	660
gattcttttc	aatatccttc	acatgtcctc	agccgagggt	tggttcaaag	ccatcggtac	720
ctgtggctcc	cacataataa	ctgttggcct	attctatgaa	tttgggctga	tactcatgt	780
taagttatca	tctgattggt	atattgggtca	ggggaagttt	ctctcagtg	tttacacgaa	840
tgaggtaccc	atgtgtaacc	ccctcattta	tagcctcagg	aacaaggatg	tcaaacttgc	900
tctaaggaa	accctaata	aaattacaaa	ctgagtagag	ccaatggtgc	tgcttagcc	960
cctctccaat	tgc					973

&lt;210&gt; 837

&lt;211&gt; 992

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g687 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 837

atgagataga	taaatcagac	acaagtgata	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atttatcgta	ttattgggtg	tctacctggt	cactgtgctt	120
ggaaatctgc	ttctaattct	ccttgttcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgtc	tctggctgac	ctctatttct	ctaccaacat	acttctcag	240
gcactagtcc	acctgctttc	cataaacaac	ctcattgcat	tcacactttc	tctaactcaa	300
cttctctttt	tcctcatttt	tggtgacccc	agtgcgcctt	tattgcagtg	atgtcctata	360
atccctatgt	tgcaatctgc	aatcctctgc	attaccctaa	catcatgacc	tggaaagtgt	420
gtgtccagct	ggcaacagga	tcatggacca	gtggcattct	ggtgtctgtg	gtagacacca	480
ccttcacact	gaggtacccc	taccgaggca	gtaacagcat	tgctcatttc	ttttgtgagg	540
ccctctgact	attgatctta	gcataccag	acacccatgc	atcagagatg	gccatttatc	600
ttacgggggt	tgtgattctc	ctcatacctg	tttttctgat	tctggtatcc	tatggccgta	660
tcatagtaac	tgtggtcaag	atgaagtcaa	ctgtggggag	tctcaaggca	ttttctacct	720



gtggctccca	cctcatgggtg	gtcatacttt	taaattggatc	agcaatactc	acttgcata	780
cacccaagtc	ttccaaacag	cagtaaaaat	cggtgtctgt	tttctatgca	atagtaactc	840
ccatgcttaa	ttccctcatc	tatagcctga	gaaacaagga	tgtgaaggca	gctctgagga	900
aagtagccac	aaggaatttc	ccatgaaggc	ttggaatctc	acactgacag	tgagctcaga	960
gaaccttttg	gcttcctact	tcaaagactt	gc			992

&lt;210&gt; 838

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g688 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 838

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgatttctat	cacgtgcacc	cagctcattc	accaacccat	gtatttcttc	180
ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgaaccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttgagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttgttg	tactggggga	tttatacatt	ctgccagtca	gtttcttctc	480
accatctctg	taccattttg	tggcccaa	gatatagatc	actactctcg	cgatgtgtat	540
cctttgctg						549

&lt;210&gt; 839

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g689 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 839

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgagcgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	gtgatggcct	atgacctgtt	tgtagccatc	180
tgtaaccttc	tatatcgttc	agccatcttg	aaccctgttg	tccgtggctt	cctagatttg	240
ttgtctttgt	tgttggtttt	tttttttttc	tctcagtctt	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attccgaatt	tcttctggga	360
accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	acaacatgta	420
tttccctgct	gccgtatttg	gttttcttcc	catctcgggg	acctttttct	cttactgtaa	480
aattgtttcc	tccattctga	gggtttcatc	atcaggtggg	aagtacaaac	cttctccacc	540
tgtgggtctc	acctgtcagt	tgtttgctga	ttttatggag	caggcgttgg	agggtacctt	600
ggttcagatg	tgatcatctt	cccagaaaag	ggtgcagtgg	cctcagtgc	gtacgtacac	660
ggtggtcacc						670

&lt;210&gt; 840

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g690 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 840

atggacgtca	ggctcatctg	caccaccgta	cccaagatgg	ccttcaacta	cttgtctggc	60
agcaagtcca	tttctatggc	tggtgtgccc	acacaaatct	tcttctgtgt	atcactgctt	120
ggctctgaat	gctttctgtt	ggctgttatg	tcttatgact	gctacattgc	catttgccac	180
cctctaagat	acaccaatct	catgagaccc	aaaatttgta	gacttatgac	tgcttctctc	240

tggatcctgg	gctctacaga	tggaatcatt	tatgctgtag	ccacattttc	cttctcctac	300
tgtgggtctc	gggaaatagc	ccacttcttc	tgtgagttac	cttccctact	aatcctctca	360
tgcaatgaca	cgtcaatatt	tgaaaagggt	atttttcattt	gctctatagt	aatgcttggt	420
ttccctgttg	caatcatcat	tgcttccctat	gctggagtta	ttctggctgt	cattcacatg	480
ggatctggag	agggtcgtcg	caaagctttc	acgacctgtt	cctctcacct	catgggtggtg	540
ggaatgttct	atggagcagg	tttgttcatg	tacatacagc	ccacatctga	tcgctcccca	600
acgcaggaca	agctgggtgc	tgtattctac	accatcctca	ctccc		645

&lt;210&gt; 841

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g691 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 841

aatctcctcc	ccgtgtggac	ccctggaagc	agggtgccct	tcattgatcac	aaattttctgt	60
ctccgagaag	caaggcatgt	cctttcccaa	gaaacttttc	cagaatcaca	aacttttctc	120
actcttttga	gggatgaatg	tattttctgca	gactgtgatg	gcctatgacc	actttgtggc	180
catctgtcac	cccctgcact	acagggtcat	catgaatcct	gggatctttg	gactgtgggt	240
tctggtgtcc	tggagcatga	gtgccctgaa	ttcctcactg	caaagcagaa	tgtgttgca	300
ctgtccttct	gcacaaactt	ggaaatcccc	ccattttttt	ctgtgaactt	aatcagttga	360
tctgtcttgc	ctgttctaac					380

&lt;210&gt; 842

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g692 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 842

tttgttgatt	tctgttatcc	caccacgatt	acacccaaac	tgctggagaa	cttgggtgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	atcatgcagt	tattctttgt	ctgcatattt	120
gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gtcccttgtt	agtggctacg	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgccgt	cgttctgtgt	360
tcttggctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
ataagcggcc	tggtgatcat	tctcactccc	tatgctttca	ttttatcac	tgtcatgaag	480
acgccttcca	ctggggggcg	caagaaagcg	ttctccacgt	ctgcctccca	cttgacggcc	540
attaccattt	tccatgggac	tatccttttc	ctctactgtg	ttcctaactc	caaaagtctg	600
tggctcatgg	tcaagggtggc	ctctgtcctt	tacacagtgg	tcattccc		648

&lt;210&gt; 843

&lt;211&gt; 643

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g693 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 843

ttgccagaca	ttggtttcac	cttggccacg	gtccccaaga	tgattgtaga	catgcaatca	60
catagcagaa	tcattctccca	tgagggtgtg	ctgacacaga	tacctttctt	tgtccttttt	120
gtatgtatag	atgacatgct	cctgactgtg	atggcctatg	actgatttgt	ggccatctgt	180
cacccctgc	actaccagc	catcatgaat	cctcacctct	gtgtcttctt	agtgttgatg	240
tctttttctt	tagcctgttg	gattcctagc	tgcaacaactg	gattgtttaca	attcacctgc	300
ttcaagaatg	tggaaatctc	taattttttc	tgtgactgat	ctcaacttct	caaccttgcc	360

tgttctgact	gtcatcagta	acatattcat	acgttttagat	agtactatat	ttggctttct	420
tcccatttca	gggatccctt	tgtcttacta	taaaattgtg	ccctccattc	taagaattcc	480
attgtcagat	gggaagtata	aagccttctc	cacctgccc	tctcacctgg	caattgtttg	540
cttattttat	ggaacaggca	ttggcatgta	cctgacttca	gctgtgtcac	cagccccag	600
gaatggtgtg	gtggcatcag	tggtgtacgc	tatggtcacc	ccc		643

&lt;210&gt; 844

&lt;211&gt; 652

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g694 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 844

ttgcctgaca	tcggtttcac	ccccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctatgc	aggctgcctg	actgtgatgt	ctctctttgc	cattttttgga	120
ggcatggaag	agacacatgc	tcctgaatgt	gatggcctat	gtccggtttg	tagccatctg	180
tcaccctcta	tatcattcag	ccatcatgaa	cccgtgttcc	tgtggcttct	tacttttgtt	240
gtcttttttt	tttctcggtc	ttttagacgc	ccagctgcac	aacatgattg	ccttacaaat	300
gacctgcttc	aaggatgtgg	aaattcctaa	tttcttctgt	gaccttctc	aactccccca	360
tcttgcatgt	tgtgacacct	tcaccaataa	cataatcatg	tattttcctg	ctgccatatt	420
tggttttctt	cccatctcgg	ggaccctttt	ctcttactat	gaaattgttt	cctccattct	480
gagggtttca	tcataagggtg	ggaagtataa	ggccttcgcc	acctgtgggt	ctcacctgtc	540
agtcgtttgc	tgattttatg	gaacaggcgt	tggagggtac	ctcagttcag	atgtgtcatc	600
ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtggtcaccc	cc	652

&lt;210&gt; 845

&lt;211&gt; 692

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g695 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 845

ttgcctgaca	tcggtttcac	ctccaccaca	gtcgccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggetgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	tatgaccggg	ttgtagccat	180
ctgtcacct	ctatatcggt	cagccatctt	gagcccggtg	ttctgtgcct	tcctagattt	240
gttgtctttg	ttttgttttg	ttttgttttg	ttttgttttg	ttttgttttg	ctcagtcttt	300
tagactccca	gctgcacaac	ttgattgcct	tacaaatgac	ctgcttcaaa	gatgtggaaa	360
ttcctaattt	cctctgggaa	ccttctcaac	tcccccatct	tgcatgttgt	gacaccttca	420
ccaggaacat	caacatgtat	ttccctgctg	ctgtattttg	ttttcttccc	atctcgggga	480
ccttttctct	tacaatggag	taaaattgtt	tcctccactc	tgagggtttc	atcatcagggt	540
gggaagtata	aaccttctcc	acctgtgggt	ctcacctgtc	agttgtttgc	tgattttgtg	600
gaacaggcgt	tggagggtac	ctcggttcag	atgtgtcatc	ttccccgaga	aagagtgcag	660
tggcctcagt	gatgtacacg	gtggtcaccc	cc			692

&lt;210&gt; 846

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g696 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 846

atgctgggcta	gaaacaactc	cttagtgact	gaattttattc	ttgctggatt	aacagatcgt	60
ccagagttcc	ggcaaccctt	ctttttcctg	ttcctagtga	tctacattgt	caccatggta	120
ggcaaccttg	gcttgatcac	tcttttcggg	ctaaattctc	acctccacac	accaatgtac	180

tatttctctt	tcaatctctc	cttcattgat	ctctgttact	cctctgtttt	cactcccaaa	240
atgctaata	acttttgtgc	aaaaaagaat	attatctcca	atgttgggtg	catgactcgg	300
ctgtttttct	ttctcttttt	cgatcatctc	gaatgttaca	tgttgacctc	aatggcatat	360
gacgcctatg	tggccatctg	taatccattg	ctgtataaag	tcaccatgtc	ccatcagggtc	420
tgttctatgc	tcaacttttg	tgtttacata	atgggattgg	ctggagccac	ggccccacac	480
gggtgcatgc	ttagactcac	cttctgcagt	gctaataatca	tcaaccatta	cttgtgtgac	540
atactcccc	tcctccagct	ttcctgcacc	agcacctatg	tcaacgaggt	ggttgttctc	600
attgttgtgg	gtactaatat	cacggtagcc	agttgtacca	tcctcatttc	ttatgttttc	660
attgtcacta	gcattcttca	tatcaaattc	actcaaggaa	gatcaaaaagc	cttcagtact	720
tgtagctctc	atgtcattgc	tctgtctctg	ttttttgggt	cagcggcatt	catgtatatt	780
aatattcttt	ctggatctat	ggagcaggga	aaagtttctt	ctgttttcta	cactaatgtg	840
gtgcccattg	tcaatcccc	catctacagt	ttgaggaaca	aggatgtcaa	agttgcactg	900
aggaaagctc	tgattaaaat	tcagaggaga	aatatatctc			939

&lt;210&gt; 847

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g697 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 847

atgaccatgg	aaaattattc	tatggcagct	cagtttgtct	tagatgggtt	aacacagcaa	60
gcagagctcc	agctgcccct	cttcctcctg	ttcctgggaa	tctatgtggg	cacagtagtg	120
ggcaacctgg	gcattgattct	cctgattgca	gtcagccctc	tacttcacac	ccccatgtac	180
tatttctctc	gcagcttgctc	cttcgtcgat	ttctgtctatt	cctctgtcat	tactcccaaa	240
atgctgggtg	acttcctagg	aaagaagaat	acaatccttt	actctgagtg	catgggtccag	300
ctctttttct	ttgtgggtctt	tgtgggtggct	gaggggttacc	tcctgactgc	catggcatat	360
gatcgctatg	ttgccatctg	tagccactg	ctttataatg	cgatcatgtc	ctcatgggtc	420
tgtctactgc	tagtgctggc	tgccttcttc	ttgggctttc	tctctgcctt	gactcataca	480
agtgccatga	tgaaactgtc	cttttgcaaa	tcccacatta	tcaaccatta	cttctgtgat	540
gttcttcccc	tcctcaatct	ctcctgctcc	aacacacacc	tcaatgagct	tctacttttt	600
atcattgcgg	ggtttaacac	cttgggtgccc	accctagctg	ttgctgtctc	ctatgccttc	660
atcctctaca	gcattcctca	catccgctcc	tcagagggcc	ggtccaaaagc	ttttggaaca	720
tgcagctctc	atctcatggc	tgtgggtgatc	ttctttgggt	ccattacctt	catgtatttc	780
aagccccctt	caagtaactc	cctggaccag	gagaaggtgt	cctctgtatt	ctacaccacg	840
gtgatcccca	tgctgaacct	tttaatatat	agtctgagga	ataaggatgt	gaagaaagca	900
ttaaggaagg	tcttagtagg	aaaa				924

&lt;210&gt; 848

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g698 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 848

atggcacctg	gaaatggctc	tttcgtgact	gaattcattc	tggcgggatt	aacacatcag	60
ccagatctcc	agtcctctct	gttcttctctg	tttctagtaa	tctatgtggg	cactctgttg	120
ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttctctc	ttacttctgc	cttcatagat	ctctgttatt	cttctgtgtt	tacacccaaa	240
atgctaata	actttatttc	agagaagaat	attatctcct	tcaaggggtg	catgacccaa	300
cttttctttt	tctgtttttt	ttgggtcattt	ctgaatgtta	tgtgctgacg	tcaatggcgt	360
atgatcgctg	tggccatctg	taaccacttt	ctgtatcaca	ttgccatgtc	tcctacagtg	420
tgtctccagc	ttatgttttg	ttcctatttg	atggcctttt	ctgggtgccat	ggccccacact	480
ggatgcattg	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
atcctccttc	tgtccagctc	ctcctgcacc	agcacctaca	tcaatgagct	gggtggttttc	600
actgtgggtg	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatggtttc	660
atcctctcca	gcattcctca	tatcagttcc	aaggagggca	ggtccaaaagc	tttcagcact	720

tgcagttccc	atataattgc	tgtttctctg	ttctttggat	cagggtgcatt	tatgtatctc	780
aacctcatctt	ctgctgggtc	catggataag	agaaaaattat	cttctgtctt	ttatacaaat	840
gtggttccca	tgttgaaccc	cttaattctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960
agtcacaaga	cagggatatt	ctgt				984

&lt;210&gt; 849

&lt;211&gt; 940

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g699 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 849

atgaaaccag	ggaatgagac	acaaatttca	caattccttc	tcctgggact	ttcagaggaa	60
ccagaattgc	agcccttctt	ctttgggcta	tttctgtcca	tgtacctggt	caccgtgctc	120
gggaacctgc	tcatacatct	ggccacaate	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctt	ccaacctgtc	ctttgcagac	atctgttttg	tgtctaccac	tgtcccaaag	240
atgctggtga	acatccagac	acagagcaga	gtcatcacct	atgcagactg	catcaccacg	300
atgtgtcttt	ttatactctt	tgtagtgttg	gacagcttac	tcctgactgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccctcg	cactacacag	tcattatgaa	ctcctggctc	420
tgtggactgc	tggttctggg	gtcctggatc	gtgagcatcc	tatatctctt	gttacaagac	480
ataatggcat	tgcagctgtc	cttctgtaca	gaattgaaaa	tccttcattt	tttctgtgaa	540
cttaatcagg	tcataccact	tgccgtgttc	gacactttta	ttaatgacat	gatgatgaat	600
tttacaagtg	tgctgctggg	tgggggatgc	ctcgctggaa	tattttactt	actttaagat	660
actttgttgc	atatgttcga	tctcatcagc	tcaggggatg	aataaagcac	tttccacctg	720
tgcattctac	ctctcagttg	tctccttatt	ttattgtaca	ggcgtagggt	tgtaccttag	780
ttctgtctga	accataact	cactctcaaa	tgctgcagcc	tcggtgatgt	acactgtggt	840
cacctccatg	ctgaaccctt	tcattctacag	cctgaggaat	aaagacataa	acagagctct	900
gaatcgattc	ttcagagagc	agaaacagga	gggccatttt			940

&lt;210&gt; 850

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g700 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 850

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagtcggg	cctcgtcttg	ctgtccctgt	ccctgtccct	gaatctgggc	120
acggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccatgtact	tcttctcttc	caacctgtgc	tgggctgaca	tcggtctcac	ctcgccacag	240
gttcccaagg	tgattctgga	tatgcagtcg	catagcagag	tcattctctca	tgtgggctgc	300
ctgacacaga	tgtctttctt	ggcctttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	gctgctttgt	agccatctgt	cgccctctgc	actaccaggt	catagtgaat	420
cctcacctct	gtgtcttctt	cgtttttggt	tccttttttc	ttaacctgtt	ggattcccag	480
ctgcacagtt	ggatttgtgt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
ttctgtgacc	cctctcagct	tctcaacctt	gcctgttctg	acagcgctcat	caatagcata	600
ttcatatat	tcgatagtag	tatgtttggg	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	ttgtccccct	cattctaagg	atgtcatcgt	cagatgggaa	gtataaagcc	720
ttctccacct	atggctctca	cctaggagtt	gtttgctggg	tttatggaac	agtcattggc	780
atgtacctgg	cttcagccgt	gtcaccaccc	cccagggaatg	gtgtgggtggc	atcagtgatg	840
taggctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggaacata	900
caaagtggcc	tgcggagggt	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttcttggt	t					971

&lt;210&gt; 851

&lt;211&gt; 1014

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g701 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 851

```

cccattgagc agggaaatta caccagggtg aaggaatctc ttttttcaag gactgaccca      60
gtcccaagag ctgagcttgg tcttatttct tttcttattt tttgtgtact cagcaactgt      120
gctgggtaac ctctcatca tggctgtggt gacctgtgag tctcgcttc acacccccac      180
gtacttcctg ctctgcaatc tctctgtgtt gggtatctgc ttctctcca tcaactgtcg      240
gaagggtgcta atagaccttt caagcagaaa gaccatctcc ttcaatggtt gcatgacaca      300
gatgtttttc ttccacctcc tcgggtggac agacgttttt tctctctttg tgatggcggt      360
tgaccaatac atggccatct tcaagccctt gcactgtgtg accatcgtga gtaggggaca      420
gtgctccctt acatcgtgag tagggggcgt gagtgaggcg caggcctcat catggcttcc      480
tgggtggggg gtttgtccac tccattgtgc aggtatttct gttgctcca ctcccttctg      540
tggacatcat atgattgatg gtttctactg tgatgtcccc caggctctca aacttgctg      600
caccacacac tttgctcttg aggtcttaat gatttccaat aatggcttga tctctatgct      660
gtgggttcata tttctctca tatcttacac ggtcatcttg atgatgttga ggtctcacac      720
tgaggaaaggc aggaggaaaag ccattgccac ctgcacctcc cacatcactg tggtagccct      780
gcatttcgtg ccctgcatct atgtgcatgc ccagccttca ctgccctccc caggacaga      840
gctgtctcca tcacctttac agtcattatt cctgtcctga accccatgat ctacaccctg      900
aggaaccagg agatgaagtc agccttgagg aggcggaaga aaagaccttc tggaaaggga      960
tagatgctac gaagtcacaga ttgaaaatc agaactgaaa agtatttctt cata      1014

```

&lt;210&gt; 852

&lt;211&gt; 1004

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g702 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 852

```

tctacatacc cgcagaatct aacagatgtc tctttattcc tctcctaga agctcagagg      60
atccagaaca gcagcctgtc ctgctgggc tggtcctgtc catgtgcctg gtcacggtgc      120
tggggaacct gtcacatc ctggccgtca gccctgactc ccacctccac acccccatgt      180
acctcttctt ctccaacctg tcttgcctg acatcggttt cactccagc atgggtccca      240
agatgattgt ggacatctaa tctcacagca gactcatctc ctaggcaggc tgcctgactc      300
ccatgtctct ctttgcattt tttggaggca tggaaagagag acatgctcct gagtgtgatc      360
cctatgaccc gttttagacc atctgtcacc ctctatatca ttcagccatc atgaacctgt      420
gtttctgtgg ctttctagtt ttgtgtctt tttttctca gtctcttta gacgccagg      480
tgcacaactt gattgcctta caaatgacct gcttcaagga tgtggaaatt cctaatttct      540
tctgggaacc ttctcaactc ccccatcttg catgttgcca cacttcacc aataacataa      600
tcatgtattc cctgctgcc atatttggtt ttcttccat ctgggggacc ctttctctt      660
actataagat tgtttctcc attctgaggg ttctcatc aggtgggaag tataaggcgt      720
gtccacctg tgggtctcac ctgtcagttg tttgctgatt ttatggaaca ggcttttggg      780
ggtacctcag ttcagatgtg tcatcttccc cgggaaaggc tgcagtggcc tcagtgtgt      840
acacggtggt caccacctg ccgaaccctt tcatctacag cctgagaaac agggatatta      900
aaagcgctct gcggcgccg caggcgagca cagtctaag tcaatatctc cttatctgtt      960
ccatgccttt ttagtgtgtg gtaaaaaag gcagcaaggt caaa      1004

```

&lt;210&gt; 853

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g703 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 853

atgaaaaact	gtaccagggt	aaaagaattt	attttccttg	gcctaaccce	gaatggggac	60
acaagattgg	tcctatttct	tttcctactc	ttgggtgtaca	tgacgactct	gctgggaaac	120
ctccatcatca	tgggtactgt	cacctgtgaa	tcttgccctc	acatgcccac	gtattttttg	180
ctccataaatt	tatctattgc	cgatatctgc	ttctactcca	tcacagagcc	caagggtctg	240
gtggaccttc	tgtctgagag	aaagaccatc	tccttcaatg	gttgcttcac	tcagatgttt	300
ctcttccacc	ttattggagg	ggtggatgca	ttttctctat	cagtgtatggc	attggatcaa	360
tatgtggcca	tttccaagtc	cctgcactat	gcgaccatca	tgagtagaga	ccgttgcatt	420
gggctcacag	tggctgcctg	gttggggggc	tttgtccact	ccattgtgca	gattaccctg	480
ttgctccac	tccttttctg	tggaccaaatt	gttcttgaca	ctttctactg	tgatgttccc	540
caggttctca	aactcgccca	tacagacatt	ttcatacttg	agctgttgat	gatttccaac	600
aatggactgc	tcaccacact	gtgggttttc	ctgtcctctg	tgctctacat	ggatcatatta	660
tcattactca	agtctcaggc	aggatagggc	aggaggaaag	tcattctccac	ctgcacctcc	720
cacatcactg	tgggtgacct	gcattttgtg	ccctgcactc	atgtctatgc	ccggcctttc	780
actgccctcc	ccacggataa	ggccatctct	gtcaccttca	ctgtcatctc	ccctctgctc	840
aacccttgat	ctacactctg	agaaaccatg	agatgaagtc	aaccatgaag	agactgaaga	900
ctctgacctt	ctgataggaa	atagaccagt	gcttccctcc	ttctc		945

&lt;210&gt; 854

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g704 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 854

cacacagagc	cacggaatct	cacaggtgtc	tgaaaagtgc	tcctgggact	ctctctgaga	60
ggatccagaa	ctgcagccca	tcctcgctgg	gctgtccctg	tcctatgtatc	tggtcacggt	120
gctgaggaa	gtgctcatca	tcctggctgt	cagctctgac	tcacacctcc	acacccccat	180
gtacttcttc	ctctccagcc	tgtgctgggc	tgacatcggt	ttcacctcgg	ccactgttcc	240
caagatgact	gtggacatgc	agtcgcatag	cagagtcac	tcctatgtga	gctgcctgac	300
acagatatct	ttcttggtcc	tttttgcatg	tatggaagac	atgctcctgt	gatggcctat	360
gacagagtgt	tggccatctg	tcacccccctg	cactatccag	tcacatgaa	tcctcacctt	420
cgtgtcttct	tagttttgct	gtcctttttc	cttagcttgt	tggattccca	gctgcacagt	480
tggatttgt	tacaattcac	cttattcaag	aatgtggaaa	actctagttt	tgtctgtgac	540
ccctctcaac	ttctcaacct	tgccgtgtct	gacagcgta	tcaatagcat	attcatatat	600
ttcgatagta	ctatgttttg	ttttcttccc	atttcaggga	tccttttatc	ttactataaa	660
attgtcccct	ccattctaag	gatgtcatca	tcagatggga	agtataaagc	cttctccacc	720
tatggctctc	aactggcagc	tccttgctga	ttttatggaa	caggcattgg	catgtacctg	780
acttcagctg	tggcactacc	ccccagggaat	ggtgtcgtgg	catcagtgat	gtaggctgtg	840
gtcacccccca	tgctgaactt	tttcatctac	agcctgagaa	acaggggacat	acaaagtgcc	900
ctgcggaggc	tgcgcagcag	aacagtcgaa	tctcatgatc	tggtccatcc	ttttcttctg	960
gt						962

&lt;210&gt; 855

&lt;211&gt; 952

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g705 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 855

aagcagcagg	aaaatggggac	ctgtctgggtg	acagaattcc	tgatgatggg	attctccaac	60
ctcccacacc	tgaggaaacac	actcttcacc	ctgttcttcc	ttacctacct	ggtcaccctc	120
ggtggcaacg	tcaccatcat	caccatcacc	catgcggata	ggccccgcca	cactcccacg	180
taccacttcc	tgggtgtgct	gtccctctcg	gagacctgct	atacacgctg	gtcaccatcc	240
ccagcatgct	ggctcatctg	ctgatggaga	ccaggccatc	tcctaccctg	gctgtcaggc	300
tcagatgttt	ttcttcttgg	gtctgggatg	cagccactgc	ttcctcctta	ccctgatggg	360
ttatgaccgc	tatgtggcca	tctgccacc	cctgcgtac	tctatggtca	tgagaccac	420
cgtttgcctc	tgccctgggg	ccctgggttt	ctgtctggg	ttctcggtgg	ccttgatcga	480

```

gaccagcatg atcttctcat cgcccttttg cggcgagagac cacgtggagc acttcttctg 540
tgacatcgcc ccggtgctga agctcagctg cgccaagagt gccagcaagg cgctgggcat 600
ctttttctctg agcgctcctgg tgggtgctgat gtccttcgtc ccgatcctct tctcctatgc 660
cttcatcggtg gctgccatcg tgaggatttc cttggcagcc ggccggcgca aggccttctc 720
cacctgtgtg gccacgtca ccgtggctgt agtacatttt gactgcgcct ccatcatcta 780
cttgcggtccg gaggccgggg ccaaccccgga ccaggaccgc ttggtggctg tgttctacac 840
gggtggtgatg ccactgctga accctgtggt gtgcactctg tggacaagg aggtgagagt 900
ggctctgagg aggaccctgg cgtggagccg tggggttttt aaataagaat ct 952

```

&lt;210&gt; 856

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g706 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(339)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 856

```

ctgctggacc acttcatctg tgagctgccg gcgttgctca agctggcctg cggaggcgac 60
ggagacacta ccgagaacca gatgttcgcc gcccgcgctg tcatcctgct gctgccgttt 120
gccgtcatcc tggcctccta cgggtccgtg gcccgagctg tctgttgcat gcggttcagc 180
ggaggccgga gggaggcgcg tgggcacgtg ttgggtccca cctgacagcc gtctgcctgt 240
tctacggctc ggccatctac acctacctgc agcccgcgca gcgctacaac cagcacgggn 300
ncagnttcgt atcgtctctc tacacccgtg gtcacaccc 339

```

&lt;210&gt; 857

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g707 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 857

```

atggatcaga gaaattacac cagagtgaag gaatttacct tcctgggaat tactcagtcc 60
cgagaactga gccaggctct atttaccttc ctgttttttg tgtacatgac aactctaattg 120
ggaaacttcc tcatcatggt tacagttacc tgtgaatctc accttcatac gcccatgtac 180
ttcctgctcc gcaacctgtc tattcttgac atctgctttt cctccatcac agctcctaag 240
gtcctgatag atcttctatc agagacaaaa accatctcct tcagtggctg tgtcactcaa 300
atgttcttct tccaccttct ggggggagca gacgtttttt ctctctctgt gatggcggtt 360
gaccgctata tagccatctc caagcccctg cactatatga ccatcatgag tagggggcga 420
tgcacaggcc tcatcgtggg cttcctgggt ggggggcttg tccactccat agcgagatt 480
tctctattgc tccactccc tgtctgtgga cccaatgttc ttgacacttt ctactgcgat 540
gtccccagg tctcaaact tgctgcact gacaccttca ctctggagct cctgatgatt 600
tcaaataatg ggtagtcag ttggtttgta ttcttcttcc tcctcatatc ttacacggtc 660
atcttgatga tgctgaggtc tcacactggg gaaggcagga ggaaagccat ctccacctgc 720
acctcccaca tcaccgtggt gacctgcat ttcgtgccct gcactctatgt ctatgcccg 780
cccttcaactg cctccccac agacactgcc atctctgtca ccttcaactgt catctccct 840
ttgctcaatc ctataattta cagctgagg aatcaggaaa tgaagtggc catgaggaaa 900
ctgaagagac ggctaggaca atcagaaagg attttaatt 939

```

&lt;210&gt; 858

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g708 nucleotide)

&lt;220&gt;



## &lt;223&gt; Synthetic construct

&lt;400&gt; 858

gtagccatat	gtaatccctt	gctttatcca	gtgatgatgt	ccaacaaact	cagcgctcag	60
ttgctaagta	tttcatatgt	aattggtttc	ctgcatcctc	tggttcattgt	gagtttacta	120
ttgcgactaa	ctttctgcag	gtttaacata	atacattatt	tctactgtga	aatttttacaa	180
ctgttcaaaa	tttcatgcaa	tggtccatct	attaacgcac	taataatatt	tatttttgggt	240
gcttttatac	aaatacccac	tttaatgact	atcataatct	cttataactcg	tgtgctcttt	300
gatattctga	aaaaaaagtc	tgaaaagggc	agaagcaaag	ccttctccac	atgcggcgcc	360
catctgcttt	ctgtctcatt	gtactacgga	actctgatct	tcatgtatgt	gcgtcctgca	420
tctggcttag	ctgaagacca	agacaaagtg	tattctctgt	tttacacgat	tataattccc	480
ctgcta						486

&lt;210&gt; 859

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g709 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 859

atgtactact	tcctctgcca	cctggccttg	gtagacgcgg	gcttactac	tagcgtgggtg	60
ccgccgctgc	tgcccaacct	gcgcggacca	gcgctctggc	tgccgcgcag	ccactgcacg	120
gccagctgtg	gcgcacgcgt	ggctctgggt	tcggccgaat	gcgtcctcct	ggcggtgatg	180
gctctggacc	gcgcggccgc	agtgtgccgc	ccgctgcgct	atgcggggct	cgtctccccg	240
cgctatgtc	gcacgctggc	cagcgccctc	tggttaagcg	gcctcaccaa	ctcggttgcg	300
caaaccgcgc	tcctggctga	gcggccgctg	tgccgcgccc	gcctgctgga	ccacttcatt	360
tgtgagctgc	cgccgttgct	caagctggcc	tgccgaggcg	acggagacac	taccgagaac	420
cagatgttcg	ccgcccgcg	ggtcactctg	ctgctgccgt	ttgccgtcat	cctggcctcc	480
tacggtgccg	tgcccgagc	tgtctgttgc	atgcggttca	gcggaggccg	gaggaggcg	540
gtgggcacgt	gtgggtccca	cctgacagcc	gtctgcctgt	tctacggctc	ggccatctac	600
acctacctgc	agcccgcgca	gcgctacaac	caggcacggg	gcaagttcgt	atcgctcttc	660
tacaccgtgg	tcacacctgc	tctcaaccgc	ctcatctaca	ccctcaggaa	taagaaagtg	720
aagggggcag	cgaggaggct	gctgcggagt	ctggggagag	gccaggctgg	gcag	774

&lt;210&gt; 860

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g710 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 860

atgcagagag	ccaatcactc	cacagtgacc	caattcatcc	tcgtcggctt	ctctgtcttc	60
ccccacctcc	agctgatgct	cttctgtctg	ttctgtctga	tgtacctgtt	cacgctgctg	120
ggcaacctgc	tcattcatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
ctcttctctg	gcgccctctc	cgtctccgag	atcctctaca	ccgtggccat	catccccgcg	240
atgctggccg	acctgctgtc	caccacgcgc	tccatcgctt	tcctggcctg	tgccagtcag	300
atgttctctt	ccttcagctt	cggcttcacc	cactccttcc	tgctcacggt	catgggtac	360
gaccgctacg	tggccatctg	ccacccctcg	cgtacaacg	tgctcatgag	ccgcggggc	420
tgccgctgcc	tggtgggctg	ctcctgggct	ggtggcttgg	tcatggggat	ggtggtgacc	480
tcggccatth	tcacctcgc	cttctgtgga	cacaaggaga	tccaccatth	tgtttgccat	540
gtgccacctc	tggtgaagtt	ggcctgtgga	gacgatgtgc	tggtgtgggc	caaaggcggtg	600
ggcttgggtg	gtatcacggc	cctgctgggc	tgthttctcc	tcatcctcct	ctcctatgcc	660
ttcatcggtg	ccgccatctt	gaagatccct	tctgctgaag	gtcggaaaca	ggccttctcc	720
acctgtgcct	ctcacctcac	tgtggtgggc	gtgactatg	gctttgcctc	cgtcatttac	780
ctgaagccca	aaagtcccca	gtctctggaa	ggagacacct	tgatgggcat	cacctacacg	840
gtcctcacac	ccttctcag	ccccatcatc	ttcagcctca	ggaacaagga	gctgaaggtc	900
gccatgaaga	agaccttctt	cagtaaaactc	taccagaaaa	aaaatgta		948

<210> 861  
 <211> 674  
 <212> DNA  
 <213> Unknown (H38g711 nucleotide)

<220>  
 <223> Synthetic construct

<400> 861  
 ttgcctgaca tcgggtttcac ctccaccacg gtccccaaga tgattgtgga catccagtct 60  
 cacagcagag tcctctccta tgcgggctgc ctgatcagat gtctctcttt gccacttttg 120  
 gaagcatgga agagaggcat gctcctgagt gtgatggcat atgaccggtt tgtagccatc 180  
 tgtcaccctc tatatcggtc agccatcttg aaccctgat tctgtggctt cctagatttg 240  
 ttgtctttgt tttttttgt ttgtttgttt tgtttttctc agtcttctag actcccagct 300  
 gcacaacttg attgccttac aaatgacctg ctccaaggat gtggaaattc ctaatttctt 360  
 ctgggaacct tctcarctcc cccatcttgc atgttgtgac accttcacca ggaacatcaa 420  
 catgtatttc cctgctgccg tatttggttt tcttccatc tcagggaacct tttctcttac 480  
 tgtaaaattc tttctccat tctgagggtt tcatcatcag gtgggaagta taaaccttct 540  
 ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaacaggc gttggagggt 600  
 acctcggttc agatgtgtca tcttccccga gaaagrgtgc agtggcctca gtgatgtaca 660  
 ygggtggtcac cccc 674

<210> 862  
 <211> 653  
 <212> DNA  
 <213> Unknown (H38g712 nucleotide)

<220>  
 <223> Synthetic construct

<400> 862  
 ttgcctgaca tcgggtttcac ctccaccatg gtccccaaga tgattgtgga atccaatctc 60  
 acagcagagt catctcctat gcaggccgcc tgactcagat gtctctcttt gccatttttg 120  
 gaggcatgga agagagacat gctcctgagt gtgatggcct atgaccggtt tgtagccatc 180  
 tgtcaccctc tatgtcatc agccatcacg aaccctgtt tctgtggctt tctagttttg 240  
 ttgtcttttt tttttctcag tcttttagac gccagctgc acaacttgat tgccttaca 300  
 aggacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaattcccc 360  
 gtcttgcatg ttgtggcacc ttcaccaata acataatcat gtatttccct gctgccatat 420  
 ttggttttct tcccatctcg gggaccttt tctcttacga taaaattgtt ttctccatc 480  
 tgagggttcc atcatcagggt gggaagcata aggcctctc caccaggggg tctcacctgt 540  
 cagttgtttg ctgattttat ggaacaggcg ttggagagta cctcgggtca gatgtgtcat 600  
 cttccccgag aaagggtgca gtggcctcag tgatgtacac ggtggtcacc ccc 653

<210> 863  
 <211> 648  
 <212> DNA  
 <213> Unknown (H38g713 nucleotide)

<220>  
 <223> Synthetic construct

<400> 863  
 ctgggtggact ttggatactc ctgagctgtc actcccaagg tcatggctgg gttccttata 60  
 gaagacaagg tcatctctta caatgcatgt gctgctcaaa tgtatatctt tgtagctttt 120  
 gccactgtgg aaaattacct cttggcctca atggcctatg accgctatgc agcagtgtgc 180  
 aaaccctac attacaccac aaccatgaca acaactgtgt gtgctcgtct ggccataggg 240  
 tcctacctct tgggtttcct gaatgcctcc atccacatg gggacacatt tagtctctct 300  
 ttctgtaagt ccaatgaagt ccatcacttt ttctgtgata ttccagcagt catgggttctc 360  
 tcttgctctg atagacatat tagcgagctt gttcttattt atgttgtgag cttcaatatc 420  
 tttatagctc tcctgggttat cttgatatcc tacacattca tttttatcac catcctaaag 480

atgcactcag	cttcagtata	ccagaagcct	ttgtccacct	gtgcctctca	tttcattgca	540
gtcggcatct	tctatgggac	tattatcttc	atgtacttac	aaccagctc	cagtcactcc	600
atggacacag	acaaaatggc	acctgtgttc	tatacaatgg	tcatcccc		648

&lt;210&gt; 864

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g714 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 864

attgttgaca	tatcctatgc	ttccaactat	gtccccaaga	tgctgacgaa	tcttatgaac	60
caggaaagca	ccatctcctt	ttttccatgc	ataatgcaga	cattcttgta	tttggctttt	120
gtcacgtag	agtgtctgat	tttgggtgtg	atgtcctatg	atcgctatgc	ggacatctgc	180
caccccttac	gttacaatat	cctcatgagc	tggagagtgt	gcactgtcct	ggctgtggct	240
tcttggtgt	tcagcttcct	cctgggtctg	gtccctttag	ttctcatcct	gaggctgccc	300
ttctgcgggc	ctcatgaaat	caaccacttc	tgtgaaatcc	tgtctgtcct	caagttggcc	360
tgtgtcgaca	cctgggtcaa	ccaggtggtc	atctttgcag	cctgcgtgtt	catcctgggtg	420
gggccactct	gcctgggtgt	ggtctcctac	ttgcgcaccc	tgcccgccat	cttgaggatc	480
cagtctgggg	agggccgcag	aaaggccttc	tccactgct	cctccacact	ttgcgtgggtg	540
ggactcttct	ttggcagcgc	cattgtcacg	tacatggccc	ccaagtcccg	ccatcctgag	600
gagcagcaga	aagttctttc	cctgtttttac	agccttttca	atcca		645

&lt;210&gt; 865

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g715 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 865

gtggccatct	gtaaaccctt	tcattatgtg	gtcatcatga	acaacagggt	gtgtacctta	60
ttagttctct	gctgttgggt	ggctggcttg	atgatcattg	ttccaccact	tagcttaggc	120
ctccagctcg	aattctgtga	ctccaatgcc	attgatcatt	ttagctgtga	tgcaggctct	180
ctcctaaaga	tctcatgctc	agatacatgg	gtaatagaac	agatgggttat	acttatggct	240
gtatttgac	tcattatcac	cccagtttgt	gtgattctgt	cctacttgta	catagtcaga	300
acaattctga	agttcccttc	tgttcagcaa	aggaaaaagg	ccttttctac	ctgttcatcc	360
cacatgattg	tggtttccat	tgcctatgga	agctgcatct	tcattctatat	caagccctct	420
gcaaaagatg	aggtggccat	aaataaagga	gtttcagttc	ttactacttc	tgctgcaccc	480
ttgttg						486

&lt;210&gt; 866

&lt;211&gt; 670

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g716 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(670)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 866

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctcta	tgagggtctg	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	cgtgatggcc	tacgaccagt	ttgtagccat	180
ctgtcacctt	ccatatcggt	cagccatctt	gaaccctgtg	ttctgtggct	tccaagattt	240

gttgtccttg	tntttttt	tttttttt	tttttctca	ggcttttaga	ctcccagctg	300
cataacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaatttc	taatgtcttc	360
tgggaacctt	ctcaactctc	ccatcttgca	tgttgtgaca	ccttcaccag	gaacatcagt	420
atttcctgc	tgccatattt	ggttttcttc	ccatcttggg	gacccttttc	tcttactgta	480
aaattgtttc	ctccattctg	agggtttcat	catcaggtgg	gaagtataaa	ccttctccac	540
ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggtgttg	gagggtagct	600
cagttcagat	gtgtcatctt	ccctgagaaa	ggctgcagtg	gcctcagtga	tgtacaagat	660
ggtcaccccc						670

&lt;210&gt; 867

&lt;211&gt; 654

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g717 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 867

ttggctgaca	tcggtttcac	ctccaacacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgctgttttt	120
ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
ctgtcaccct	ctatatatt	cagccatcat	gaacccatgt	ttctgtggct	tcctagtttt	240
gtgttttttt	tttttctcag	tcttttagac	tcccagctgc	acaatttgat	tgccctacaa	300
atgacctgca	tcaaggatgt	ggaaattcct	aatttcttct	gtgacccttc	tcaactcccc	360
catcttgcat	gttgtgacac	cttcaccatt	aacatagtc	tgtatttccc	tgccgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ctaaaattgt	ttcctccatt	480
ctgagggttt	catcatcagg	tgggaagtat	aaagccttct	ccacctgtgg	gtctcacttg	540
tcagttgttt	gctgagttta	tggacacagg	gttggagggt	acctcagttc	agatgtgtca	600
tcttcctga	gaaaggctgc	agtggcctca	gtgatgtaca	cggtgggtcac	cccc	654

&lt;210&gt; 868

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g718 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 868

ttgattttct	tcttaatcta	tccgcttata	ctgggtgggt	atgaccagat	cctgggtgggt	60
gtgatggcag	aggccagcct	tcacaagcct	gtgtacttct	tcctgataaa	cctctcagcc	120
ctagacatcc	tctccactac	agtcactgtc	cccaagacgc	tgccctgtgt	cttgcttggg	180
gaccacttcc	tcagcttccc	tgccctgttc	ctacagatgt	acctgttcca	cagcttctcc	240
tgctcagaag	ccttcatact	gggtggtcatg	gcctatgacc	gctatgtagc	tatctgccac	300
ccactgcaat	accctgttct	catgaaccca	cagaccaatg	ctgtcttggc	aaccgggtgcc	360
tggctcactg	cctctctcct	gccatttcca	gcagtagtac	agaccttcca	gatggcattt	420
gacagcattg	ctgacatcta	ccactgtctc	gtgtatcatc	tggctgtggg	ccaggcctcc	480
tgctctgata	ccacccccag	accttcattg	gtttctgcat	cgccatgggt	gtgtccttcc	540
tcccccttct	cctgggtgctt	ctctcctatg	cccacatctt	gacctgggtg	cttcgcatta	600
actcccaaga	aggacgctcc	aaagccttct	ccacctgcag	ctcccatctc	ccggtagtggt	660
gcacctacta	ctcatccatt	gccatagcct	atgtggccta	cagcgctgac	ctgccccctg	720
acttccacgt	catgggcaat	gtgtacatg	tcttcttctt	cctcttcttc	ttcttcttcc	780
tcttctctct	cttctctctc	ctctctgtct	tctcttctct	cttcttctcc	ttctccttcc	840
tcttctctct	cttctctctc	tcttctctct	tcttctctct	tt		882

&lt;210&gt; 869

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g719 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 869

atggagatgg	aaaactgcac	cagggtaaaa	gaatttattt	tccttggcct	gacccagaat	60
cggaagtgga	gcttagtctt	atttcttttc	ctactcttgg	tgtatgtgac	aactttgctg	120
ggaaacctcc	tcatcatggt	cactgttacc	tgtgaatctc	gccttcacac	gcccattgat	180
tttttgctcc	ataattttatc	tattgccgat	atctgcttct	cttccatcac	agtgcccaag	240
gttctgggtg	accttctgtc	tgaagaaaag	accatctcct	tcaatcattg	cttcaactcag	300
atgtttctat	tccaccttat	tggaggggtg	gatgtatttt	ctctttcggg	gatggcattg	360
gatcgatatg	tggccatctc	caagcccctg	cactatgcga	ctatcatgag	tagagaccaa	420
tgcattgggc	tcacagtggc	tgcctgggtg	gggggctttg	tcactccat	cgtgcagatt	480
tccttggtgc	tcccactccc	tttctgcgga	cccaatgttc	ttgacacttt	ctactgtgat	540
gtccacgggg	tcccaaaact	ggcccataca	gacattttca	tacttgaact	actaatgatt	600
tccaacaatg	gactgctcac	cacactgtgg	tttttctctc	tcctgggtgc	ctacatagtc	660
atattatcat	tacccaagtc	tcaggcagga	gagggcagga	ggaaagccat	ctccacctgc	720
acctcccaca	tcaactgtgt	gacctgcat	ttctgtgccc	tgcattctatg	tctatgcccg	780
gcccttcaact	gccctcccga	tggataaggc	catctctgtc	accttcaactg	tcatctcccc	840
tctgtctaac	cccttgatct	acactctgag	gaaccatgag	atgaagtcag	ccatgaggag	900
actgaagaga	agacttgtgc	cttctgatag	aaaa			934

&lt;210&gt; 870

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g720 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 870

acaatgcagc	aaaataacag	tgtgcctgaa	ttcatactgt	taggattaac	acaggatccc	60
ttgaggcaga	aaatagtgtt	tgtaatcttc	ttaattttct	atatgggaac	tgtgggtggg	120
aatatgctca	ttattgtgac	catcaagtcc	agccggacac	taggaagccc	catgtacttc	180
tttctatttt	atttgtcctt	tgcagattct	tgcttttcaa	cttccacagc	ccctagatta	240
attgtggatg	ctctctctga	aaagaaaatt	ataacctaca	atgagtgcac	gacacaagtc	300
tttgcactac	atttatttgg	ctgcatggag	atctttgtcc	tcattctcat	ggctgttgat	360
cgctatgtgg	ccatctgtaa	gcccttgcgt	tacccaacca	tcattgagcca	gcaggctctgc	420
atcatcctga	ttgttcttgc	ctggataggg	tctttaatac	actctacagc	tcagattatc	480
ctggccttaa	gattgccttt	ctgtggaccc	tatttgattg	atcattattg	ctgtgatttg	540
cagcccttgg	tgaacttgc	ctgcatggac	acttacatga	tcaacctgct	gttgggtgtct	600
aacagtgggg	caatttgcct	aagtagtttc	atgattttga	taatttcata	tattgtcatc	660
ttgcattcac	tgagaaacca	cagtgcacaa	gggaagaaaa	aggctctctc	cgcttgcaag	720
tctcacataa	ttgtagtcat	cttattcttt	ggccccatga	tattcatata	tacacgcccc	780
ccgaccactt	tccccatgga	caagatgggtg	gcagtatttt	atactattgg	aacacccttt	840
ctcaatccac	tcattctacac	atctgaggaa	tgcagaagtg	aaaaatgcca	tgagaaag	898

&lt;210&gt; 871

&lt;211&gt; 943

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g721 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 871

atggagtggg	gaaatgtcac	cagagtaaaa	gaatttatat	ttctgggact	tactcaatcc	60
caagaccaga	gtttggtctt	gtttcttttt	ttatgtcttg	tgtacatgac	gactctgctg	120
ggaaacctcc	tcatcatggt	caccgtgacc	tgtgagtctc	gccttcacac	ccccatgtac	180
ttcctgctcc	gcaatctagc	catccttgac	atctgcttct	cctccacaac	tgctcctaaa	240
gtcttgctgg	accttctgtc	aaagaaaaag	accatatacct	atacaagctg	catgacacag	300
atatttctct	tccacctcct	tggtggggca	gacatttttt	ctctctctgt	gatggcggtt	360
gactgctaca	tggccatctc	caagcccctg	cactatgtga	ccatcatgag	tagagggcaa	420

tgactgccc	tcattctctgc	ctcttgatg	gggggctttg	tccactccat	cgtgcagatc	480
tcctgtgtgc	tgctctctccc	tttctgtgga	cccaatgttc	ttgacacttt	ctactgcat	540
gtcccccagg	tcctcaaact	cacttgact	gacacttttg	ctcttgagtt	cttgatgatt	600
tccaacaatg	gcctgggtcac	taccctgtgg	tttatcttcc	tgcttggtgc	ctacacagtc	660
atcctaata	cgctgaggtc	tcaggcagga	gggggcagga	ggaaagccat	ctccacttgc	720
acctccccac	atcactgtgg	tgaccctgca	ttttgtgccc	tgcatctatg	tctatgcccc	780
gcccttctact	gccctcccca	cagaaaaggc	catctctgtc	accttctactg	tcattctcccc	840
tctgctgaac	cctttgatct	acactctgag	gaaccaggaa	atgaagtcag	ccatgagaag	900
actgaagaga	agactcgtgc	cttctgaaag	ggaatagaaa	aca		943

&lt;210&gt; 872

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g722 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 872

atgctggggc	taaaccacac	ctccatgtct	gaattcatcc	tcgtcgggctt	ctctgccttc	60
ccccacctcc	aactgatgct	cttctgtctg	ttcctgtctga	tgtacctgtt	cacgtgtctg	120
ggcaacctgc	tcattcatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
ctcttctctgt	gcgtcctctc	agtctccgag	atcctctaca	ccgtggccat	catcccgcg	240
atgctggccg	acgtgtgtc	caccagcg	tcctgcgct	tcctggcctg	tgccagtcag	300
atgttcttct	ccttcagctt	cggcttcacc	cactccttcc	tgctcacctg	catgggtac	360
gaccgctacg	tggccatctg	ccacccctg	cgctacaacg	tgctcatgag	cccacggggc	420
tgccgctgcc	tgggtggctg	ctcctgggct	gggtggctcg	tcattggggat	gggtgtgacc	480
tcggccattt	tccaactgac	tttctgtgga	tcctcatgaga	tcagcattt	tttatgtcat	540
gtgccacctc	tgttgaagtt	ggcctgtgga	aataatgtac	cagctgtggc	cctgggcgtg	600
ggcttggtat	gtatcatggc	actgctgggc	tgttttctcc	tcattcctct	ctcctatgcc	660
ttcatcgtgg	cgcacatctt	gaagatccct	tctgctgaag	gtcggaaaca	ggccttctcc	720
acctgtgcct	ctcaccttat	tgtggtcatt	gtgcactatg	gctttgcctc	tgtcatctac	780
ctcaagccca	aaggccccca	ctctcaggag	ggtagacacc	tgatggccac	cacctacgca	840
gtcctcacgc	ccttctctcag	ccccatcatc	ttcagcctca	ggaacaaaga	actgaagggtt	900
gccatgaaga	ggaccttcct	cagcacactc	tattcctcag	gc		942

&lt;210&gt; 873

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g723 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 873

atgcctgggc	agaactacag	aaccatatct	gaatttatcc	tctctggctt	ctcagccttc	60
ccccagcagc	tcctgcctgt	cttggtcctg	ctgtacctcc	tgatgttctt	gttcacattg	120
cttggcaacc	ttcttatcat	ggccacagtt	tggattgaac	gcagactcca	cacacccatg	180
tacctcttct	tgtgtgccct	ctccatctct	gagattctgt	tcactgttgc	catcacccct	240
cgcattgctg	ctgatctgct	cttcacccat	cgttccatca	cctttgtggc	ttgtgccatt	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcat	ggtcattggc	360
tatgatcact	acgtgaccat	ctgccaccga	ctgcattaca	acatgcta	gagtcctcgt	420
ggctgtgccc	atcttgtggc	ctggacctgg	gctgggtggc	cggcatggg	gatgatggtg	480
acaatgatgg	tttttcacct	cactttctgt	gggtctaata	tgatccacca	ttttctctgt	540
catgtgcttt	ccctcttgaa	gttggcctgt	gggagcaaga	catcatctgt	catcatgggt	600
gtgatgctgg	tgtgtgtcac	agccctgata	ggctgtttgt	tcctcatcat	cctctccttt	660
gtcttcattg	tggctgcat	cttgaggatt	ccttctgctg	agggccggca	caagactttc	720
tccacttggt	tatccacact	cactgtgggt	gtcatgcact	atagttttgc	ctcccttacc	780
tacctcaaac	ccaaggcct	ccattctatg	tacagtgtatg	ccttgatggc	caccacctat	840
actgtcttca	cccccttct	cagcccaatc	attttcagtc	taaggaaaca	ggagctgaag	900
aatgccataa	ataaaaactt	ttgcagaagg	ttctgccctc	taagctcc		948

<210> 874  
 <211> 484  
 <212> DNA  
 <213> Unknown (H38g724 nucleotide)

<220>  
 <223> Synthetic construct

<400> 874  
 ggatggaaat acaagcacct tcaacatctc ctgcaccaag ttcttccttg tgggtttccc 60  
 tggacttcga gagggtggc cccttctggt cctgcctctt gtcttcctct ttgtgaccat 120  
 catctctgcc aatgccctgg tcatccacac agtgggtggc cggcaaaatc tgcacagcc 180  
 tacgtgtatg ctcatcactg tgctcctggc tgtcaatatt cgtgctgcca cagccgtgat 240  
 gcctaaaatg ctggagggct ttgtatatta tgctaacccc atatcgctgc atggccgcct 300  
 ggcctagggtg ttctttatct acttcaccct cctcctggac tacaacttcc tctggccctg 360  
 gccctggact ggttactttg ccatctgcca cccactctgc ttttctgacc tgatgacctc 420  
 ccagctgctg ggactgctgg ccattcttgc ctttgaacaa agccctggga gtgaccccg 480  
 ccct 484

<210> 875  
 <211> 595  
 <212> DNA  
 <213> Unknown (H38g725 nucleotide)

<220>  
 <223> Synthetic construct

<400> 875  
 gtagccatct ggccaccctc tctgttttca aactgaatga cttcccagct ggctgggatt 60  
 gctggccatt cttgccttga cacagagctg gggagtgaac gtgccttttg tagtactaac 120  
 tgcaaaagcc gatttctgcc ggacagcagt gattcgacac ttcacctgtg agtgcattgc 180  
 actgctgagc atagcttgtg gagacctgac cttcaacaac tggctggggc tggctatgtg 240  
 tttggtcact gtaatctctg atatggccct gctggggacc tcctacaccc acatcatcta 300  
 tgctgccttc cggatctctt cttggggagc ccaagccaag gccttacaca cgtgtggctc 360  
 ccacctactg gtcactctct ccatctacgt ctctggtctt tccacttcca tcaccttctg 420  
 agtagccaag actgtgtccc agaatgtcca gaatctactc agtgccatat acttgctgct 480  
 tccaggagcc ttgaatcctg tcatttatgg ggtgaggact agggagatcc agcaacatgt 540  
 agaaaagatg ctctgtgaaa aggaacacag ccagaaggct ggggagaagc caaag 595

<210> 876  
 <211> 944  
 <212> DNA  
 <213> Unknown (H38g726 nucleotide)

<220>  
 <223> Synthetic construct

<400> 876  
 ttcagtcaga acttgctgat ctctgggtct gggtcctttg tcctgctggg gatgccggga 60  
 ctggaggctc tgcattgctg gctctctgtg cctgtgtgac tgctctacat ggcagctttg 120  
 gtagggaatg cccttctagt ggggctgggt ggtcgtgac aaggcactct gggcaccat 180  
 gtaccagctg ctgtggcttc tggcagctgc tgattttgtt ctggccacat ccacagtgcc 240  
 caaagctctg gctgtacttt ggggcttgtc tagtgagata tcatttggag gctgcttggc 300  
 tcaactcttt gttgccatg tgtcaatcat tgccacattg ctgagtcctc agtgctgctg 360  
 tccacggccg tagactgcca gcctttgcgc tatggggcgt tgctggccca gtttgtggta 420  
 ggtctagtgg ctctgactac catgacccgt gatgtctgtg tcatgtacac cctgtgatcc 480  
 gtgtcaagaa actgccttac tgtggacagt gggccctgcc ccacacctac tgcgaacaca 540  
 tgggtgtggc ttgcctggca tgtggagata cgtgccccat catcaggatg ggactggcca 600  
 ccacactgct ctccccagcc ctggacctag ggctcatagg tgcttcctat gccctcattt 660  
 tccgtgctgt ctgccgtctg ccatcccatg ttgcctgcca caaggctctg ggtaactgag 720

ggacctatgc	tagcatcatt	ggtctcttct	acacacctgc	cctcttctcc	ttccttgctc	780
actgttttgg	gtgtcacaca	gtgcccaccc	atattcacat	cctactggct	aacctctacg	840
cagtgggtgt	cccagcttct	aatcctgtgg	tctatggagt	gcagactcag	cagagctcag	900
aggctcagga	acttgcttca	acttttcttg	gcaggagcag	tgaa		944

&lt;210&gt; 877

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g727 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 877

atgaattggg	aaaatgagag	ctccccaaaa	gagtttatac	tacttggtct	ctcagatagg	60
gcttggttac	aaatgccctt	ttttgtggct	ctgttaatat	catacacaat	caccatattt	120
ggcaatgtgt	ccatcatgat	ggtgtgcatt	ctggatccca	aacttcatac	tcccatgtat	180
ttctttctca	ctaattcttc	catcttagat	ctctgtata	ccacaactac	agtcctctcat	240
atgttggttaa	atatgggttg	caacaaaaag	accatcagct	atgctggctg	tgtggccac	300
ctcatcatct	tcctggccct	aggtgctaca	gagtgtctcc	ttctggctgt	tatgtccttt	360
gacagatatg	tggtgttttg	cagacccctc	cactatgtag	tcacatgaa	ttattggttc	420
tgccaaagga	tggcagcctt	ctcatggctc	attggtttcg	gcaactcagt	gctgcagtct	480
tccttgactc	ttaacatgcc	acgtgtgtgt	caccaggaag	tggaaccactt	tttctgtgag	540
gtgcctgcac	ttctcaagtt	gtcatgtgct	gacacaaagc	ctattgaggc	tgagctcttc	600
ttcttttagtg	tactaattct	tctaattcca	gtgacattga	tcctcatctc	ctatggcttc	660
atagctcaag	cagtattaaa	aatcagggtca	gcagaaggac	ggcaaaaagc	atttgggaca	720
tgtgggtccc	acatgattgt	ggtgtccctc	ttttatggaa	cagccattta	tatgtactct	780
caaccacctt	catccacctc	taaggactgg	ggaaagatgg	tttccctctt	ctatggaatc	840
atcacatcca	tgttgaactc	cctcatctac	agccttagaa	ataaagatat	gaaggaggcc	900
ttcaagaggc	tgatgccaaag	aatctttttc	tgtaagaaa			939

&lt;210&gt; 878

&lt;211&gt; 968

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g728 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 878

ggcacattga	atttaagtag	cttcaatcca	ggactcttca	ttctgttggg	gatcccaggg	60
ctggagtggg	tctgcatctg	gatgggaatt	ctctccttta	ccagttacct	tgtctccctt	120
gcagggaatg	tcacctctct	ctaccttata	actgtggaac	acaacctcca	taaaccatg	180
ttttccttcc	tctctatacc	ggcctctgca	aacctcatat	tatgcattac	atatttcccc	240
aaaacatttg	ggatattcta	gctgaaagct	cagaaaaata	tatttcctgg	atgcttcacc	300
agggtttttt	tttttggtct	acttcacttt	agcttttttt	ctggacttgg	ccatcttgtt	360
gggtctggca	tttgatcatt	acatgaccat	tggtttcctt	ctgagatata	ccagtggctt	420
gacacctcaa	cacttggcaa	gattgtgggtg	agcattgatt	gaaggtttaa	taacattttg	480
cccattgatt	tcctggggaa	gcatttgccc	ttctgcagaa	cacacattaa	ttctaacaca	540
tactgtgagc	acataggtgt	ggccctgctt	tcctatgctg	atatctccat	caatatctgg	600
tatgacttta	ctatattggg	aatgactatt	atctcagatc	tgatcctcac	tgatatttcc	660
tacacctca	cccttcatgc	tgttttccac	cttccatcca	gtgatgccct	tctgaaggcc	720
ctaagcacct	gtgtttctca	tgctcagtgc	attctcatgt	tgtacacacc	aacctgtctt	780
tctgccccta	ctcatcactt	tgccagagct	atctcttgca	ctttttacat	tatgtttgtg	840
ggcctctata	gggcaatccc	tcctgtactc	aattccataa	ttatggagta	aaaacaaagc	900
agattggaaa	caaggtcata	cttttattct	ttcttaaagg	gatgcagtga	tatgaggatg	960
agaatatg						968

&lt;210&gt; 879

&lt;211&gt; 1011

&lt;212&gt; DNA



<213> Unknown (H38g729 nucleotide)

<220>

<223> Synthetic construct

<400> 879

atgaaaaaaa	atgcaagttt	tgaagacttc	tttattctac	ttggattttc	taactggcct	60
catctggaag	tagttctctt	tgtggttatc	ttgatcttct	acttgataac	actgatagga	120
aacctgttca	tcatacatct	gtcatacctg	gactceccatc	tccacactcc	catgtacttc	180
ttcctttcaa	atctctcatt	tctggatctc	tgtctacacca	ccagctctat	ccctcagttg	240
ctggtgaatc	tctggggccc	ggaaaagacc	atctcttatg	ctggttgtag	agttcaactt	300
tactttgttc	tgcactggg	aaccgcagag	tgtgtcctac	tgggtggtag	gtcctatgat	360
cgttatgcag	ctgtgtgtag	acctttgcat	tacactgtcc	tcatgcaccc	tcgtttctgc	420
cgcttggttg	ctgcggcttc	ttgggtaagt	ggtttttaca	cctcagcact	tcattcctcc	480
tttactttct	ggataccctt	atgtagacat	cgcttagtgg	atcacttctt	ctgtgaagct	540
ccagcacttc	tgcgattatc	atgtgttgat	acctaggcaa	atgagctgac	cctcatgggc	600
atgagctcca	tttttggtct	catacctctc	atcctcatcc	tcacttccta	tgggtgccatt	660
gcccgggctg	tactgagcat	gcaatcaacc	actgggcttc	agaaagtgc	taggacatgt	720
ggagcccata	ttatggttgt	atctctcttt	ttcattccag	tcatgtgcac	gtatctccag	780
ccaccatcag	aaaattctca	agatcaaggc	aagttcattg	ccctctttta	cactgttgct	840
acacctagtc	taaaccctct	aatctacact	ttcagaaaca	aggatgtaag	aggggcagtg	900
aagagactaa	tggggtggga	atgggggatg	tgacagggaa	atcatggttg	ctgttggttt	960
tcctagggtc	ttatccattt	tgaaagggtg	tttcctctgc	tctttgtgat	t	1011

<210> 880

<211> 956

<212> DNA

<213> Unknown (H38g730 nucleotide)

<220>

<223> Synthetic construct

<400> 880

atggccatgt	acaacatgag	tgaccatggt	acaggcctgt	tcatacctttt	gggtatccct	60
ggacttgagc	agtaccacgt	ctggatcagc	atcccattct	gcttaatcta	tctcatggct	120
gtcgtggcca	agagtatcct	tctctacctc	attgtggtag	agcacagtct	tcatgcaccc	180
atgttctttt	tcctttccat	gctggccatt	actgatctca	tattgtccac	cacatgtgtc	240
cccaaaacac	ttagcatctt	ctggtttggt	ccccaaacag	tttccttggc	tgtctcaccc	300
aattattctt	tctgcactat	agctttgtgt	tggactcagc	tatactgctg	gccatggcat	360
ttgaccgcta	tatggccatt	tgtccaccct	tgagatacac	tactattctg	actcccaaaa	420
ccattgtcaa	aattgctgtg	ggaatatgtt	tccgaagttt	ctgtgttttt	gtcccgtgtg	480
ttttccttgt	gaatcgttta	cccttctgca	ggacacacat	cattttctac	acatactgtg	540
agcacatagg	tgttgcccag	cttgccctgtg	ctgatatctc	catcaaatatc	tgggtgtggat	600
tttgtgttcc	catcatgacg	gtgatgacag	acgtgatcct	cattgtctgc	tcctacaccc	660
tcatgtctctg	tgggtgtctt	tgcctcccct	cccaagatgc	ccgtcagaag	gccctttgct	720
cctgtgggtc	ccatgtctgt	gttatcctca	tattctatac	accagcattc	ttctccatcc	780
ttgcccacgc	ctttgggcat	aatgtccctc	atacctttca	tattatgttt	gccaaccttt	840
atgtaatcat	tccacctgct	ctcaacccta	ttgtctacag	aataaagacc	aagcaaattcc	900
agaacagaat	ccttttgctc	tttcccaagg	gggtccagtg	atagggtgcct	gagctc	956

<210> 881

<211> 933

<212> DNA

<213> Unknown (H38g731 nucleotide)

<220>

<223> Synthetic construct

<400> 881

atgaatgatg	atggaaaagt	caatgctagc	tctgaggggt	actttatttt	agttggattt	60
tctaattggc	ctcatctgga	agtagttatc	tttgtggttg	tcttgatctt	ctacttgatg	120

acactgatag	gaaacctggt	catcatcacc	ctgtcatacc	tggactccca	tctgcacaca	180
ccaatgtact	tcttcctttc	aaacctctca	tttctggatc	tctgctacac	caccagctct	240
atccctcagt	tgctgggtcaa	tctctggggc	ccggaaaaga	ccatctotta	tgctgggtgc	300
atgattcaac	tttactttgt	tctcgcaactg	ggaaccacag	agtgtgtcct	actggtgggtg	360
atgtcctatg	accgttatgc	agctgtgtgt	agacctttgc	attacactgt	cctcatgcac	420
cctcgtttct	gccacctgct	ggctgtggct	tcttgggtaa	gtggttttac	caactcagca	480
cttcattcct	ccttcacctt	ctgggtacct	ctgtgtggac	accgccaagt	agatcacttt	540
ttctgtgaag	ttccagcact	tctgcgatta	tcgtgtgttg	ataccatgt	caatgagctg	600
accctcatga	tcacaagctc	catatttgtt	ctcatacctc	tcacctcat	tctcacttct	660
tatggtgcca	tcgtccgagc	tgtactgagg	atgcagtcaa	ccactgggct	tcagaaagtg	720
tttgaacat	gtggagctca	tcttatggct	gtatctctct	ttttcattcc	ggccatgtgc	780
atatactctc	agccaccatc	aggaaattct	caagatcaag	gcaagttcat	tgccctcttt	840
tatactgttg	tcacacctag	tcttaacct	ctaacttaca	ccctcagaaa	caaagttgta	900
agaggggcag	tgaagagact	aatgggggtg	gaa			933

&lt;210&gt; 882

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g732 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 882

tttattcatg	ccctctcagt	cattgaatcc	atcattgtgc	tggccatggc	ctttgagcgt	60
tatgtggcca	tatgccaccc	actgtgccat	gctgaagtgc	tcaacagtac	agtaacagcc	120
catattggca	tcgtagctgg	ggtacgggga	tccctctttt	tttcccact	ggctctgctg	180
ataaagacgc	tgggcttatg	ccactcctat	gtgctctcgc	actcctattc	gctccaccag	240
gatgtagcga	acttgtccta	tgcg				264

&lt;210&gt; 883

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g733 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 883

gttgccatct	gtaacccttt	gcgctacett	acagtcata	acccccagct	atgccttttg	60
ttggttcttg	cctgctgggt	tgggggtttt	atccactcta	tcatgcaggt	catactagtc	120
atccagctgc	ctttctgtgg	gccaatgaa	ctggacaact	tctactgtga	tgctctacaa	180
atcatcaagc	tggcctgcat	ggacacctat	gtggtagagg	tgctgggtgat	agccaacagt	240
ggctctgctg	ctcttgtctg	cttcttggtc	ttactattct	cttatgctat	catcctgatc	300
accctgagaa	cacgcttctg	ccagggccag	aacaaggtcc	tctctacctg	tgcttctcac	360
ctgacagtgg	tcagcctgat	cttcgtgcc	tgcgattcca	tctatttgag	gcctttctgc	420
agcttctctg	tgataagat	attctccttg	ttttacacag	tgattacacc	tatgttg	477

&lt;210&gt; 884

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g734 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 884

atgtcagctc	ccaaccactc	cactgccaat	catgatatgt	ttgtcctcat	tggcgttcct	60
ggcctgaagg	agctgcacgt	gtggatctcc	atccccctct	gtctgatgta	cctgggtggct	120
gtgtcaggaa	atggtctcct	tgtctgtgtg	gtggcagtgg	agcacagtct	tcataaacct	180
atgtaccttt	tcctctccat	gctggcattt	tgggatctga	ttctatccac	atctgcagta	240

```

cccaaagcct tgagcatttt ctggtttgat gatgtggaca tctcctttgg tggctgtgtc 300
actcagctct tttttatgca ttttgccctt gtagcggagt caggcattct cttgaccatg 360
gctttcgacc gctatgtggc catctgctac ccattgaggt atagcaccat acttagccac 420
agtgttattg gcaaaattgg ggggtgtcgtg gtgttcagga gttttgcaac tgtcttctcc 480
atcgtcttcc ttgtgaagcg tctgcccctc tgccggacaa acatcattgc ccacaccttc 540
tgtgaacaca tggggctggc aaagctagggt tgttctgaaa tcaccatcaa tatttggtat 600
ggaatctctg taccactact cagtgttacg ttagatatgg tgacaatagt catctcctag 660
gggctcatag ttcaagcagt cttcaggctg ccctcccttg gtgcttggat gaaagcactc 720
agcacctgtg gttcccatgg cagtgtcatc ctcatgttct gccttccagg aattttcact 780
gtcattgttc agcgctttgc ctgaaaattt cccaagtatg tccacatcct gctggccaat 840
ctctatgttc ttgttcccc ccatgatgaac ccaattatct atggagtaaa gactaaacag 900
attcagaaaag gggttgcctt tgtgttttct ccaaaaggaa aatgttgc 948

```

&lt;210&gt; 885

&lt;211&gt; 1087

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g735 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 885

```

atgccactaa ctaatgaaag ccaccctgaa gaatttattc tgctaggcct tgcagaccgc 60
ccttggttag agcttcctct gtccactagt cttcttataa tgtaccctat agccgtgatg 120
ggaaacatca caatcattct catgtccagg ttagactctc gtcttcatag ccccatgtac 180
tttttctcca ccaacctctc ctttttggac atgtgttata ccacaagcat tgtccctcag 240
atgctgttta aactgggaag ctctaagaag accatcagct atatgggggtg tgcggttcag 300
ctttatttct ttcacataat ggggggaaca gaatgtttgc ttttggtat tatgtccttt 360
gatcgctatg tggccatctg cagacctctt cactacaccc tcatcatgaa tcagcgcgtc 420
tgtatcctta gtttccaccg tgtggctaata tgggaataatc tatgctgtct cagaggccac 480
tgccacatta caattgccac tgtgtgtctt aataaactgg accacttgggt gtgtgagatt 540
cctgttctga taaagattgc ctgtggtgaa aagggttcta acgagctcac actctctgtg 600
gtatgcattt ttatgttagc tgtccacta tgcctaattc ttgcttccta tgctagtatt 660
ggaagtgtgt tatttaagat caaatcttcc aagggaagga aaaaggcctt tgggacatgc 720
tcctcccatc ttattgtagt tttcttattt tatggcccag ccatcagcat gtaccttcag 780
ccccctcct ccactcctcaag ggatcaaccc aagttcatgg ccctcttcta tggagtgggtg 840
actccctcac tcaacccttt tatctacacc ctgcggaata agaattgtaaa gggggcatta 900
cgcaacttgg tgaggagcat ttcagcttta agtgatagtg ggtagacata aaatgaagtt 960
attgaacagt tagagttagt tgctatggtt ttatctaaca aattcttgtc tcataatcaa 1020
atatcgcttt acatgttctt gcaaaatatg ttatgtctcc gagactcttt gtaaacatgt 1080
tcagcaa 1087

```

&lt;210&gt; 886

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g736 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 886

```

tttattcatg ccctctcagc cattgaatcc accatcctgc tggccatggc ctttgaccgt 60
tatgtggcca tctgccaccc actgcgcoat gctgcagtgc tcaacaatac agtaacagcc 120
cagattggca tctgtgctgt ggtccgcgga tccctctttt ttttccact gcctctgtgtg 180
atcaagcggc tggccttctg ccactccaat gtgtctctgc actcctattg tgtccaccag 240
gatgtactga agttggccta tgcagacact ttgcccaatg tggatatagg tcttactgcc 300
attctgctgg ccatggcggt ggacgcaatg ttcactctct tgcctatttt tctgataata 360
cgaacggttc tgcaactgcc ttccaagtca tagcgggcca aggccttttg aacctgtgta 420
gtacacattg gtgtggtact cggcttgat gtgccactta ttggcacttc aagtggtcac 480
cggtttggga acaaactt

```

<210> 887  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g737 nucleotide)

<220>  
 <223> Synthetic construct

<400> 887  
 atgatgatta aaaaaaatgc aagttcggaa gacttcttta ttctacttgg attttctaata 60  
 tggcctcagc tggaagtagt tctctttgtg gttatcttga tcttctacct gatgacactg 120  
 acaggaaacc tggtcatcat catcctgtca tacgtggact cccatctcca cacaccaatg 180  
 tacttcttcc ttccaaccc ctcatttctg gatctctgcc acaccaccag ctctatccct 240  
 cagttgctgg tgaatctccg gggcccggaa aagaccatct cgtatgctgg ttgcatgggt 300  
 caactttact ttgttcttgc actgggaatc gcagagtgtg tctactgggt ggtgatgtcg 360  
 tatgatcgtt atgtagctgt gtgtagacct ttgcattaca ctgtcctcat gcaccctcgt 420  
 ttctgccact tggtggctgc ggcttcttgg gtaattgggt ttactatctc agcacttcat 480  
 tcttcttcta ctttctgggt accccttctg ggacatcgcc tagtggatca cttcttctgt 540  
 gaagttccag cacttctgcg tttatcatgt gttgacaccc atgcaaata gctgaccctc 600  
 atggctcatg gctccatttt ttgtctcata cctctcattc tgattctcac tgcctatgggt 660  
 gccattgccc gggctgtact gagcatgcaa tcaaccactg ggcttcagaa agtggttagg 720  
 acatgtggag cccatcttat ggttgtatct ctcttttcca ttccagtcac gtgcatgtat 780  
 ctccagccac catcagaaaa ttctcctgat cagggcaagt tcattgccct cttttatact 840  
 gttgtcacac cgagtcttaa tctctaatc tacactctca gaaacaagca tgtaaaaggg 900  
 gcagcgaaga gactattggg gtgggagtgg gggaag 936

<210> 888  
 <211> 453  
 <212> DNA  
 <213> Unknown (H38g738 nucleotide)

<220>  
 <223> Synthetic construct

<400> 888  
 cggcgcgtgt gcgcgccccg cctgctggac cacttcatct gtgagctgcc ggcgttgctc 60  
 aagctggcct gcggaggcga cggagacact accgagaacc agatgttcgc cgcccgcggtg 120  
 gtcatectgc tgccgggggt tgccgtcacc ctggcctcct acggtgccgt ggcccgagct 180  
 gtctgttgca tgccgttcaa cggaggccgg aggaggcggt tgggcacgtg tgggtccac 240  
 ctgacagccg tctgcctgtt ctacggctcg gccatctaca cctacctgca gcccgcgag 300  
 cgctacaacc aggcacgggg caagttcgta tcgtcttctt acaccgtggt cacacctgct 360  
 cttaaccgcg tcatctacac cctcaggaat aagaaaatga aaggggcacc gaggaggctg 420  
 ctgcggagtc ttgggagagg ccaggctggg cag 453

<210> 889  
 <211> 1014  
 <212> DNA  
 <213> Unknown (H38g739 nucleotide)

<220>  
 <223> Synthetic construct

<400> 889  
 aaagtcaatg ctagctctga ggggtacttt attttagttg gattttctaa ttggccttat 60  
 ctggaagtag ttctctttgt gggtattttg atcttctgct tgatgacact gataggaaac 120  
 ctgttcatca tcatcctgac gtacctggac tccatctcc atactccctt gtatttcttc 180  
 ctttcaaata tctcatttct ggatctctgc tacaccacca gctctatccc tcagttgctg 240  
 gtcagtctct ggggtgtgga aaagaccatt tcttatgtcg gttgcatgggt tcaactttac 300  
 ttttttctca cactgggaac cacagagtgt gtcctactgg tggatgatgc ctatgaccgt 360  
 tatgcagctg tgtgtagacc tttgcattac actgtcctca tgcactctcg tttctgccac 420  
 ttgttggctg tggcttcttg ggtaagtgggt tttacaaacc cagcacttca ttctctcttc 480

accttctggg	tacctctgtg	tggacaccgc	caaatagatc	actttttctg	tgaagttccg	540
gcacttttat	gattatcatt	tgtcaatacc	cgtgaaaata	aactgaccct	catgatcaca	600
agctccattt	ttgttctgct	acttctcacc	ctcattttca	cttcctatgg	tgctattgcc	660
caggctgtac	tgaggatgca	gtcaaccact	gggcttcaga	aagtatttgg	aacatgtgga	720
gctcatcata	tggttgatc	tctcttttcc	attccggcca	tgtgcatgta	tctccagcca	780
ccatcaggga	attctcaaga	tcaaggcaag	ttcattgctc	tcttttatac	tggtgttaca	840
cctagtctta	accctcta	ctacaccctc	agaaacaaag	atgtaagagg	ggtagtgaag	900
agactaaggg	gggtggagtg	agcctgtgtt	tgtgtgat	taacaatata	atggagtctt	960
tcctcacaat	gattcatcca	tctgttcatt	tatcaacat	tcttttatc	actc	1014

&lt;210&gt; 890

&lt;211&gt; 656

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g740 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 890

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagacagaca	tactcctgag	tgtgatggcc	tatgaccagt	ttgtagccaa	180
atgtcaccct	ctatatcatt	cagccatcat	gaaccctgt	tctgtggctt	tctacttttg	240
ttgtcttttt	tttttccctc	agtcttttag	atgccagct	gtacaatttg	attgccttac	300
aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctt	ctgtgaccct	tctcaactcc	360
cccattctgc	atgttgtgac	accttcaaca	ataacataat	cctgtatttc	cctgatgccca	420
tatttggttt	tcttcccatc	tcggggacac	ttttctctta	cgataaaaatt	gtttcctcca	480
ttctgagggt	ttcatcgta	gggtggagg	ataaagccct	ctccacctgt	gggtctcacg	540
tgctcagttg	ttgctgagtt	tatggaacag	gcgttggagg	gtacctcagt	tcggatgtgt	600
cattttcccc	cagaaagggt	gcagtggcct	cagtgatgta	cgcggttgct	accccc	656

&lt;210&gt; 891

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g741 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 891

atgattataa	tttgcaatga	cagccacagt	gatttcatcc	ttctgggctt	ctctaacaag	60
ccacatttgg	agaagatact	ttttggatca	tttttatttt	ttattttttg	actcttgacg	120
gaaatatggg	catagttctt	gtgtccttga	aggatccaaa	actccacatc	cctatgtatt	180
tctttctttc	caacctttcc	ttggtagacc	tctgtttgac	cagcagctgt	gttccacaga	240
tggtgattaa	cttctggggc	ccagaaaaga	ccatcagcta	cattggctgt	gccattcaac	300
tctatgtttt	tttgtggctt	ggggccacgg	aatatgtcct	tcttgttgct	atggctgtgg	360
attgttatgt	agcagtgtgt	catccactgc	aaaataccat	gatcatgcac	ccaaaacttt	420
gtctgcagct	ggctatcttg	gcatggggga	ctggcttggc	ccagtctctg	atccagtccc	480
ctgccaccct	ccggttaccc	ttctgtctcc	agcggatggg	ggatgatgtt	gtttgtgaag	540
tcccagctct	gattcagctc	tccagtactg	atactacctc	cagtgaatt	cagatgtcta	600
tcgccagtgt	tgctctctg	gtgatgcctt	tgatcattat	cctttcctct	tctggtgcta	660
ttgctaaggc	tgtgctgaga	attaagtcaa	ctgcaggaca	gaagaaagca	tttggcacct	720
gcactctctc	ccttcttgg	gtttctctct	tttatggcac	tgtcacagg	gtctaccttc	780
aacaaaaaaa	tcaactatct	catgaatggg	gcaaatttct	cactcttttc	tacactgtag	840
taaccccaac	tcttaatccc	ctcatctaca	ctctaaggaa	caaggaggta	aaggaggcac	900
taataagatt	ggggaggagg	acctgggatt	cccagaataa	ctaacaagg	taacatatgt	960
ttacctttgc	t					971

&lt;210&gt; 892

&lt;211&gt; 651

&lt;212&gt; DNA

<213> Unknown (H38g742 nucleotide)

<220>

<223> Synthetic construct

<400> 892

ttgcctgaca ttggtttcac cttggccacg gtccccaaga tgatggagac atgcaatcac	60
atagcagagt catctcccat gcaggctgtc tgacacagat acctttcttt gtcctttttg	120
tatgtataga tgacatgtct ctgactgtga tggcctataa ctgatttggt gccatctgtc	180
acccctgca ctaccagtc atcatgaatc ctcacctctg tgtctcttta gttttggtgt	240
cctttttcct tagcctgttg gattcccagc tgcacagctg gattgtgtta cacaactcac	300
cttcttcaag aatgtgaaa tctataattt tttttctgtg acctatctca acttctcaac	360
cttgccctgt ctgacagcat catcaataac atattatgta ttttagatat ccttatattt	420
ggttttcttc ccatttcagg gatccttttg tcttactata aaattgtctc ctccattcca	480
agaattccat cgtcagatgg gaagtataaa gccttctcca cctgtggctc tcacctggca	540
gttggttgct tattttatgg aacagggctt gtagggtagc tcagttcagc tgtgttacca	600
tccccagga agagtatggt ggcttcagtg atgtacactg tggtcacccc c	651

<210> 893

<211> 373

<212> DNA

<213> Unknown (H38g743 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 893

ttctctcttt aggccaactt acagcgcaga ggagcgcttt ctctgtctgg gtttctccga	60
ctggccttcc ctgcagccgg tctctctcgc ccttgtctc ctgtgtacc tctgacctt	120
gacgggcaat tcgggcgctg gtgtgtcttg gcnngnngg acctacgcct gcanacncac	180
gatgtatgna ctacttcctc tgccacctgg ccttggtaga cgcgggcttc actactagcg	240
tggtgcccgc gctgtggcc aacctgcgc gaccagcgt gctntgncgc gcagccactg	300
cacggcccga gctgtgcgca tcgctggctc tgggttcggc cgaatgcgct ctctggcggt	360
gatggctctg gan	373

<210> 894

<211> 648

<212> DNA

<213> Unknown (H38g744 nucleotide)

<220>

<223> Synthetic construct

<400> 894

atattagaaa ttctgttcac aaccgtcagt ataccaagt ttctgggtaa cattatttca	60
ggagataaaa ccatttcctt taataattgc atagttcagt tatttttctt cattctcttg	120
ggagtcacag agttttacct tctggctgcc atgtcctatg accgctatgt ggccatctgc	180
aagcctctgc attacttgag tatcatgaat cgaagagtct gcacactgct tgtttttact	240
tcttggtctg tttcattctt aatcatatc ccagactca tgttgctttt aaagcttgat	300
tactgtagggt ctaatattat tgaccatttt acctgtgatt attttccact gctgcaactt	360
gcttggtcag acacaaaatt cttagagggt atgggatttt cttgtgctgc gtttactcta	420
atgttcactt tggcattaat atttctgtcc tacatataca ttatcagaac aattttgaga	480
attccttcta ctagtcagag gacaaaggcc ttttcacat gttcttccca catggttggt	540
atctccatct cttatggcag ctgcattttt atgtacatta aacctcagc aaaagataga	600
gtgtccttga gcaaggaggt ggcaatacta aacacctcag tagccccc	648

<210> 895

<211> 659  
 <212> DNA  
 <213> Unknown (H38g745 nucleotide)

<220>  
 <223> Synthetic construct

<400> 895  
 tttcctgaca tcggtttcac ctccaccaca gtccccaaga tgattgtgga catccagtct 60  
 cacagcagag tcattctcta tgcaggctgc ctgactcaga tgtctctctt tgccattttt 120  
 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatgaccggg ttgtagccat 180  
 ctgtcaccct ctatatcgct cagccatctt gaaccctgtt ttctgtggct tcctagattt 240  
 gttgtctttt ttttttttcc ctcagtcctt tagactccca gctgcacaac ttgattgcct 300  
 tacaaatgac ctgcttcaag gatgtggaaa ttcttaattt cttctgtgac cttcttcaac 360  
 tcccccatct tgcattgtgt gacaccttca ccaataacat aatcatgtat ttccctgctg 420  
 ccatatttgg tttcttccag atctcgggga cccttttctc ttactataaa attgtttcct 480  
 ccattctgag ggtttcatca tcagggtggga actataaagc cttctccacc tgtgggtctc 540  
 acctgtcagt tgtttgctga ttttatggaa caggcgttgg aggggtacct agttcagatg 600  
 tgtcatcttc cctgagaaag gctgcagtgg cctcagtgat gtacatgggtg gtcacacc 659

<210> 896  
 <211> 804  
 <212> DNA  
 <213> Unknown (H38g746 nucleotide)

<220>  
 <223> Synthetic construct

<400> 896  
 atgatggcac tcattttcac agactcccat ctccaaagcc caatgtattt cttcctcaat 60  
 gtccctctctg ttcttgatat ttgttactct tctgtgggtca cacctaagct cttgggtcaac 120  
 ttccctggct ctgacaagtc catctctttt gagggctgtg tgggtccagct cgccttctt 180  
 gtagtgcatt tgacagctga gagcttccctg ctggcctcca tggcctatga ccgcttccca 240  
 gccatctgtc aacccctcca ttatggttct atcatgacca gggggacctg tctccagctg 300  
 gtagctgtgt cctatgcatt tgggtggagcc aactccgcta tccagactgg aaatgtcttt 360  
 gccctgcctt tctgtgggccc caaccagcta acacactact actgtgacat accacccctt 420  
 ctccacctgg cttgtgcca caccagccaca gcaagagtgg tcctctatgt cttttctgct 480  
 ctgggtcacc ttctgcctgc tgcagtcatt ctacctcct actgcttgggt cttgggtggcc 540  
 attggggagga tgcgctcagt agcagggagg gagaaggacc tctccacttg tgcctcccac 600  
 tttctggcca ttgccatttt ctatggcacc gtgggttttca cctatgttca gcccattgga 660  
 tctactaaca ataccaatgg ccaagtagtg tccgtcttct acaccatcat aattcccatg 720  
 ctcaatccct tcatttatag cctccgcaac aaggaggtga agggcgctct gcagaggaag 780  
 cttcaggtca acatttttcc cggc 804

<210> 897  
 <211> 949  
 <212> DNA  
 <213> Unknown (H38g747 nucleotide)

<220>  
 <223> Synthetic construct

<400> 897  
 atggacttgg gaaatcaaac aagagtttca gaatttttac tcttgggatt ttcccaagac 60  
 ctagaggatc aacagttgct ctttgcactg tttctgtcca tgtacctggt caccgttctg 120  
 gggaacctgc tcattatcct ggccatcagc tctgactccc acctccacac ccccaggtag 180  
 ttcttctctt ccaatctgtc cctggctgac atcggtttca cctccaccgc agtccccaaag 240  
 atgctggtga acatccagggt gcagagcaat gccatcagct atgcagactg catcgcccag 300  
 atgtatgttt ttcatggttt ttggaggcat ggacacattt ctcttcaccg tgatggccta 360  
 tgaccgggat gtggccatct gtcacccctt gtactactgt gtcaccagga acccctgcct 420  
 ctgtggcctg ctgggttctt tgtcctgggt cctcagcttg tcatactccc tgatccagag 480

tctgttggtg	ctgcgggtgt	ccttctgcac	cagttgagtc	attcagcact	tttactgtga	540
gcttgctcag	gtcctcaggc	ttacctgtct	agacacacat	gtcaattaca	tcctgctcta	600
cgtgggtggc	ggccttcttg	acttttgtgc	cttctcaggg	atccttttct	cctacaccca	660
aattgtctcc	tacatcctga	gaatctcatc	cacagatggg	aaacacaaag	ccttttctac	720
ctgtggatct	catctgtttg	tggtttcttt	attctatggg	acaggccttg	gtgtgtatct	780
tagttccaat	gcacgtcctt	cttcctgggt	gggcatgggt	gcctcgggtc	tgtacactgt	840
ggcaccccc	atgctgaacc	ccttcattcta	ttgcttgctg	aacaggggaca	tcaagaggac	900
cctagaaaca	ctgcttggga	gaatgctgta	tgctcaatga	cggggacat		949

&lt;210&gt; 898

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g748 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 898

atggagaatt	gtacggaagt	gacaaagttc	attcttctag	gactaaccag	tgtcccagaa	60
ctacagatcc	ccctctttat	cttggttcacc	ttcatctacc	tcctcactct	gtgtgggaac	120
ctggggatga	tgttgctgat	cctgatggac	tcttgctctc	acaccccat	gtacttttct	180
ctcagtaacc	tgtctctggt	ggacttttga	tactcctcag	ctgtcactcc	caagggtcatg	240
gctgggttcc	ttagaggaga	caagggtcatc	tcctacaatg	catgtgctgt	tcagatgttc	300
ttctttgtag	ccttgggccac	ggtggaaaat	tacttggttg	cctcaatggc	ctatgaccgc	360
tatgcagcag	tgtgcaaacc	cctacactac	accaccacca	tgacggccag	tgtagggtgc	420
tgtctggccc	taggctcata	tgtctgtggc	ttcctaaatg	cctcattcca	cattgggggc	480
atattcagtc	tctctttctg	taaatccaat	ctgggtacatc	actttttctg	tgatgttcca	540
gcagtcattg	ctctgtcttg	ctctgataaa	cacactagtg	aggtgattct	ggtttttacg	600
tcaagcttta	atatcttttt	tgttcttcta	gttatcttta	tctcctactt	gttcatattc	660
atcaccatct	tgaagatgca	ttcagctaag	ggacacccaa	aagcattgtc	cacctgtgcc	720
tctcacttca	ctgcagtcct	cgtcttctat	gggacagtaa	tcctcatcta	cttgacagccc	780
agctccagcc	actccatgga	cacagacaaa	atggcatctg	tgttctatgc	tatgatcatc	840
cccattgctg	accctgtggt	ctacagcctg	aggaacagag	aagtcagaa	tgcattcaag	900
aaagtgttga	gaaggcaaaa	atttcta				927

&lt;210&gt; 899

&lt;211&gt; 938

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g749 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 899

atgcacacca	tgggtggagaa	ccacacccaa	gtcacctggt	tccgcctgct	gggacttaca	60
gagcaggagg	agctcagagg	cactctcttt	gtgctcttcc	tgctcatgca	ttcagtcact	120
gttatgggca	acctgggaat	gatcactctg	atccatgcag	acccacagct	ccacaccccc	180
atgtatttct	tcctgagcgt	cctatccttc	atagactcct	cgttttccac	agtggacacc	240
cccaggctgc	tggagagctt	cctcatctca	agccaatcca	tctcctttgc	aggctgtatg	300
gtccagatgg	ccctcatgat	cctccatggt	actgctgagt	gtctgctcct	ggccatcatg	360
gcctatgacc	gattcaccgc	catctgccac	cctctcctct	atcacactat	tatatcccaa	420
tgtctgtgtg	ccctgctggt	ggtagacctg	tatactgttt	ctggtgcaa	ttcagctttg	480
ctgactgggt	gcatctttaa	gctgccctac	tgtggcccca	atgtcattaa	ccactatttc	540
tgtgacatcc	cccctgtgct	ccaacttgcc	ggtgcagata	ctacgagggt	gagaccatta	600
tcttctcatt	gtgtgccttg	ctcatcctct	ttaccatcac	cattatccca	gtctcctatg	660
cctacatcct	cgtgaccatt	tgcaggatgc	gtccctgtca	agcccagagc	aaagctctct	720
ccacctgtgc	ctcccacctc	accatcatct	gcctcttcta	tagcaccatc	accttcatgt	780
atgctcagcc	aagctctcac	aattccatgg	aacacaacaa	ggtcattgtct	gtcttctaca	840
ctgtgttcat	ccgcaggctg	aacctctga	tctacagcct	gaggaaataa	gatgtaaaat	900
atgctttgaa	gaggagatgc	ctgtgcaagc	tgtcttca			938



<210> 900  
 <211> 942  
 <212> DNA  
 <213> Unknown (H38g750 nucleotide)

<220>  
 <223> Synthetic construct

<400> 900  
 atggaaaata agacagaagt aacacaattc attcttctag gactaaccaa tgactcagaa 60  
 ctgcagggtc ccctctttat aacgttcccc ttcattctata ttatcactct ggttggaac 120  
 ctgggaatta ttgtattgat attctgggat tctgtctcc acaatcccat gtactttttt 180  
 ctcagtaact tgtctctagt ggacttttgc tactcttcag ctgtcactcc catcgatcatg 240  
 gctggattcc ttatagaaga caaggatcct tcttacaatg catgtgctgc tcaaattgat 300  
 atctttttag cttttgccac tgtggaaaat tacctcttgg cctcaatggc ctatgaccgc 360  
 tatgcagcag tgtgcaaacc cctacattac accacaacca tgacaacaac tgtgtgtgct 420  
 cgtctggcca taggctccta cctctgtggt ttcctgaatg cctccatcca cactggggac 480  
 acatttagtc tctctttctg taagtccaat gaagtccatc actttttctg tgatattcca 540  
 gcagtcattg ttctctcttg ctctgataga catattagcg agcttgttct tatttatgtt 600  
 gtgagcttca atatctttat agctctcctg gttatcttga tatcctacac attcattttt 660  
 atcaccatcc taaagatgca ctcagcttca gtataccaga agcctttgtc cacctgtgcc 720  
 tctcatttca ttgcagtcgg catcttctat gggactatta tcttcatgta cttacaaccc 780  
 agctccagtc actccatgga cacagacaaa atggcacctg tgttctatac aatgggtcatc 840  
 cccatgctga accctctggt ctatagtctg aggaacaagg aagtgaagag tgcattcaag 900  
 aaagttgttg agaaggcaaa attgtctgta ggatggtcag tt 942

<210> 901  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g751 nucleotide)

<220>  
 <223> Synthetic construct

<400> 901  
 atgaacaact ctgacactcg catagcaggc tgcttctca ctggcatccc tgggctggag 60  
 caactacata tctggctgtc catccccctc tgcatcatgt acatcgctgc cctggaaggc 120  
 aatggcatcc taatttgtgt catcctctcc caggcaatcc tgcatgagcc catgtacata 180  
 ttcttatcta tgctggccag tgctgatgtc ttgtctctca ccaccacat gcctaaggcc 240  
 ctggccaatt tgtggctagg ttatagccac atttcccttg atggctgcct cactcaaaag 300  
 ttcttcattc acttctctt cattcactct gctgtcctgc tggccatggc ctttgaccgc 360  
 tatgtggcca tctgtctccc cctgcgatat gtcacaatcc tcacaagcaa ggatcattggg 420  
 aagatcgta ctgccaccct gagccgcagc ttcattcata tgtttccatc catctttctc 480  
 cttgagcacc tgcactattg ccagatcaac atcattgcac acacattttg tgagcacatg 540  
 ggcattgccc atctgtcctg ttctgatata tccatcaatg tctggatagg gttggcagct 600  
 gctcttctct ccacaggcct ggacatcatg cttactatg tttcctacat ccacatcctc 660  
 caagcagtct tccgcctcct ttctcaagat ccccctcca aggccctgag tacctgtgga 720  
 tcccatatct gtgtcatcct actcttctat gtccctgccc ttttttctgt ctttgcctac 780  
 aggtttggtg ggagaagcat cccatgctat gtccatattc tcctggccag cctctacgtt 840  
 gtcattcctc ctatgctcaa tcccgttatt tatggagtga ggactaagcc aatactggaa 900  
 ggggctaagc agatgttttc aaatcttgcc aaagga 936

<210> 902  
 <211> 994  
 <212> DNA  
 <213> Unknown (H38g752 nucleotide)

<220>  
 <223> Synthetic construct

<400> 902

```

agcattcttt tcctttatct ctcattgctg caggcatcct ctgattttct aataacattg      60
atgaagaact gtacagaagt gacagagttc atcctcctgg gactaaccaa tgctccagag      120
ctacaagtcc ccctccttat catgttcact ctcataatcc ttgtcaatgt gggtggaaac      180
ctggggatga ttgttttaat tggttgggac attcatctcc acactcccat gtattttttc      240
ctcagtcacc tgtctctagt ggacttttgt tactcttcag ctgtcactcc cacagtcata      300
gctgggctcg ttataggaga caaggtcacg tcttacaatg catgtgctgc tcaaagtgtc      360
ttttttgcag cctttgccac tgtggaaaat ttctctctgg cctcaatggc ctatgaccgc      420
tatgatgcag tgtgcaaacc cctacattac accaccacca tgacaacaag tgtgtgtgca      480
tgtctggcta taatctgtta tgtctgtggt ttcttgaatg cctccataca cattggggaa      540
acattgtctc tctttctgta tgtccaatga agtccattgc tttttctgtg atgttccacc      600
agtcatggct ctgtcttgct gtgatagaca tgtgaatgag ctagtcttca tttatgtagc      660
cagtttcaat atcttttctg ccattcctagt tatcttgatc tctacctat tcatatttat      720
caccatccta aagatgcact cagcttcagg ataccagaag gctttgtcca cctgtgcctc      780
ccacctcact gcagtcacga tcttctatgg gactattatc ttcatgtact tacagcccag      840
ctctggtcac tccatggaca cagacaaact ggcatctgtg ttctatacta tgatcatccc      900
catgctgaac cccctggtct atagcctgag gaacaacgaa gtgaagagcg cattcaagaa      960
agttattgag aaggcaaaat tgtctctatt attg                                     994

```

&lt;210&gt; 903

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g753 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 903

```

atgtcagatt ccaacctcag tgataaccat cttccagaca ccttcttctt aacagggatc      60
ccagggctgg aggctgccca cttctggatt gccatccctt tctgtgccat gtatcttgta      120
gcactggttg gaaatgctgc cctcatcctg gtcattgccg tggacaatgc tcttcattgca      180
cctatgtacc tcttctctg ccttctctca ctcacagacc tggctctcag ttctaccact      240
gtgcccaaga tcttgcccat tttgtggctc catgctgggtg agatttcctt tgggtggatgc      300
ctggcccaga tgttttgtgt ccattctatc tatgctctgg agtcctcgat tctacttgcc      360
atggcctttg ataggtatgt ggctatctgt aacccattaa ggtacacaac cattctcaac      420
catgctgtca taggcagaat tggtcttggg gggctattcc gtagtggtggc tattgtctcc      480
cccttcatct tcttgctgag gcgactcccc tactgtgggc accgtgtcat gacacacaca      540
tactgtgagc atatgggcat cgcccgactg gcctgtgccg acatcactgt caatattgtc      600
tatgggctaa ctgtggctct gctggccatg ggactggatt ccattctcat tgccatttcc      660
tatggcctta tcttccatgc agtcttccac cttccatctc atgatgccc gacacaaagct      720
ctgagtacct gtggctccca cattggcacc atcttggttt tctacatccc tgccttcttc      780
tccttctcca cccaccgctt tggtcaccac gaagtcccca agcatgtgca catctttctg      840
gctaactctc atgtgctggg gcctcctgta ctcaatccta ttctctatgg agctagaacc      900
aaggagattc ggagtcgact tctaaaactg cttcacctgg ggaagacttc aata                                     954

```

&lt;210&gt; 904

&lt;211&gt; 989

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g754 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 904

```

cacatagaac cagggaaatga tacacagatt tcagaatttc ttcttctggg actttcagat      60
aaaccagaat tgcagccctt cctctttggg ctgttcttct ccatgtacct gggtcactgtg      120
cttgggaatc tgctcatcat cctggccaca atctcagact cccacctcca caccctcatgt      180
acttcttctc ctccaacctg tcttttgctg acatctgttt catctctact acaatcccaa      240
agatgctcgt aaacatccag acacagagca gagtcatcac ttatgcaggc tgcacaccc      300
agatgtgctt tttgtactc ttagaagcac tggacagctt actcctgacc gtgatggcct      360
atgaccagtt tgtggccatc tgtcaccctc tgcactacat ggtcatcatg agccctggt      420
tctgtggact gctggttctg gcatcctgga tcatcatgag cccctggctc tgtggactgc      480

```

tggttctggc	atcctggatt	atcagtgatc	tggtttcctc	attacatagc	ttgatgggtgc	540
tgctactgcc	cttctgcaca	gattttccaa	ttccacattt	tgtctatgaa	cttaatcagg	600
tcacccgcct	tgccggttct	gataccttct	ttaatgacat	ggcgatgtat	tttgcagtag	660
ggccactggg	tggagttccc	ctcgtcggga	tctgtactt	gtactgtaag	atagttttct	720
ccatacgtgc	aatctcatca	gctcagggga	agtacaaggc	attttccacc	tgtgcatctc	780
atctctcagt	tgtctcctta	ttttatggta	ggagcctagg	ggtgtacttt	agttctgctc	840
ctacccaaaa	ctctcactca	ggtgctgcag	cttcagtgat	gtacactgtg	gtcaccacca	900
tgctgaaccc	cttcactctgc	agtctgagga	ataaagacat	aaagagagct	ctgaatcaat	960
tcacagggt	agtgcattc	ttcaggaag				989

&lt;210&gt; 905

&lt;211&gt; 932

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g755 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 905

accacatcta	tagatgataa	tacagaggta	aatgaattca	tatgactagg	actaaccaaa	60
gccccagaac	tacaggtcca	cctctttgtc	ttattttaact	tcactctacct	cttcactctg	120
agtgggaacc	tggggatgat	gctgctgac	ctgctggact	ctcgtctcca	cacttccatg	180
tactttttcc	tcagtaacct	gtctctgggt	gacttttgct	actcagaaac	tgctactcca	240
aagatgatgg	ctgggttgct	gatagctcac	aaggctcatct	cctacaatgt	atgtgctgct	300
cagatgttct	tttttgcagt	ctttgctact	gtggaaagt	acttcttgac	ttcagtggcc	360
tatgattgct	acagagtaat	gtgtaaacc	ctacattaca	ccaccaccat	gacaacaaat	420
gtgtgtgctt	ctctggccat	acatgcatgt	cttaggttta	ctgactgctg	ctgttgacat	480
tgagagacatt	ttatgtccaa	tgagatccat	cactttttct	gtgatattct	ggcagtcag	540
actctgactt	gctctaataa	acatattaat	gagttgatcc	ttgttcctac	ttcaagctat	600
attttttacc	ctcctagtta	tcttgatttc	ctgcttggtt	gtatttgat	ttgtcaccat	660
tttaaagatg	ctctctttaa	gtatacaaga	aggttttatc	tacctatggt	tctcacctca	720
ctgcagttcc	tttattttat	gagactgtcc	tcatacacata	tgtgcagcca	agttctatca	780
tttcatgaac	acagaaaaaa	ttgtatctgt	gtttcatatt	atggttatcc	ccatgctaata	840
ccctgtgggt	tatagcctga	gaaacaacga	ggtcaagagt	gcattcaaga	ctgtttgttg	900
aggaaacaaa	atattttctg	ggtttagtct	tt			932

&lt;210&gt; 906

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g756 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 906

atggggggct	ttgggactaa	catctcaagt	actaccagct	tcactctaac	aggcttccct	60
gagatgaagg	gtctggagca	ctggctggct	gcccttctgc	tgctgctttg	tgctatttcc	120
ttcctgggca	acatcctcat	cctctttatc	ataaagggaag	agcagagctt	gcaccagcca	180
atgtactact	tcctgtctct	tttttctggt	aatgacctgg	gtgtgtcctt	ttctacattg	240
cccactgtac	tggtgctgt	gtgttttcat	gccccagaga	caacttttga	tgcttgctg	300
gcccagacgt	ctttcatcca	cttttctctc	tgacagagt	ttggcatcct	actggccatg	360
agttttgacc	actatgtggc	catctgtaac	ccgctgcgct	atgccacagt	gctcactgat	420
gtcctgtgg	cccacaatgg	catatccatt	gtcatccgca	gcttctgcat	ggtattccca	480
cttcccttcc	tctgaagag	actgccttcc	tgtaaggcca	gtgtggtact	ggccatttcc	540
tactgtctgc	atgcagacct	gattcggctg	ccctgtggag	acactaccat	caacagcatg	600
tatggcctgt	tcattgtcat	ctctgccttt	ggtgtagatt	cactgtcat	cctcctctcc	660
tatgtgtca	ttctacattc	tgtgtgtcca	ttgcctccag	gggtgagagg	cttaagacac	720
tcgaacacat	gtgtgtcaca	tatctatgca	gtgctgatct	tctatgtgcc	tatggttagt	780
gtgtccatgg	ttcatcgatt	tgggagcat	gctctggaat	atgtgcacaa	gttcatgtct	840
ctttgtacct	gccaatgtct	taccgcaatt	atctattcca	tcaagactaa	ggagattcgc	900
aggagactac	acaagatggt	attgggagct	aagttctgat	cgaag		945

<210> 907  
 <211> 989  
 <212> DNA  
 <213> Unknown (H38g757 nucleotide)

<220>  
 <223> Synthetic construct

<400> 907  
 atggaaccag agaatgatac acgaatttca gaatttccgac ttctgggatt ttcagaagaa 60  
 cccagactgc aacgatttccg atttctcttt ggagtgttct tatccatgta cctcatcatt 120  
 gtatttggaa acttgcttat catcctgggt atcattttat gctccacact ccacacctcc 180  
 atgtacttct ttctctccaa cctgtccttt gtagacatct gttttgcctc caccagggtc 240  
 ccaaagatgc tgggaatat ccaggcacag agcaaagtca tcacctctgc aggctgcatc 300  
 acccagatgt actttttcat acattttgta ggattggaca gcttcctcct gactgtgatg 360  
 gcctatgacc ggtttgtggc catctgtcac cccctgtact acacggtcat catgaaccct 420  
 caactctgtg gattgcttgt tctggtatcc tggatcacia gtgtcttgca ttccttatta 480  
 catagcttaa tgggtctgca gttgtcctta tgcagagagt tggaaatccc ccacttttcc 540  
 tgtgaactta atcagggtcat ccaccttgcc tgtcttgaca cctttcttaa tgacatgggtg 600  
 atgtatctgg cagctgtgct gctgggtggg gggatgtctc gctgggatcc tttactctta 660  
 ctctaagaca gtttctcca tatgtcaat ctcatcagct caaggggaagt ataaggcatt 720  
 ttccaactgt ccattctacc tctcagttgt ctcttctgtt tactgtacaa gcctaggagt 780  
 gtaccttagc tcggctgcat cccacaactc acaactcagg gcaatagcct cagtgtatga 840  
 cactgtggtc acccccatgc tgaaccctt catctacagc ctgaggaata aggacataaa 900  
 gagggctctg aagaattctt tgggagggaa actagaaaag ggccagttgt cctagggctg 960  
 aagctatatc catgattgca aggtcaca 989

<210> 908  
 <211> 960  
 <212> DNA  
 <213> Unknown (H38g758 nucleotide)

<220>  
 <223> Synthetic construct

<400> 908  
 atggaagag gaaaccaaac agaagtggga aactttctcc tcctgggatt cgcagaggac 60  
 tctgacatgc agcttctcct ccattgggctg ttctctctcca tgtacctggg taccatcatc 120  
 ggaaacctgc tcatcatcct gaccatcagt tcagactccc acctccacac ccccatgtac 180  
 ttcttctctc ccaacctgtc ctttgtctgac atctgtttca catccacgac tgtcccaaag 240  
 atgctgggta atatccaaac acaaagcaaa atgatcactt ttgcaggctg cctcactcag 300  
 atattttttt tcattgcatt tggatgcctg gacaatttgc tcctgaccat gacggcctat 360  
 gaccgcttcg tggccatctg ttacccctcct cactacacgg tcatcatgaa cccccggctc 420  
 tgtggactgc tggttctggg gtccctgggtc atcagtgtca tgggttctct gcttgagacc 480  
 ttgaccattt tgaggctgtc ctccctgcaca aatatggaaa ttccgcaact tttttgtgat 540  
 ccttccgaag tcctgaagct ggcctgttct gacaccttca tcaataacat cgtgatgtgt 600  
 tttgtgacca ttgtcctggg tgttttctct ctctgtggaa tcctattctc ttattctcag 660  
 attttctcct ccgtcctaag agtatcatct gccagaggcc agcacaagc ctttaccacc 720  
 tgtgggtccc acctctcagt ggtcagcttg ttctatggca ctggccttgg ggtctatctc 780  
 agttctgcag ttacaccacc ttctaggaca agtctggcag cctcgggtgat gcacaccatg 840  
 gtcaccccca tgetgaacct ctcatctac agcctgagga acaaggacat gaaggggtca 900  
 ctggggagac tcctcctcag ggcaacgtct ctcaaagagg ggaccattgc taagctctca 960

<210> 909  
 <211> 981  
 <212> DNA  
 <213> Unknown (H38g759 nucleotide)

<220>  
 <223> Synthetic construct

&lt;400&gt; 909

tatacagacc	cacagaatct	aacagatgtc	tttatattcc	tcctcctaga	actctcagag	60
gatccagcac	tgagctggg	cgtcactggg	ctgtgcctgt	gtgcctgggc	acggtgctgt	120
ggaacctgct	cagcatcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
tcttctctctg	caacctgtcc	ttgcctgaca	tcgggtttcac	ctccaccacg	gtccccaaga	240
tgatcgtgga	catccaatct	cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	300
tgtctctctc	tgccattttt	ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	360
tatgaccagt	ttgtagccat	ctgtcaccct	ctgtatcatt	cagccatcat	gaacccgtgt	420
ttctgtggct	tcctgggtttt	gttgtctttt	tttttctcag	tcttttagac	tcccagctgc	480
aaaacttgat	cgccttacia	atcacctgct	tcaaggatgt	ggaaattcct	aatttcttct	540
gtgaccttct	tcaactcccc	catcttgcat	gttgtgacac	cttcaccaat	aacattatca	600
tgtattttccc	tgctgccata	tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	660
ataaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggagctat	aaagccttcg	720
ccacctgtgg	atctcacctg	tcagttgttt	gctgatttta	tggaaacaggc	gttgagggtg	780
acctcagttc	agatgtgtcg	tcttccctga	gaaagcgtgc	agtggcctca	gtgatgtaca	840
cagtggctcac	ccccatgctg	aatcccttga	tctacagcct	gagaaacagg	gatattaaag	900
gtgtcctgtg	gcagccgtgc	agccgcacgg	cagcacagtc	tcattctaat	atcttatctg	960
ttccattcct	tttgcaggat	g				981

&lt;210&gt; 910

&lt;211&gt; 628

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g760 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 910

tcagtgaagt	acttgaatga	aagtttccca	gaggatttca	ttctcatggg	ctttgtcaaa	60
tatccatggc	tggaattttct	tctcttctgt	gtcctcttga	ccttctacat	gttcacattg	120
ttgggaaata	gtgctattat	tctggctctct	caactagatt	cccaacttca	tagtctatg	180
tatttctctc	tcaccagtct	ttcctgtctta	tattctctgtt	tcaccaccac	aacagtacct	240
caaagtctgt	tcaatttagg	gggccaaca	agaacatcac	ttaaattaggc	tgtatggccc	300
aggcctatgt	atttcaactgg	ctagcctgta	ttgaatgtgt	ccttcttggc	atcgtggcct	360
tagactgcta	tgtggctgtc	tgtaagcctc	caaggtagac	tataatcata	gaccataagg	420
tctgcctgca	cctgtccagc	actgcttggc	taattgggtct	ggccaattca	ctgctgcagt	480
caacaatcac	aattcagttg	cccctgtaga	ggtgtatagc	tcagatcttc	cttttagttag	540
agtctgtcac	ctaacagtct	ctaactgtaa	caacctttga	gatctgctac	agcattctat	600
ctgaggccaa	cttcatgctg	gggagctc				628

&lt;210&gt; 911

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g761 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 911

atggaaccag	aaaagcaaac	cgaaatctca	gaattcttcc	tccagggact	ctcagaaaag	60
ccagagcatc	agaccctcct	cttcacaatg	ttcctctcca	cataacctgg	caccatcatt	120
ggaaatgcc	tcattatcct	ggccatcatc	acggactctc	acctccacac	acccatgtac	180
ttctttctct	tcaacctctc	actcgttgac	accctattat	cctccaccac	cgtccccaag	240
atgctagcga	acatccaggc	tcagagcaga	gccatcccct	ttgtgggctg	cctcaccag	300
atgtatgcct	tccacctgtt	cgggaccatg	gacagcttcc	tcctggcagt	aatggccatc	360
gaccgcttcg	tggccattgt	ccaccacag	cgttacttgg	ttctcatgtg	ctcccctgtc	420
tgtgggctgc	tgctgggagc	atcatggatg	atcaccaacc	tccagtctct	catacacacc	480
tgccctcatg	ctcaactgac	cttctgcgcc	ggctctgaaa	tctccactt	cttctgtgac	540
ctcatgcccc	tgctgaagct	ctccggctca	gacacgcaca	ccaacgagct	gggtgatctt	600
gcttttggca	ttgtcgtggg	caccagccca	ttctcctgca	tccttctctc	gtacatccgc	660

atcttctgga	cagtctttaa	gatcccttct	actcggggca	agtggaaagc	cttctccacc	720
tgtggcttac	acctcactgt	ggtgtcactg	tcctatggga	ccatctttgc	tgtgtactta	780
cagcccacat	ccccagctc	ctcccagaag	gacaaggcag	ccgcccta	gtgtggggtg	840
ttcatcccca	tgtcaaccc	ctttatctac	agcatacgga	acaaggatat	gaaggcagcc	900
ctggggaagc	tcacgggcaa	agtggccgctc	ccctgtccta	ggcca		945

&lt;210&gt; 912

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g762 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 912

atggctccga	ccaacctcac	atctgcccc	gtgttccctc	tcctcggcct	ggtggacgga	60
acagacgccc	acccgctgct	gttccctgctc	tgccttggca	tctatctgct	caacgccttg	120
agcaacctga	gcatggtggc	gctggtgaga	tcggacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcacctgag	cctcgtggac	gtctgcttta	ccaccgtcac	ggtccccagg	240
ctgctggccg	gcctgctcca	ccggggccag	gccatatact	tcaggcgctg	ctttgccgag	300
atgtacttct	tcgtggctct	gggcatcacc	gagagctacc	tcctggcggc	catgtcctac	360
gaccgcgcga	cggcggcgtg	ccggccccctg	cgctacggcg	cgctgggtgac	gccatgggag	420
tgcgcctcgc	tggtgctgct	gtcgtgggccc	gtgacgcacc	tgcactcgct	gctgcacacg	480
ctgctcctct	ccgcgctctc	ctaccctctac	cccacccccg	tgcgccccct	cttttgcgac	540
atgacggtga	tgtcagctt	ggcgacctcg	gacacgtccg	ccgcggagac	ggccatcttc	600
tcgaggggccc	tggcgtgggt	gttggccccg	ctgctcctcg	tgctcctttt	cctacgcgcg	660
cactctggtc	gcggtgctcg	gcttgccgcg	gcccgcgcgcg	cgccttctcc	tactgcgggg	720
cccacctagt	ggcggtggcg	gtggcgcttt	tctttggctc	tgctcctctc	gtgtatttcc	780
cgccgtcgtc	tgctactca	gcccgtctacg	accgcctggc	cagcgtggtc	tacgtgtca	840
tcacgccgac	cttgaacctt	ttcatcaaca	gccttcgcaa	caaagaggtc	aagggcgccc	900
tgaaaagggg	gctcagatgg	agggctgcac	cccaagaggc	gtgaggga		949

&lt;210&gt; 913

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g763 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 913

atggatggag	agaatcactc	agtggatatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagegcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tcacgtcat	tggtggtgtg	gagatggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccctc	cactatctga	ccattatgag	ccaagaatg	420
tgcctttcat	ttctggctgt	tgctgggacc	cttgggtgtc	gtcactccct	gttccaactg	480
gcatttcttg	ttaatttagc	cttctgtggc	cctaagtgtg	tggacagctt	ctactgtgac	540
cttctcgggc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggtcact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacgtcttc	660
atcctgttta	ctgttttgaa	acattcctca	ggtggttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggg	ccttttgctc	tttgggtccac	ccatgtttgt	gtatacacgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatct	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgtg	ttacaaggag	atctca			936

&lt;210&gt; 914

&lt;211&gt; 954

&lt;212&gt; DNA

<213> Unknown (H38g764 nucleotide)

<220>

<223> Synthetic construct

<400> 914

atgtggcaga	agaatcagac	ctctctggca	gacttcaccc	ttgaggggct	cttcgatgac	60
tcccttacc	accttttct	tttctccttg	accatgggtg	tcttccttat	tgcggtgagt	120
ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttctgtctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaac	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaaccag	300
cacttctct	atttgtgtct	aggtgggtgt	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcatccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggctgtcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcaactccc	tttctgtggg	cctcggaag	tctaccactt	ctactgtgag	540
ttcccagctg	ttgtgaagtt	ggtatgtggc	gacatcactg	tgtatgagac	cacagtgtac	600
atcagcagca	ttctcctcct	cctccccatc	ttcctgattt	ctacatccta	tgtcttcac	660
cttcaaagt	tcattcagat	gcgtctcatc	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacgggtgt	ttctcttttg	tttgggtgct	gcattctctc	ctacatgaga	780
cccaggctcc	agtgcactct	attgcagaac	aaagtgtggt	ctgtgttcta	cagcatcatt	840
acgcccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tggtatcacc	cagtgcattc	aacgactgca	attg	954

<210> 915

<211> 309

<212> DNA

<213> Unknown (H38g765 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(309)

<223> n = A,T,C or G

<400> 915

acgtgtgtgc	ccacagcctn	gctggncac	ttcatctgtg	agctgccggc	gttgctcaag	60
ctggcccgcg	gagcatcgga	gacactaccg	agaaccagat	gttcgccgcc	cgcgtgggtca	120
ttctgtgtct	gccgtttgce	gtcatcctgg	cctcctacgg	tgcggtggcc	gagctgtctg	180
ttgtatgcgg	ttcagcggag	gccggagagg	gcggtgggca	cgtgtgggtc	ccactgacag	240
ccgtctgcct	gttctacggc	tcggcatcta	cacctacctg	cagcccgcgc	agctaacaac	300
caggcacgg						309

<210> 916

<211> 313

<212> DNA

<213> Unknown (H38g766 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(313)

<223> n = A,T,C or G

<400> 916

attcatgcc	tctcagccat	tgaatccacc	atcctgtctg	ccatggcctt	tnaccgttat	60
gtggccatct	gccacccact	gcgccatgct	gcagtgtctca	acaatacagt	aacagcccag	120
attggcatcg	tggctgtggt	ccgcggatcc	ctcttttttt	tcccactgcc	tctgtgtatc	180
aagcggctgg	ccttctgcca	ctccaatgtc	ctctcgcatc	cctattgtgt	ccaccaggat	240
gtaatgaagt	tggcctatgc	aagacanttt	gcccaatgtg	gtatatggtc	ttaactgncc	300

atTTTtggTtg gTc

313

&lt;210&gt; 917

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g767 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 917

atggaaacag	gaaatcaaac	acatgcccac	gaatttctcc	tcctgggatt	ttcagcaacg	60
tcagagattc	agttcattct	ctttgggctg	ttcctctcca	tgtacctagt	cactttcacc	120
gggaacctgc	tcatcatcct	ggccatatgc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ttttgctgac	ctctgtttta	cctccacgac	tgteccaaag	240
atgttactga	atatactgac	acagaacaaa	ttcataacat	atgcaggctg	tctcagtcag	300
atTTTTTTTT	tcacttcatt	tggatgcctg	gacaattttac	tcttgaccgt	gatggcctat	360
gaccgcttcg	tggccgtctg	tcacccctcg	cactatacgg	tcatcatgaa	ccccagctc	420
tgtggactgc	tggttcttgg	gtcctgggtg	atcagtgtca	tgggttcctc	gctcgagacc	480
ttgactgttt	tgaggctgtc	cttctgcacc	aaaatggaaa	ttccacactt	tttttTgtgat	540
ctacttgaag	tcctgaagct	cgcctgttct	gacaccttca	ttaataacgt	ggtgatatac	600
tttgcaactg	gcgtcctggg	tgtgatttcc	ttcactggaa	tatttttctc	ttactataaa	660
attgttttct	ctatactgag	gatttcctca	gctgggagaa	agcacaaagc	gttttccacc	720
tgtggttccc	acctctcagt	ggtcaccttg	ttctatggca	cgggcttttg	ggtctatctc	780
agttctgcag	ccacaccatc	ttctaggaca	agtctgggtg	cctcagtgat	gtacaccatg	840
gtcaccccca	tgctgaacct	cttcactctac	agcctgagga	acacggacat	gaagagggcc	900
ctggggagac	tcctcagtag	ggcaacattt	tttaatgggtg	acatcactgc	aggactttca	960

&lt;210&gt; 918

&lt;211&gt; 937

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g768 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 918

atgggggaca	accaatcacg	ggtcacagaa	ttcctcctgg	ttggattcca	gctcagtgTg	60
gagatggaag	tgctcctctt	ctggatcttc	tcctgttat	atctcttcag	cctgctggca	120
aatggcatga	tcttggggct	catctgtctg	gatcccagac	tgcgcacccc	catgtacttc	180
ttcctgtcac	acttggccgt	cattgacata	tactatgctt	ccagcaattt	gctcaacatg	240
ctggaaaacc	tagtgaaaca	caaaaaaac	tatctcgttc	atctcttgca	ttatgcagat	300
ggctttgtat	ttgacttttg	ctgctgcagt	gtgcatgatt	ttggtggTga	tgtcctatga	360
cagattttgtg	gcgatctgcc	atccctcgca	ttacactgtc	atcatgaact	ggagagtgtg	420
cacagtactg	gctattactt	cctgggcctg	tggattttcc	ctggccctca	taaatactaat	480
tctccttcta	aggctgccct	tctgtgggcc	ccaggaggTg	aaccacttct	tcggtgaaat	540
tctgtctgtc	ctcaaaactgg	cctgtgcaga	cacctggatt	aatgaaattt	ttgtctttgc	600
tggTggtgtg	tttgtcttag	tcggggccct	ttccttgatg	ctgatctcct	acatgcgcat	660
cctcttggcc	atcctgaaga	tccagtcaaa	ggaggggccg	aaaaaagcct	tttccacctg	720
ctcctcccac	ctctgtgtgg	ttgggcttta	ctttggcatg	gccatggTgg	tttacctggT	780
cccagacaac	agtcaacgac	agaagcagca	gaaaattctc	accctgtttt	acagcctttt	840
caaccatttg	ctgaaccccc	tcactctacag	cctgcggaat	gctcaagtga	agggtgcctt	900
atacagagca	ctgcagaaaa	agaggaccat	gtgaatg			937

&lt;210&gt; 919

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g769 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 919

atggaaccag	gaaatgatac	acaaatttca	gaatttcttc	ttctgggatt	ttcacaagaa	60
cctggactgc	aacccttcct	ctttgggctg	ttcctgtcca	tgtacctgg	cactgtgctc	120
gggaacctgc	tcatcctcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctct	ccaacctgtc	ctttgctgac	atttgtgtta	cttccaccac	cattccaaaa	240
atgtgatga	acatccagac	acagaacaaa	gtcatcacct	acatagcctg	cctcatgcag	300
atgtattttt	tcatactctt	tgctggattt	gaaaacttcc	tcctgtccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcaccccttg	cactacatgg	tcattatgaa	ccctcacctc	420
tgtggactgc	tggttctagc	atcctggacc	atgagtgttc	tgtattcctt	gtacaaaatc	480
ttaatggtag	tacggctgtc	cttctgcaca	gccttagaaa	tccccactt	tttctgtgaa	540
cttaatcagg	tcatccaact	tgcttgttct	gatagctttc	ttaatcacat	ggtgatatat	600
tttacagttg	cgctgctggg	tggagggtccc	ctgactggga	tcctttactc	ttactctaag	660
ataatttctt	ccatcacatg	aatctcatca	gtcaggggga	agtacaaggc	attttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatgggtg	caatcctagg	ggtgtacctt	780
agttctgctg	ccaccgcaa	ctcacactca	agtgaacacg	cctcagtgat	gtacactgtg	840
gtcaccccca	tgtgaaccc	ctttatctat	agtctgagga	ataaagacat	aaagagggtc	900
ctgggaatac	atttgttggtg	gggaacaatg	aaagggaat	ttttcaagaa	gtgcccc	957

&lt;210&gt; 920

&lt;211&gt; 222

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g770 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 920

ggagacacta	cagagaacca	gatgttcgcc	gcccgcgtgg	tcctcctgct	gctgccgtat	60
gacgtcatac	tggcctccta	aggtgccgtg	gcccagctg	tctgttgcat	gcgggttcagc	120
ggaggaccga	ggagggcgct	gggcacgtgt	gggtcccacc	cgacagccgt	ctggctgttc	180
taaggctcgg	gcaaataaac	ctatctgcaa	gccgcgcagc	ta		222

&lt;210&gt; 921

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g771 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 921

atgaaatcat	ggaacaatac	aataatttta	gaatttcttc	tcctgggaat	ttcagaggaa	60
ccagaattgc	aggccttcct	ctttgggctg	ttcctgtcca	tgtacctgg	cactgtgctc	120
gggaacctgc	tcatcctcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctct	ccaacctgtc	cttcgtaggc	atctgttttg	tctctaccac	tgtcccgaag	240
atgtgggtga	acatccagac	acacaacaaa	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	tcttactctt	tgtaggattg	gataacttcc	ttctgaccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccctctg	cactacatgg	tcattatgaa	ccctcaactc	420
tgtggactgc	tggttctggc	atcctggatc	atgagtgttc	tgaattccat	gttaciaaagc	480
ttaatgggtg	tgccactgcc	cttttgtaca	cacatggaaa	tccttcattt	tttctgtgaa	540
attaatcagg	tgggtccact	tgccctgttct	gacacctttc	ttaatgacat	agtgatgtat	600
ttcgcagtag	cgctgctggg	cgggtgggtccc	ctcactggga	tcctgtactc	ttactctaag	660
atagtttctt	ccatactgtc	aatctcatca	gtcaggggga	agtataaggc	attttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatggta	catgcttagg	ggtgtacctt	780
agttctgctg	ccaccacaaa	ttcacacaca	ggtgctgcag	cctcagtgat	gtacactgtg	840
gtcaccccca	tgtgaaccc	cttcatctac	agtctgagga	ataaacacat	aaagggtgct	900
atgaaaacat	tcttcagagg	aaagcaa				927

&lt;210&gt; 922

&lt;211&gt; 246

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g772 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 922

atgggtcacag agttcctccc actgggattt ctcctggggc caaggattca gatgctcctc	60
cttgggctct tctccctggt ctatgtcttc acccgcgtgg ggaatgggac catccccggg	120
ctcatctcac tggactccag actccacacc cccatgtact tcttcctctc acacctgggc	180
gtcgtcaaca tcgcctatgc ctgcaacaca gtgccccaga tgctgggtgaa cctcctgcat	240
ccagcc	246

&lt;210&gt; 923

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g773 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 923

ctcatggacc tcaagctcat ctgcaccacc gtaccaaga tggccttcaa ctacctgtct	60
ggcagcaagt ccatttctat ggctgggtgt gtcacacaaa ttttcttcta tatatcactg	120
tctggctctg aatgttttct tttggctggt atggcttatg accgctatat tgctatttgc	180
cacctcttaa gatataccaa tctcatgaat cctaaaattt gtggacttat ggctaccttc	240
tcctggatcc tgggctctac agatggaatc attgatgctg tagccacatt ttccttctcc	300
ttttgtgggt ctggggaaat agccacttc ttctgtgaat tcccttccct actaatcttc	360
tcattgcaatg acacatcaat atttgaagag gttattttca tctgctgtat agtaatgctt	420
gttttccctg ttgcaatcat cattgcttcc tatgctcgag ttattctggc tgcattcac	480
atgggatctg gagagggtcg ttgcaaagct ttcacgacct gttectctca cctcatggtg	540
gtgggaatgt actatggagc agctttgttc atgtacatac ggccacatc tgatcactcc	600
ccaacgcagg acaagatggt gtctgtattc tacaccatcc tcaactccc	648

&lt;210&gt; 924

&lt;211&gt; 916

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g774 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 924

atgaaaccag ggaatgatac acgaatttca gaatttcttc ttctaggact ttcagcagaa	60
ccagaattgc agcccttctt ctttgggctg ttctgtcca tgtacctggt caccgtgctc	120
gggaacctgc tcatcatcct ggccacaatc tcagactccc acctccacac ccccatgtac	180
ttcttctctt ccaacctgtc ctttgcagat atcagttttg tgtctaccac tgtcccgag	240
atgctggtga atatccagac gcagagcaga gtcacacct atgcaggctg catcaccag	300
atgtgctttt tctactatt tgcagtgttg gacagccttc tcttagctgt gatggcctat	360
gatcggtttg tggccatctg tcatcctctg tactacacaa tcatcatgaa ccctcagttc	420
tatagactgg attcttagtg tctgaattc tctgttaca agcttaatgg tgttgccact	480
gcccttctat acagacatag caatccccca ctttttctgt gaacttaatc agataatctg	540
cattgcctgt tctgacacct ttcttaatga catcatgata tattgtgcaa ctgtgctgct	600
gggcgggtgt cccctcactg gaatccttta ctcttactct aagatagttt cctccatacg	660
tgcaatctca tcagctcagg ggaagtacaa ggcattttcc acctgtgcat ctcacctctc	720
agttgtctcc ttgttttatg gtacaagcct aggaatgtac cttagttctg ctgcaaccca	780
caactcacc ccaagtgcac cagcctcagt gatgtacact gtggtcaccc ccatgctgaa	840
cccctttatc tacagtctga ggaataaaga cctaaaggat gctctgaaac gcttcttcag	900
aaggaagcaa taaaag	916

&lt;210&gt; 925

<211> 360  
 <212> DNA  
 <213> Unknown (H38g775 nucleotide)

<220>  
 <223> Synthetic construct

<400> 925  
 ttttccctct cacacctggc ggttggtgac attgcctacg cctgcaacac ggtgccccgg 60  
 atgctggtga acctcctgca tccagccaag cccatctcct ttgcgggccg catgatgcag 120  
 acctttctgt tttccacttt tgctgtcaca gaatgtttcc tcctggtggt gaagtccaat 180  
 gatttgtaag tggccatctg ccacccctcc cgatatttgg ccatcatgac ctggagagtc 240  
 tgcataccac tcgcggtgac ttcttggaac actggagtc ttttatcctt gattcatctt 300  
 gtgttacttc tacctttacc cttctgtagg cccagaaaaa tttatcactt tttttgtgaa 360

<210> 926  
 <211> 643  
 <212> DNA  
 <213> Unknown (H38g776 nucleotide)

<220>  
 <223> Synthetic construct

<400> 926  
 ttgcctgaca tcggtttcac ctccaccacg gtccccaaga tgattgtgga atccaatctc 60  
 acagcagagt catctcctat gcaggctgcc tgactcagat gtctctcttt gccatttttg 120  
 gaggcatgga agagagacat gctcccagat gtgatggcct atgaccgggt ttagccatc 180  
 tgtcaccttc tatatcattc agccatcatg aaccctgtgt tctgtggctt cctagttttg 240  
 ctgtcttttt tttctttctt tttctcagct gcacaacttg attgccttac aaatgacctg 300  
 cttcaagaat gtgggaattc ctaatttcct ctgtgacctt tctcaactcc cccatctcac 360  
 atgttgtgac accttcacca atcacataat catgtatttc cccgctgcca tatttggtt 420  
 tcttcccatc tcggggaccc ttttctctta ccattgtaatt gtttcctcca ttctgagggg 480  
 ttcatcatca ggtgggaagt ataaagcctt ctccacctat gggctcacc tgtcagatgt 540  
 ttcttgattt tatggaacag gcgttgagg gtacctcagt tcagatgtgt catcttcccc 600  
 gagaaagact gcagtgacct cagtgtatgta cgcagtggtc acc 643

<210> 927  
 <211> 498  
 <212> DNA  
 <213> Unknown (H38g777 nucleotide)

<220>  
 <223> Synthetic construct

<400> 927  
 gtgaaaaatc agacaatggt cacagagttc cttctatttg gatttttctt gagcccaagg 60  
 atacacatgc tcctcttttg gctcttctac ctgttctatg tcttcacctt gctggggaat 120  
 gggaccatcc tggggctcat ttactggac tccatactcc acaccccat gtacttcttc 180  
 ctataacacc tgtccgtcgt caacatcgcc tatgcctgca acacagtgcc ccagatgctg 240  
 gtgaacctcc tgcattcagc caagcccatt tactttgctg gctgcatgac atatacttt 300  
 ctctttttga gatttgaca tactgaatgc ctctgttggt tgctgatgtc ctacgattgg 360  
 tacgtggcca tcttgacacc tctccgatat atcatcatta tgacctgtaa agtcttcac 420  
 atctctgcca tcactttcat gtacatgtgg ttctttctg tcttggtcca tgaagcctc 480  
 atactaagac tgcctttt 498

<210> 928  
 <211> 276  
 <212> DNA  
 <213> Unknown (H38g778 nucleotide)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 928

caa	atg	ag	ct	tgt	tgt	aat	ctt	tgc	ctt	ct	gg	ctg	aat	gc	aatt	tgt	tta	aact	cg	ca	ct	60	
gg	cc	t	a	t	a	g	a	g	a	g	g	a	c	c	c	c	c	c	c	c	c	c	120
t	c	t	a	a	g	a	g	a	g	c	c	a	t	a	t	c	t	t	t	t	t	t	180
t	g	g	t	c	a	c	t	g	t	g	a	c	a	a	c	a	a	c	a	a	c	a	240
c	t	t	c	t	c	t	g	t	g	a	c	a	a	c	a	a	c	a	a	c	a	a	276

&lt;210&gt; 929

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g779 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 929

t	t	c	t	c	t	g	a	t	c	c	t	c	a	a	t	t	c	a	a	t	c	a	60
c	a	a	g	t	a	c	c	a	a	c	c	a	c	a	c	a	c	a	c	a	c	a	120
g	g	a	g	a	t	a	t	g	a	t	g	a	t	g	a	t	g	a	t	g	a	t	180
t	t	c	c	t	t	t	g	c	a	t	a	c	c	a	a	a	t	t	t	t	t	t	240
c	t	g	t	g	a	t	g	c	a	a	t	a	t	c	c	c	t	g	c	a	c	c	300
t	t	t	t	g	t	g	a	a	a	t	g	t	c	a	t	t	t	t	t	t	t	t	360
t	c	t	g	t	c	a	g	a	c	a	c	t	t	a	t	g	t	t	a	t	g	t	420
a	t	t	a	t	t	c	c	a	t	t	c	a	t	g	t	t	a	t	t	a	t	t	480
g	t	t	c	c	a	t	c	t	t	c	c	a	a	g	g	t	c	c	a	a	a	a	540
g	t	g	a	c	c	t	t	g	t	a	a	a	t	t	g	g	t	a	a	a	a	a	600
a	c	t	g	t	g	a	a	t	t	c	c	a	t	g	a	t	t	c	c	a	a	a	645

&lt;210&gt; 930

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g780 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 930

a	g	c	a	a	c	c	t	a	c	t	a	c	t	a	a	t	t	c	a	a	t	c	60
a	a	c	a	t	g	c	a	g	a	t	t	c	t	c	a	a	t	c	c	c	c	c	120
c	t	t	t	t	g	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	180	
g	t	a	g	c	c	a	t	c	t	c	t	c	a	c	c	a	c	c	a	c	c	a	240
c	t	t	g	t	g	t	g	c	t	g	c	a	c	a	t	t	c	a	t	t	c	a	300
a	c	t	a	g	g	t	t	g	t	g	a	a	a	c	a	a	t	g	t	a	t	t	360
c	t	g	t	g	a	a	c	t	g	c	t	a	a	t	t	c	a	a	t	a	a	t	420
g	g	g	c	t	t	g	t	t	g	t	t	a	a	c	t	t	c	a	c	a	c	a	480
t	c	c	a	t	t	c	a	g	g	t	c	c	c	t	t	c	a	a	g	g	c	a	540
c	a	c	c	t	g	t	c	t	g	t	a	a	c	a	a	t	t	a	t	t	g	c	600
g	c	t	a	a	a	c	t	a	a	c	t	a	a	a	c	t	a	a	a	c	t	a	657

&lt;210&gt; 931

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g781 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 931

a	t	g	g	a	a	c	a	g	a	g	g	t	a	a	c	a	a	c	a	a	a	60
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	----

```

ctgcagatcc cactcttcat agtcttcctt ttcattctacc tcatcactct gggtgggaac 120
ctggggatga ttgaattgat tctactggac tctgtctcc acaccccat gtacttcttc 180
ctcagtaacc tctccctggt ggactttggt tattcctcag ctgtcactcc caaggtgatg 240
gtgggggttc tcacaggaga caaattcata ttatataatg cttgtgccac acaattcttc 300
ttctttgtag cctttatcac tgcagaaagt ttctcctgg catcaatggc ctatgaccgc 360
tatgcagcat tgtgtaaacc cctgcattac accaccacca tgacaacaaa tgtatgtgct 420
tgcttgcca taggctccta catctgtggt ttctgaatg catccattca tactgggaac 480
actttcaggc tctccttctg tagatccaat gtagttgaac actttttctg tgatgctcct 540
cctctcttga ctctctcatg ttcagacaac tacatcagtg agatggttat tttttttgtg 600
gtgggattca atgacctctt ttctatcttg gtaatcttga tctcctactt atttatattt 660
atcaccatca tgaagatgcg ctacactgaa ggacgccaga aggccttttc tacttggct 720
tcccacctta ctgcagtttc catcttttat gggacaggaa tctttatgta cttacgacct 780
aactccagcc atttcatggg cacagacaaa atggcatctg tgttctatgc catagtcatt 840
cccattgtga atccactggt ctacagcctg aggaacaaag aggttaagag tgcctttaa 900
aagactgtag ggaaggcaaa ggcctctata ggattcatat tt 942

```

&lt;210&gt; 932

&lt;211&gt; 562

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g782 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 932

```

gcaacaaagg agctgtgttt tcttggggta tatattccca aaggcgatgc ctgctggaaa 60
tgactcctct gggcctgcat ttactcttgc taggttgaca agttgtctcc atgggtggga 120
acctggcctt gattgctcta attggctgaa attcatacct tcccaccccc aagctctggt 180
ttctttcacc cagtccttcc ctgatctcta ttgtcctggt tgcaccccca gaatgctcat 240
gacttttcta tcaaagaaaa acatcttcta tgtcagggtg atgactcagc tgtcgcagct 300
tttctttctc ttattgttcc tactctatta aataccacgt gttgatgttc atagcctgtg 360
gttgcttagt ggccatctac aatccatcat tgcagaggt caccatgtct cctcagggtg 420
gagagagaga gaggatggat ttgctgggaa cactcccaca cagggcacat acttaggccg 480
aacttgtgta atattgatgt catcaatcat catcttatga cagcctcttg gtcctctaag 540
tttctgttac cagcacctgt gc 562

```

&lt;210&gt; 933

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g783 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 933

```

atgactgggg gaggaatat tacagaaatc acctatttca tctgtctggg attctcagat 60
tttcccagga tcataaaagt gctcttctact atattcctgg tgatctacat tacatctctg 120
gcctggaacc tctccctcat tgttttaata aggatggatt cccacctcca tacacccatg 180
tatttcttcc tcagtaacct gtccttcata gatgtctgct atatcagctc cacagtcccc 240
aagatgctct ccaacctctt acagggaacag caaactatca cttttgttgg ttgtattatt 300
cagtacttta tcttttcaac gatgggactg agtgagtctt gtctcatgac agccatggct 360
tatgatcggt atgctgcat ttgtaacccc ctgctctatt catccatcat gtcaccacc 420
ctctgtgttt ggaatgtact gggagcctac atgactggcc tcaactgctt tttattccaa 480
attggtgctt tgcttcaact ccacttctgt ggggtctaag tcatcagaca tttcttctgt 540
gacatgcccc aactgttaat cttgtcctgt actgacactt tctttgtaca ggtcatgact 600
gctatattaa ccatgttctt tgggtagtag agtgccctag ttatcatgat atcctatggc 660
tatattggca tctccatcat gaagatcact tcagctaaag gcaggccaaa ggcattcaac 720
acctgtgctt ctcatctaac agctgtttcc ctcttctata catcaggaat ctttgtctat 780
ttgaggtcca gctctggagg ttcttcaagg tttagacagat ttgcatctgt tttctacact 840
gtggtcattc ccatgttaaa tcccttgatt tacagtttga ggaacaaaga aattaaagat 900
gccttaaaga ggttgcaaaa gagaaagtgc tgc 933

```

<210> 934  
 <211> 935  
 <212> DNA  
 <213> Unknown (H38g784 nucleotide)

<220>  
 <223> Synthetic construct

<400> 934  
 atgactgggg aaaggaacag tacgagaatt acaaagttca ttctcttggg attctctgaa 60  
 ttcccaaaga accctatttt cctcttttca atattcctag ggatctacct cctgacagtg 120  
 tcctggaaca taaacctcat cacccttatac aggacgactc ccatctgcat acacctatgt 180  
 acttttttct tagtaatctg tcgtttcttg acatctgcta tgtttccact atagcccca 240  
 agatgctctc agacttcttc aagaagcata aattcatctc ctttatgggg tgcagtatgc 300  
 agtacttttt cttctctagc ctaggtctaa ctgagtgtctg tcttctggca gccatggctt 360  
 atgatcgata tgctgccatt tgcaaccctc tgctctacag ggccatcatg tttcccaccc 420  
 tctgctgca gatggtggca ggatcttgta taactggatt cttaggctca tttatccaac 480  
 tctgtgccct gcttcagctc catttctgtg ggccaaatgt catcaacct tttctctgtg 540  
 atctgcccc gctgctgatt ctatctgtt ctgacacct tttctttcaa gtcatgacct 600  
 ctgtttcac agtgatcttt ggactcacgt ctgtcttagt tatcatgata tcttatgggt 660  
 atatcattgc caccattctg aagatcacct cagctgaagg cagagccaaa tctttcaaca 720  
 cttgtgcttc tcaccttaca gcagtgatec ttttctttgg ctcaggtatc tttgtttata 780  
 tgtatcctaa tgctggtgat tccctgagcc aaaacaagtt ggcatcagtc ttatacacag 840  
 ttacaatccc catgttaaat ccagtgtctc acagcctgag gaacaaggaa atcaaagatg 900  
 ctctaaccag atggaagaag agaacttctt cctgg 935

<210> 935  
 <211> 1330  
 <212> DNA  
 <213> Unknown (H38g785 nucleotide)

<220>  
 <223> Synthetic construct

<400> 935  
 atgactgtgg aaaggagtag catgacaatt acaaagttca ttctcttggg attctctgaa 60  
 tattcaaaga ccactatttt tctcttttca gtattcctag ggatataacct cctgaccatg 120  
 tcctgaaacg tgagtctcat cgcccttatac aggacggact cccatctaca tgcacctgtg 180  
 tactttttcc ttagtaatcc gtcttttctg gacatctgct gtgtttccac tatagcccc 240  
 aagatgccct cagacttttt caagaagcat aaattcattt ctttatggg gtgcaccatg 300  
 cagtacttct ctagcctgaa tgtgactgag tgctgtcttc ttacagccat ggttatgat 360  
 taatatgctg ccatttgtga tctctgtctc tacacagcca tcatgtcacc tgctctctgt 420  
 atgccaatgg tggcaggatc ttgtacaact ggatactttg tctcatttat ccaactctgt 480  
 gccttgcttc tgctccattt ctgtgagtca aatagcagcc atttcttttg tgacctgccc 540  
 caactgctga ttctatcctg ttctcatact gttttttttt tctcaagtca tgaccactat 600  
 gctcacagta acctttatac tcacctctat cttggttatc atgataactt atggttatat 660  
 cattgccaac attcatctct tttatgggat gcaccatgta atacttcttc tctagcctgg 720  
 gtctgactga gtgctgtctt ctggaagcta tggcttataa ttgatatgct gccatttgtg 780  
 accctctgct ctacatggcc atccatgtcc ccaacctctg tgtgcacata atggttgaa 840  
 cctgtataac tattatcttt ggctcattta tccaactatg tgctttgctt cagctccatt 900  
 tctgtgggcc aaatagcaac catttcttct gtgacctgcc ccaactcttg atcctatctt 960  
 gctatgacac ctttttctgt caagtcatga catccatgct tacagtggta tttggactca 1020  
 catctgtctt agttatcatg atattttatg gctatgtcat tgctaccatt ctgaagatca 1080  
 tctcagtga aggcaggtct aaggcttcca aactggtgg ttctccctga tagcagtgc 1140  
 tctctctat tgetcaagaa tctttgtcta tatgtgctct cactctgatg cttctctgag 1200  
 tagaaacaag gtggattcta ttgtatacac tgtggtgatc cccaggttga atccattgat 1260  
 ctacagcctg agtgacaagt aaatcaaaga tgccttaaag agatggacga agagaatatt 1320  
 ctctggcct 1330

<210> 936

<211> 930  
 <212> DNA  
 <213> Unknown (H38g786 nucleotide)

<220>

<223> Synthetic construct

<400> 936

atgggggaaa	atcagacaat	ggtcacagag	ttcctcctac	tgggatttct	cctggggccca	60
aggattcaga	tgtcctctt	tgggctcttc	tccctgttct	atatcttcac	cctgctgggg	120
aacggggcca	tcctggggct	catctcactg	gactccagac	tccacacccc	catgtacttc	180
ttcctctcac	acctggctgt	cgtcgacatc	gcctacaccc	gcaacacggg	gccccagatg	240
ctggcgaaac	tcctgcaccc	agccaagccc	atctcctttg	ctggctgcat	gacgcagacc	300
tttctctgtt	tgagttttgg	acacagcgaa	tgtctcctgc	tgggtgctgat	gtcctacgat	360
cgttacgtgg	ccatctgcca	ccctctccga	tactccgtca	tcatgacctg	gagagtctgc	420
atcacccctgg	ccgtcacttc	ctggacgtgt	ggctccctcc	tggctctggc	ccatgtgggt	480
ctcatcctaa	gactgccctt	ctctgggccc	catgaaatca	accacttctt	ctgtgaaatc	540
ctgtctgtcc	tcaggctggc	ctgtgctgac	acctggctca	accagggtgt	catctttgca	600
gcctgcgtgt	tcttctcgtt	ggggccaccc	agcctgggtg	ttgtctccta	ctcgcacatc	660
ctggcgggcca	tcctgaggat	ccagtctggg	gaggggccga	gaaaggcctt	ctccacctgc	720
tcctcccacc	tctgcgtggg	gggactcttc	tttggcagtg	ccatcatcat	gtacatggcc	780
cccaagtccc	gccatcctga	ggagcagcaa	aaggctcttt	ttctatttta	cagttttttc	840
aaccacaacac	ttaacccctt	gatttacagc	ctgaggaacg	gagagggtcaa	gggtgccttg	900
aggagagcac	tgggcaagga	aagtcattcc				930

<210> 937

<211> 942

<212> DNA

<213> Unknown (H38g787 nucleotide)

<220>

<223> Synthetic construct

<400> 937

atggaaagac	aaaatcaaag	ctgtgtgggt	gaattcatcc	tcttggggctt	ttctaactat	60
cctgagctcc	aggggcagct	ctttgtggct	ttcctgggta	tttatctggt	gacctgata	120
gaaatgcca	ttattatagt	catcgtctcc	ctagaccaga	gcctccacgt	tcccatgtac	180
ctgtttctcc	tgaacttata	tgtgggtggac	ctgagtttca	gtgcagttat	tatgcctgaa	240
atgctgggtg	tcctctctac	tgaaaaaact	acaatttctt	ttgggggctg	ttttgcacag	300
atgtatttca	tccttctttt	tgggtggggct	gaatgttttc	ttctggggagc	aatggccttat	360
gaccgatttg	ctgcaatttg	ccatcctctc	aactacaaaa	tgattatgaa	taaaggagtt	420
tttatgaaat	taattatatt	ttcatggggc	ttaggtttta	tgttaggtac	tgttcaaaca	480
tcatgggtat	ctagttttcc	cttttgtggc	cttaatgaaa	ttaaccatat	atcttgtgaa	540
accccagcag	tgtagaact	tgcattgtgca	gacacgtttt	tgtttgaaat	ctatgcattc	600
acaggcacct	ttttgattat	tttgggttct	ttcttgttga	tactcttgtc	ttacattcga	660
gttctgtttg	ccatcctgaa	gatgccatca	accactggga	gacaaaaggc	cttttccacc	720
tgtgccgctc	acctcacatc	tgtgacccta	ttctatggca	cagccagtat	gacttattta	780
caacccaaat	ctggctactc	accggaaacc	aagaaagtga	tgatcattgtc	ttactcactt	840
ctgacaccac	tgtgtaatct	gcttatctac	agtttgcgaa	atagtgaat	gaagagggct	900
ttgatgaaat	tatggcgag	gcgagtgggt	ttacacacaa	tc		942

<210> 938

<211> 993

<212> DNA

<213> Unknown (H38g788 nucleotide)

<220>

<223> Synthetic construct

<400> 938

atgggtcacag	agttcctcct	actgggattt	ctcctgggcc	caaggattca	gatgctcctc	60
-------------	------------	------------	------------	------------	------------	----

tttgggctct	tctccctggt	ctatgtcttc	accctgctgg	ggaatgggac	catcctgggg	120
ctcatctcac	tggactccag	actccacacc	cccatgtact	tcttcctctc	acacctgggc	180
gtcgtcaaca	tcgcctatgc	ctgcaacaca	gtgccccaga	tgctgggtgaa	cctcctgcat	240
ccagccaagc	ccatctcctt	tgctggctgc	atgacataga	cctttctctt	tttgagtttt	300
gcacatactg	aatgcctcct	gttggtgctg	atgtccctacg	atcgggtacgt	ggccatctgc	360
cacctctctc	gataatttcat	catcatgacc	tggaaagtct	gcatcactct	ggccatcact	420
tcttggacat	gtgggtccct	cctggctatg	gtccatgtga	gcctcatcct	aagactgccc	480
ttttgtgggc	ctcgtgaaat	caaccacttc	ttctgtgaaa	tctgtctgtg	cctcaggctg	540
gcctgtgctg	atacctgggt	caaccagggt	gtcatctttg	cagcctgcat	gttcatcctg	600
gtgggaccac	tctgcctggg	gctgggtctc	tactcacaca	tcttggcggc	catcctgagg	660
atccagtctg	gggagggcgc	cagaaaggcc	ttctccacct	gtcctcccca	cctctgcgta	720
gtgggactct	tctttggcag	cgcatccgtc	atgtacatgg	cccctaagtc	ccgccatcct	780
gaggagcagc	agaaggctct	ttttctattt	tacagtctct	tcaaccgat	gctaaacccc	840
ctgatttaca	acctgaggaa	tgtagaggtc	aagggtgccc	tgaggagagc	actgtgcaag	900
gaaagtcatt	cctaagaggt	gtgacatttg	aactgccagc	ctcagttgtc	acgtggactc	960
ttgatgcccc	attattgcct	caatccagaa	aag			993

&lt;210&gt; 939

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g789 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 939

atggggggaca	atataacatc	catcacagag	ttcctcttac	tgggatttcc	cggtggccca	60
aggattcaga	tgtcctctct	tgggtctctc	tcctgtttct	acgtcttcac	cctgctgggg	120
aacgggacca	tactgggggt	catctcactg	gactccagac	tgcacgcccc	catgtacttc	180
ttcctctcac	acctggcggt	cgctcgacatc	gcctacgcct	gcaacacggt	gccccggatg	240
ctgggtgaacc	tcttgcaccc	agccaagccc	atctcctttg	cgggccgcat	gatgcagacc	300
ttctgttttt	ccactttttg	tgtcacagaa	tgtctcctcc	tgggtggtgat	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttgccca	tcatgacctg	gagagtctgc	420
atcacccctg	cggtgacttc	ctggaccact	ggagtctctt	tatccttgat	tcatcttggt	480
ttactttctac	ctttaccctt	ctgtaggccc	cagaaaattt	atcacttttt	ttgtgaaatc	540
ttggctgttc	tcaaacttgc	ctgtgcagat	accacatca	atgagaacat	ggctcttgcc	600
ggagcaattt	ctgggctggg	gggacccttg	tccacaattg	tagtttcata	tatgtgcac	660
ctctgtgcta	tctttcagat	ccaatcaagg	gaagttcaga	ggaaagcctt	ctgcacctgc	720
ttctcccacc	tctgtgtgat	tggactcttt	tatggcacag	ccattatcat	gtatgttgga	780
cccagatatg	ggaaccccaa	ggagcagaag	aaatatctcc	cgctgtttca	cagcctcttt	840
aatcccatgc	tcaatcccct	tatctgtagt	cttaggaact	cagaagtga	gaatactttg	900
aagagagtgc	tgggagtaga	aagggtctta				930

&lt;210&gt; 940

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g790 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 940

atgaaaagac	aaaatcaaag	ctgtgtgggt	gaattcatcc	tcttgggctt	ttctaacttt	60
cctgagctcc	agggtcagct	ctttgggggt	ttcctagtta	tttatgtggt	gacctgatg	120
ggaaatgcca	tcattacagt	catcatctcc	ttaaaccaga	gcctccacgt	tcccatgtac	180
ctgttctctc	tgaacctatc	tgtggtggag	gtgagtttca	gtgcagtcac	tacgcctgaa	240
atgctgggtg	tgtctctctac	tgagaaaact	atgatttctt	ttgtgggctg	ttttgcacag	300
atgtatttca	tccttctttt	tgggtgggact	gaatgttttc	tcttgggagc	gatggcttat	360
gaccgatttg	ctgcaatttg	ccatcctctg	aactaccag	tgattatgaa	cagaggggtt	420
tttatgaaat	tagtaatatt	ctcatggatc	tcagggatca	tgggtggctac	tgtgcagacc	480
acttgggtat	ttagtctttc	atcttctgtg	cccaatgaaa	ttaatcatct	cttctgtgag	540



```

actccccgg tactagagct tgtgtgtgca gacaccttct tatttgaaat ctatgccttc 600
acaggcacca ttttgattgt tatgggttct ttcttgttga tctcttgtc ttacattcga 660
gttctgtttg ccatacctgaa gatgccatca actactggga gacaaaaggc cttttccacc 720
tgtgcctctc acctcacatc tgtgacctg ttctatggca cagccaatat gacttattta 780
caacccaaat ctggctactc acccgaaacc aagaaactga tctcattggc ttacacgttg 840
cttaccctc tgctcaatcc gctcatctat agcttacgaa acagtgaat gaagaggact 900
ttgataaaac tatggcgaag aaaagtgtt ttacacacat tc 942

```

&lt;210&gt; 941

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g791 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 941

```

atgagtgcga acacctccat ggtgactgag tttcttcttc tcggcttctc ccacctggcc 60
gacctccagg gcttgcctct ctctgtcttt ctactatct acctgctgac cgtggcaggc 120
aatttctca ttgtgggtgt ggtctccact gatgctgccc tccagtcccc tatgtacttc 180
ttcttgcgca cctctcggc ctggagatt ggctatacgt ctgtcacggc cccctgcta 240
cttcaccacc tcttactgg cggcgccac atctctcgt ctggatgtg tctccagatg 300
ttcttcttcc tcttcttttg cgccacggag tgctgcctcc tggcagccat ggcctatgac 360
cgctatgcag ccatactgtga accctcgcg taccactgc tgctgagcca cgggtgtgt 420
ctacagctag ctgggtcggc gtgggcctgt ggggtgctgg tggggtggg ccacacctc 480
ttcatcttct ctttgcctt ctgcgcccc aataccatcc cgcagtctt ctgtgagatc 540
cagcctgtcc tgcagctggt atgtggagac acctcgctta atgaactgca gattatcctg 600
gcaacagccc tctcatcct ctgcccctt ggctcatcc tgggctccta cgggcgtatc 660
ctcgttacca tcttcggat cccatctgtt gcgggccgcc gcaaggcctt ctccacctgc 720
tctcccacc tgatcgtggt ctccctcttc tatggcaccg cactctttat ctatattcgc 780
cctaaggcca gctacgatcc ggccactgac cctctggtgt cctcttcta tgctgtggtc 840
accccatcc tcaaccccat catctacagc ctgcggaaca cagaggtaa agctgccta 900
aagagaacca tccagaaaac ggtgcctatg gagatt 936

```

&lt;210&gt; 942

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g792 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 942

```

atgtacctgg tcaactgtgt cggaacctg ctcatcatcc tggccgcaat ctcaactcc 60
tgctccaca ccccatgta cttcttctc tccaacctgt ccttcgtaga tatctgtttt 120
gcctccacca tggccccaa gatgttggtg aacatccaga cacagagcaa agtcattacc 180
tatgcagggt gcatcaccca gatgtgcttt ttgtactct ttatagtgtt ggacagctta 240
ctcctgaccg tgatggccta tgaccagtt gtggccatct gtcacccct gcactacag 300
gtcatcatga gccctcagct ctgtggactg ctggtctctg tgctcctggat catgagtgtc 360
ctaaactcca tgttacaaag cttagtgaac ttgcagttgt ccttctgcac agacttgaa 420
atccctcact tttctgtga acttaatgag atgatccacc ttgcctgttc tgacacctt 480
gtgaacaaca tggatgatga ttttgagct gtgctgctgg acggtggtcc tctcgttggg 540
atcctttatt cttactgtag gatagtttcc tccatactg caatctcgtc aactcagggg 600
aagtacaagg cactttccac ctgtgcatct cactctcag ttgtctccat attttatggt 660
acggggctag ggggtgacct tagctctact atgacccaaa acttacactc aactgtgtc 720
gcctcgggtg tgtacactgt ggtcaccccc atgtcaacc ccttcattta cagtctgagg 780
aataaagaca taaagggggc tctgacacaa ttcttcagag ggaaacaa 828

```

&lt;210&gt; 943

&lt;211&gt; 950

&lt;212&gt; DNA

<213> Unknown (H38g793 nucleotide)

<220>

<223> Synthetic construct

<400> 943

tcaattacct	gggaaaatca	ctcagtggtg	atggaatttg	tggttcctggc	ctatccctcc	60
tgcccagaac	tgcatattct	gtccttcctt	ggggtcagcc	tggtttatgg	tttgatcatc	120
actgggaaca	ttctcattgt	ggtgtccatt	cacacagaaa	cctgtctatg	cacatccatg	180
tactatttcc	tgggcagcct	ttctgggatt	gaaatatgct	acactgcagt	ggtgggtgcc	240
catatcctgg	ccaacacctt	acagtcagag	aagacatcac	tctcctgggc	tggtgccacc	300
agatggcttt	cttcattgca	ctgggcagtg	ctgattgctt	cctcttggct	gccatggcct	360
atgaccgcta	tgtggccatt	tgccaccctg	tgcagtaccc	tctcctcatg	acattgactc	420
tttgtgtcca	cttgggtgtg	gcatcagtca	tcagtggtct	gttcctgtcc	ttacaactgg	480
tggccttcat	cttctctctg	ccattctgcc	aggctcaggg	cattgagcac	ttcttttgtg	540
atgtgccacc	agtcatgcat	gttgtttgtg	ctcagagtca	cattcatgag	cagtcagtgc	600
tggtggcagc	catactagcc	attgctgtgc	ctttcttcct	catcaccacc	tcctacacct	660
tcattctggc	tgctctgtct	aagatccact	cggctgctgg	cgcaccaccg	gccttctcca	720
cctgtctctt	ccacctcact	gtggtgctgc	tgcagtatgg	ctgctgtgcc	ttcatgtacc	780
tgtgccccag	ctccagctac	aaccccaagc	aagatcggtt	catctcactg	gtgtacacat	840
tgggaacccc	actgtcctac	ccacttatct	atgccctgag	gaacagttag	atgaaagggg	900
ccgtagggag	agttcttacc	aggaactgcc	tttccagaaa	cagctaggaa		950

<210> 944

<211> 927

<212> DNA

<213> Unknown (H38g794 nucleotide)

<220>

<223> Synthetic construct

<400> 944

atggaaccag	agaatgacac	agggatttca	gaatttggtc	ttctgggact	ttctgaggaa	60
ccagaattgc	agcccttcc	ctttgggctg	tttctgtcca	tgtacctgg	cactgtgtct	120
gggaatctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctt	ccaacctgtc	ctttgcagac	atctgtttca	tctccactac	aatcccaaag	240
atgtctatta	acatccagac	acagagcaga	gtcatcacct	atgcaggctg	catcaccacg	300
atgtgctttt	ttgtactttt	tggagggtta	gacagcttac	tcctggctgt	gatggcctat	360
gatcgggttg	tggccatctg	tcatactctg	cactacacag	tcatactgaa	ccctcggtct	420
tgtggactcc	tggttctggc	atcctggatg	attgctgccc	tgaattcctt	gtcacaaagc	480
ttaatggtat	tgtggctgtc	cttctgcaca	gacttggaaa	tcctccactt	tttctgtgaa	540
cttaatcagg	tcataccact	tgctgttctt	gacacctttc	ttaatgacat	ggggatgtat	600
tttgcagcag	ggctgtctgg	tggtggtccc	cttgtgggga	tcctttgtct	ttactctaag	660
atagtttcc	ccatacgtgc	aatctcatca	gtcaggggga	agtacaaggc	atcttccacc	720
tgtgcatcac	acctctcagt	tgtctcttta	ttttgttgta	cgggcctagg	tgtgtacctt	780
acttctgtct	caaccacaaa	ctcacacaca	agtgcaacag	cctcagtgat	gtacactgtg	840
gccaccccca	tgctgaaccc	ctttatctac	agtctgagga	ataaagacat	aaagagggct	900
ctgaaaatgt	ccttcagagg	aaagcaa				927

<210> 945

<211> 942

<212> DNA

<213> Unknown (H38g795 nucleotide)

<220>

<223> Synthetic construct

<400> 945

atggagaata	atacagaggt	gagtgaattc	atcctgcttg	gtctaaccac	tgccccagaa	60
ctacaggttc	ccctctttat	catgtttacc	ctcatctacc	tcatactctt	gactgggaac	120
ctggggatga	tcataattaat	cctgctggac	tctcatctcc	acactcccat	gtactttttt	180

```

ctcagtaacc tgtctcttgc aggcattggt tactcctcag ctgtcactcc aaaggtttta 240
actgggttgc ttatagaaga caaagccatc tcctacagtgc cctgtgctgc tcagatgttc 300
ttttgtgcag tctttgccac tgtggaaaat tacctcttgt cctcaatggc ctatgaccgc 360
tacgcagcag tgtgtaaccc cctacattat accaccacca tgacaacacg tgtgtgtgct 420
tgtctggcta taggctgtta tgtcattggt ttcttgaatg cttctatcca aattggagat 480
acatttcgcc tctctttctg catgtccaat gtgattcatc actttttctg tgacaaacca 540
gcagtcatta ctctgacctg ctctgagaaa cacattagtg agttgattct tgttcttata 600
tcaagtttta atgtcttttt tgcacttctt gttaccttga ttctctatct gttcatattg 660
atcaccattc ttaagaggca cacaggtaag ggataccaga agcctttatc tacctgtggt 720
tctcacctca ttgccatttt cttattttat ataactgtca tcatcatgta catacgacca 780
agttccagtc attccatgga cacagacaaa attgcatctg tgttctacac tatgatcatc 840
cccatgctca gtcctatagt ctataccctg aggaacaaag acgtgaagaa tgcattcatg 900
aaggttggtg agaaggcaaa atattctcta gattcagttc tt 942

```

&lt;210&gt; 946

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g796 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 946

```

atgtaaaata actcaaagtt tactgatttc atcctggtag gtctaacc aa tgccacagaa 60
cttcagatcc cctcttttat cttgttcac ctcaccacc tcctcattct gactaggaac 120
ctggagatca tactgttgat cctgctggac tcttgctccc aattcccatg tactttttcc 180
tcagtaacct gtctctgctt ggataactaa ctgtcactcc cagggtcacg gctagcaggg 240
ctaggttact tagagggtag gaggctaagt tcctcgtaca atgcttgctg tgctcagatg 300
ttcttttttg tagccttggc cacagtggaa aatatcgctg ttgacatcaa tggcctatga 360
ccactatata gcagtgtgca aacccttaca ctacactacc accacgatag ccagtgtatg 420
tgctcatctg gtcataaggct cctatgtctg tggctttcta aatgcctccc tccgcatagg 480
ggacatattc agtctctctt tctgtaagtc caatcttgct catcaccttt tctgtgatgt 540
tccaccagtc atggctgtgt cttgctctgg taaacacatt agcaagaaga ttctggtttt 600
tatgtcaagc ttcaatgtct ttttggtctt tctagttatc ttgacctcct acctgttcat 660
attcatcacc atcttgaaga tgcactcagc tcagggaac ttaaaagctt tgtccacctg 720
tgcctctcac ctcatgagc tctccatctt ctatggaaact actatcttta tgcacttaca 780
gcctagctcc agccattcca tggacacaga tgaatggga tccttggtct atgctgtggt 840
catctccatg ctgaaccttg tgttctacag cctgaggagc aaagaagtca agaatgcatt 900
caaaaaggcg gttgagaagg caaaattttt cttagaactg tgattt 946

```

&lt;210&gt; 947

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g797 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 947

```

atggacaaca gcaactggac cagtgtgtcc cattttgttc tcttgggcat ttccaccac 60
ccagaagagc aaatcccact cttccttggt ttctcactca tgtacgcaat caatatttct 120
ggcaacttgg ccattcatcac actgattctc tctgtctcac gcctccacat ccccatgtac 180
atcttctcga gtaacttggc cttgacagac atctgcttca cctccaccac ggtccccaag 240
atgctgcaga ttattttctc cctacaaaag gtaatttctt acacaggctg tttagcccaa 300
acttatttct tcatttgctt cgcgctcatg gaaaacttca tcctggctgt gatggcctat 360
gacaggtaca ttgccatctg ccacctttc cactacacta tgatcctgac tagaatgctg 420
tgtgtgaaga tggtggtcat gtgccatgct ctctcccacc ttcatgccat gctgcatacc 480
tttctcatgg gccaaactaat cttctgtgca gataacagaa tccccactt cttctgtgac 540
ctctacgctc tgatgaagat ctctgcacc agcacctacc tcaacacct tatgattcac 600
acagaagggt ctgttgtaat cagtggagct ctggccttca ttactgcctc ctatgcctgc 660
atcatcctgg tggctcctcg gatccctca gccaaaggga ggtggaaaac cttttctacc 720

```

tgcggtcccc	acctcactgt	ggtggccata	ttctatggca	ccctcagttg	ggtctacttc	780
cgggcccttt	ccagctattc	agtgaccaag	ggtcgcatta	taacagtcgt	gtacacagtg	840
gtgactccca	tgctgaaccc	cttcactctac	agcctgagga	atggggatgt	caagggaggc	900
ttcatgaaat	ggatgagcag	aatgcagact	tttttcttta	ga		942

&lt;210&gt; 948

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g798 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 948

atgggttaacc	aaagctcccc	catgggcttc	ctccttctgg	gcttctctga	acacccagca	60
ctggaaagga	ctctctttgt	ggttgtcttc	acttcctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tcctgctgtc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
ctctctgacc	tctccttctt	ggacctctgc	tttaccacaa	gttggtgtcc	ccagatgctg	240
gtcaacctct	ggggcccaaa	gaagaccatc	agcttctctg	gatgctctgt	ccagctcttc	300
atcttctctg	ccctggggac	cactgagtgc	atcctcctga	cagtgatggc	ctttgaccga	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccaccccg	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggttatgagt	ctggttcaat	cgatagtcca	gacaccatcc	480
accctccact	tgcccttctg	tccccaccag	cagatagatg	actttttatg	tgaggtccca	540
tctctgatcc	gactctcctg	tggagatacc	tcctacaatg	aaatccagtt	ggctgtgtcc	600
agtgtcatct	tcgtggttgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
caggcagtgc	tgaggattaa	ctctgccaca	gcatggagaa	aggcctttgg	gacctgtctc	720
tcccatctca	ctgtggtcac	cctcttctac	agctcagtca	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcaact	840
ccttcactta	accctctcgt	atacaccctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaag	agactccagg	gaaagctgga	gagctgct		948

&lt;210&gt; 949

&lt;211&gt; 971

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g799 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 949

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatatggtc	120
acgggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	gctccacacc	180
ccccatgctt	tcttctcttc	caaactgtgc	tgagctgaca	tcggtttcac	cttggccatg	240
gttcccaaga	tgattgtgaa	catgcagtgc	catagcagag	tcactctctta	tgagggtctc	300
ctgacacgga	tgtctttctt	tgtccttttt	gcatgtatgg	aagacatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccagct	catcgtgaat	420
cctcacctct	gtgtcttctt	cgtcttggtg	tcctttttcc	ttagcccgtt	ggattcccag	480
ctgcacagtt	ggatttgtgt	actattcacc	atcatcaaga	atgtggaaat	cactaatttt	540
gtctgtgaac	cctctcaact	tctcaacctt	gcttgttctg	acagcgtcat	caataacata	600
ttcatatatt	tcgatagtac	tatgttttgt	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	ttgtcccttc	cattctaagg	atgtcatcgt	cagatgggaa	gtataaaggc	720
ttctccacct	gtggctctta	cctggcagtt	gtttgtctgat	ttgatggaa	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaatg	gtgtggtggc	gtcagtgatg	840
tatgctgtgg	tcaccccat	gctgaacctt	ttcatctaca	gcctaggaaa	gagggatata	900
caaagtgtcc	tgcgagggtc	gtgcagcaga	acagtcgaat	ctcatgatat	gttccatcct	960
ttttcttgtg	t					971

&lt;210&gt; 950

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g800 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 950

atggaaccag	agaatggtac	gaggatttta	ggattttctc	ttctgggact	ttcagaggaa	60
ccagaattgc	agcccggtat	gtttggactc	ttcctctcca	tgtatctgac	aactgtgttt	120
ggaaacctgc	tcatcctcct	ggccatctgc	tctgggtccc	acctccacac	ccccatgtac	180
ttcttctctc	ctaacctgtc	ctttgtagac	atctgtgtta	cctccaccac	agtcccaaag	240
acactgtcaa	acatccggac	acagagtaaa	gtcatcacct	atgcagggtg	catcacccag	300
atgtactttt	ttgtactctt	tatagtgttg	gacagcttac	tcttgaccgt	gatggcctat	360
gaccagtttg	tggccatctg	tcacccctcg	cactacacgg	tcatcgtgaa	ccctcggtc	420
tgtggactgc	tggttctggc	gtcctggatc	atgagtgcc	tgaattcctt	gata	474

&lt;210&gt; 951

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g801 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 951

atgatgagct	ttgcccctaa	tgtttcacac	tctccggttt	ttttgtcct	tgggttctcg	60
agagctaaca	tctcctacac	tctcctcttc	ttcctgttcc	tggctattta	cctgaccacc	120
atactgggga	atgtgacact	ggtgctgtc	atctcctggg	actccagact	gcactcacc	180
atgtattatc	tgttctgtgg	cctctctgtg	atagacatgg	ggctatccac	agttacactg	240
ccccagttgc	tggcccattt	ggtctctcat	tacccaacca	ttcctgtctc	ccgtgtcttg	300
gctcagttct	ttttcttcta	tgcatttggg	gttacagata	cacttgtcat	tgtgtcatg	360
gctctggatc	gctatgtggc	catctgtgac	cccctgcact	atgctttggt	aatgaatcac	420
caacggtgtg	cctgtctact	agccttgagc	tgggtggtgt	ccatactgca	caccatgttg	480
cgtgtgggac	tcgtcctgcc	tctttgctgg	actggggatg	ctgggggcaa	cgtaaacctt	540
cctcacttct	tttgtgacca	cgggccactt	ctgcgagcct	cttgttctga	cataattctt	600
aatgagctgg	ccatattctt	tgagggtggc	ttccttatgc	tgggcccctg	tgccctcatt	660
gtactctctt	atgtccgaat	tggggccgct	attctacgtt	tgccttcagc	tgtgtgtcgc	720
cgccgagcag	tctccacctg	tggatcccac	ctcaccatgg	ttggtttcct	ctacggcacc	780
atcattttgt	tctacttcca	gcctcccttc	cagaactctc	agtatcagga	catggtggct	840
tcagtaatgt	atactgccat	tacacctttg	gccaacccat	ttgtgtatag	cctccacaat	900
aaggatgtca	aggggtgcact	ctgcaggctg	cttgaatggg	tgaaggtaga	cccc	954

&lt;210&gt; 952

&lt;211&gt; 921

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g802 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 952

atgctgaata	caacctcagt	caccgaattt	ctcctcttgg	gagtgcagag	cattcaagaa	60
ctgcagcctt	ttctcttcgt	ggttttcttc	accatctact	tcatcagtgt	gactgggaat	120
ggagccgttc	tgatgattgt	catctccgat	cctagactcc	attcccttat	gtatttcttc	180
ctgggaaacc	tgtcctacct	ggatatctgt	tactctacgg	tgacactgcc	aaaaatgctg	240
cagaactttc	tctctacaca	caaagcaatt	tctttcttgg	gatgcataag	ccagcttcat	300
ttcttccact	tcctgggcag	cacggagtcc	atgttgttcg	ccgtgatggc	atttgacctc	360
tctgtggcta	tctgcaagcc	acttcgtctac	actgtcatca	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	ggtcattggt	tttttccatg	ccctgctgca	ctccgtaatg	480
acttctcgct	tgcaacttctg	tggttccaac	cgtatccatc	attttctctg	tgatattaag	540
ccattgctaa	agctggcctg	tgggaacact	gagcttaatc	agtggctact	cagtactgtc	600
acggggacaa	ttgccatggg	ccccttcttt	ctgacacttc	tctcctattt	ctacattatc	660

acttatctct	tcttcaagac	ccgttcttgt	agcatgctct	gtaaagcact	gtccacttgt	720
gcctcccact	tcatggtagt	tattcttttc	tatgcacctg	ttcttttcac	ctatatccat	780
cctgcgttag	agagcttcat	ggaccaggac	cggattgttg	ccatcatgta	cactgtggtc	840
actcctgtac	taaacccact	gatctatact	ttgaggaaaca	aggaagtga	gggggccttg	900
ggtagagtga	tcagaaggct	t				921

&lt;210&gt; 953

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g803 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 953

cagccacgga	atctcacaga	tgtctgagaa	ttcctcctca	tgggactctc	agaggatcca	60
gaactgcagc	ccgtcctcgc	tgggctgtcc	ctgtccatgt	atctggtcac	ggtgctgagg	120
aacctgctca	gcatacctggc	tgtcagctct	gactcccacc	tccacacccc	catgtacttc	180
ttcctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cggccacggg	tcccaagata	240
attgtggaca	tgcagtgcga	tagcagagtc	atctcttatg	tgggctgcct	gacacggatg	300
tcttttttgg	tcctttttgc	atgtatagaa	gacatgcttc	tgactgtgat	ggcctatgac	360
tgctttgtag	ccatctgtcg	ccctctacac	taccagtcga	tcgtgaatgc	tcacctccgt	420
gtcttcttag	ttttgggtgc	ctttttcctt	agcctgttgg	attcccagct	gcacagttag	480
attgtgttac	aattcacctt	cttcaagaat	gtggaaatct	ctaattttgt	ctgtgagcca	540
tctcaacttc	tcaagcttgc	ctgttctgac	agcatcatca	atagcatatt	catatatattc	600
gatagtacta	tgtttggttt	tcttcccatt	tcagggatcc	ttttgtctta	ctgtaaaatt	660
gttccctcca	ttctaaggat	ttcaacatca	gatgggaaat	ataaagcctt	ctccacctgt	720
ggctctcacc	tggcacttgt	ttgcttattt	tatggagcag	gcattggcgt	gtacctgact	780
tcagctgtgt	caccaccccc	caggaatggg	gtgggtgggt	cagtgatgta	cactgtgggtc	840
acccccatgc	tgaacccttt	catctacagc	ctgagaaaca	gggacattca	aagcaccctg	900
cggaggctgc	tcagcagaac	agtcgaatct	catgatctgt	tccatccttt	ttcttgtgt	959

&lt;210&gt; 954

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g804 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(984)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 954

atggcacctg	gaaatggctc	tttcgtgact	gaattcattc	tggcgggatt	aacacatcag	60
ccagatctcc	agtcacctct	gttcttccctg	tttctagtaa	tctatgtggg	cactctgttg	120
ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttctctt	tttaacttgc	cttcatagat	ctctgttatt	cttctgtgtt	tatacccaaa	240
atgctaata	actttatttc	agagaagaat	attatgtcct	tcaaggggtg	catgacccaa	300
ctttctcttt	nctgattttt	ttggtcattt	ctgaagggtta	tgtgctgacg	tcaatggcgt	360
atgatcgctg	tggccatctg	tacccccactt	ctgtatcaca	ttgccatgtc	tcctacagtg	420
tgtccagcgc	ttatgttttg	ttcctatttg	atgccttttt	ctggtgccat	ggccccacact	480
ggatgcagtc	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
atcctccctc	tgtccagct	ctcctgcacc	agcacctaca	tcaatgagct	ggtgggttttc	600
actgtgggtg	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatgggttc	660
atcctctcca	gcatacctcca	tatcagttcc	aaggagggtca	ggtccaaagc	tttcagcact	720
tgcagttccc	atataattgc	tgtttctctg	ttctttggat	cagggtgcatt	tatgtatctc	780
aaacctctct	ctgctgggtc	catgggataag	agaaaattat	cttctgtctt	ttatacaaat	840
gtggttccca	tgttgaacct	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960

agtcacaaga cagggatatt ctgt

984

&lt;210&gt; 955

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g805 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 955

atgggaagaa	ataacctaac	aagaccctct	gaattcatcc	tccttggact	ctcctctcga	60
cctgaggatc	agaagccgct	ctttgctgtg	ttcctcccca	tctaccttat	cacagtata	120
ggaaacctgc	ttatcatcct	ggccatccgc	tcagacactc	gtctccagac	gcccattgtac	180
ttctttctaa	gcatcctgtc	ttttgttgac	atttgctatg	tgacagtcac	tatccctaag	240
atgctggtga	acttcttata	agagacaaag	accatctctt	acagtgaagt	tctgaccag	300
atgtactttt	tcttagcctt	tggaaacaca	gacagttacc	tgctagcagc	catggccatt	360
gaccgctatg	tggccatatg	taatcccttc	cactacatca	ccattatgag	tcacagatgc	420
tgtgtccctg	tcttggttct	ctccttctgc	attccacatt	ttcactccct	cctgcacatt	480
cttctgacta	atcagctcat	cttctgtgcc	tcaaagtcca	tccatcactt	tttctgcat	540
gatcaaccag	tgctaaaatt	gtcctgttcc	tccatttttg	tcaaagaaat	cacagtaatt	600
acagaaggct	tggctgtcat	aatgaccccg	ttttcatgca	tcatcatctc	ttattttaaga	660
atcctcatca	ctgttctgaa	gattccttca	gctgctggaa	agcgtaaagc	atcttctacc	720
tgtggctctc	atctcacagt	ggtgaccctg	ttttatggaa	gcattagcta	tctctatttt	780
cagccctctg	ccaactatac	tgtcaaggat	caaatagcaa	caattatcta	caccgtactg	840
actcctatgc	taaatccatt	tatctatagt	ctgaggaaca	aagacatgaa	gcagggtttg	900
gcaaagttga	tgcacaggat	gaaatgtcag				930

&lt;210&gt; 956

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g806 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 956

atggaaattg	tctccacagg	aaacgaaact	attactgaat	ttgtcctcct	tggttcttat	60
gacatccctg	aactgcattt	cttggttttt	attgtattca	ctgctgtcta	tgtcttcata	120
atcataggga	atatgctgat	tattgttagca	gtgggttagct	cccagaggct	ccacaaacct	180
atgtatattt	tcttggcgaa	tctgtccttc	ctggatattc	tctacacctc	cgcagtgatg	240
caaaaaatgc	tggagggtct	cctgcaagaa	gcaactatct	ctgtggctgg	ttgcttgctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgctaccca	ctccactacc	cactcctgat	ggggcccaga	420
cggtagatgg	ggctgggtgt	cacaacctgg	ctctctggat	ttgtggtaga	tggactgggt	480
gtggccctgg	tggcccagct	gaggttctgt	ggccccaacc	acattgacca	gttttactgt	540
gactttatgc	ttttcgtggg	cctggcttgc	tcggatccca	gagtggctca	ggtgacaact	600
ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgtc	gagagttcct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgtcctc	cccacctagc	tgtagtgaac	acattctatg	gaacgctcat	gatcttttat	780
gttgaccctc	gtcgtgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcaccc	ctctcttcaa	tcctgtgatc	tataccatga	ggaacaagga	ggtgcatcag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

&lt;210&gt; 957

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g807 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 957

cactggaaaa	ttttaagaag	aaacagcaag	atgatacatg	aaattatata	gaccttatgc	60
caaatacctt	actcagagga	caaaacttgt	tacatacaga	tacaaagctt	gttttgtact	120
gacttggaag	tcccaaactt	tttctgtgaa	cttaattagg	tggtccaact	tgctgttct	180
gacacctttc	tcaaagacat	agtgaggat	tgtacaacta	tgctgctgag	tggtgggtccc	240
attgctggta	tttttttact	ctttctctaa	gatcatttca	tccatatgtg	caatcccatc	300
agctcagggg	aagcataaag	catttccac	ctgcgtgtct	cacctctcaa	atatgtcctt	360
attttattgt	aggagcacag	gattgtacct	tagttttgct	gctaccacac	actcatgctc	420
taatgcaact	gcctcagtg	ggcacactgt	ggttaaacc	ttactaaacg	ttttcatctt	480
aaagtcaagt	aataaagaca	taaaatgagc	tctgaaagta	ttcttcagag	gaaagcaatg	540
gaagcatcat	ttttcaaaaa	gtgca				565

&lt;210&gt; 958

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g808 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 958

atggaaaaaa	gaaatctaac	agttgtcagg	gaattcgtcc	ttctgggact	tcctagctca	60
gcagagcagc	agcacctcct	gtctgtgtct	ttctctctga	tgtatttagc	caccaccttg	120
gggaacatgc	tcatcattgc	gacgattggc	tttgactctc	acctccattc	ccctatgtac	180
ttcttcctta	gtaacttggc	ctttgttgac	atctgcttta	cgtegactac	agtccccaa	240
atggtagtga	atatcttgac	tggcaccaag	actatctctt	ttgcaggctg	cctcaccag	300
ctcttcttct	tcgtttcttt	tgtgaatatg	gacagcctcc	ttctgtgtgt	gatggcgtat	360
gatagatatg	tggcgatttg	ccaccctta	cattacaccg	ccagaatgaa	cctgtgcctt	420
tgtgtccagc	tagtggtctg	actgtggctt	gttacttacc	tccacgcctt	cctgcatact	480
gtcctaatag	cacagctgtc	cttctgtgcc	tccaatatca	tccatcattt	cctctgtgat	540
ctcaatcttc	tcctgcagct	ctcttgcctt	gacgtctcct	tcaatgtaat	gatcattttt	600
gcagtaggcg	atctattggc	tctcacgccc	cttgtctgta	tcctcgatc	ttatggactt	660
atcttctcca	ctgttctgaa	gatcacctct	actcagggca	agcagagagc	tgtttccacc	720
tgcagctgcc	acctgtcagt	ggtgggtgtg	ttttacggca	cagccatcgc	cgtctatttc	780
agcccttcat	cccccatat	gcctgagagc	gacactctgt	caacctcat	gtattcaatg	840
gtggctccga	tgtgtaatcc	tttcatctat	accctaagga	acagggatat	gaagagggga	900
cttcagaaaa	tgctttctca	gtgcacagtc	tttcagcag			939

&lt;210&gt; 959

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g809 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 959

atggatggag	gcaaccagag	tgaaggttca	gagttccttc	tcctggggat	gtcagagagt	60
cctgagcagc	agcagatcct	gttttggatg	ttcctgtcca	tgtacctggt	cacggtgggtg	120
ggaaatgtgc	tcatcactct	ggccatcagc	tctgattccc	gcctgcacac	ccccgtgtac	180
ttcttctctg	ccaacctctc	cttcactgac	ctcttctttg	tcaccaacac	aateccccaa	240
atgctgggtg	acctccagtc	ccataacaaa	gccatctcct	atgcagggtg	tctgacgcag	300
ctctacttcc	tggtctcctt	ggtggccctg	gacaacctca	tcctggctgt	gatggcatat	360
gaccgctatg	tggccatctg	ctgccccctc	cactacacca	cagccatgag	ccctaagctc	420
tgtatcttac	tcctttcctt	gtgttgggtc	ctatccgtcc	tctatggcct	catacacacc	480
ctoctcatga	ccagagtgac	cttctgtggg	tcacgaaaaa	tccactacat	cttctgtgag	540
atgtatgtat	tgtctgaggat	ggcatgttcc	aacattcaga	ttaatcacac	agtgtgtgatt	600
gccacaggct	gcttcatctt	cctcattccc	tttggattcg	tgatcatttc	ctatgtgctg	660
attatcagag	ccatcctcag	aataccctca	gtctctaaga	aatacaaaagc	cttctccacc	720
tgtgcctccc	atttgggtgc	agtctccctc	ttctatggga	cactttgtat	ggtataccta	780



aagccccctcc	atacctactc	tgtgaaggac	tcagtagcca	cagtgatgta	tgctgtgggtg	840
acacccatga	tgaatccctt	catctacagc	ctgaggaaca	aggacatgca	tggggctctg	900
ggaagactcc	tagataaaca	ctttaagagg	ctgaca			936

&lt;210&gt; 960

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g810 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 960

atgggaatgt	ccaacctgac	aagactctct	gaattttatc	tcttgggact	ctcctctcgg	60
tctgaagacc	agaggccact	ctttgccctc	tttcttatca	tatacctggt	cactttgatg	120
ggaaatctgc	tcatactctt	ggctatccac	tctgatccctc	gacttcaaaa	ccctatgtat	180
tttttccctaa	gcatcttgct	ctttgctgat	atttgctaca	caacagtcac	agtcccaaa	240
atgctcgtga	acttcttctc	agagaaaaag	accatttctc	atgctgaatg	tctggcacag	300
atgtatttct	tcctgggttt	tggaaacata	gatagttatc	tcctggcggc	tatggccatc	360
aaccgctgtg	tagccatttg	taacccattc	cattatgtca	ctgttatgaa	ccgcagatgc	420
tgtgtgttgc	tactagcatt	ccccatcact	ttctcctatt	tccactctct	cctacatgtc	480
ctcctgggtga	atcggtctac	cttttgtaca	tcaaatgtta	tccatcattt	tttttgtgat	540
gtcaaccctg	tgtgaaact	gtcctgctcc	tccacctttg	tcaatgaaat	tgtggccatg	600
acagaagggc	tggcctctgt	gatggctcca	tttgtctgta	tcatcatctc	ttatctaaga	660
attctcatcg	ctgttctcaa	gattccctca	gcagctggaa	aacacaaagc	cttctccacc	720
tgcagctccc	atctcactgt	ggtgattctg	ttttatggga	gtattagcta	tgtctatttg	780
cagcctttgt	ccagctatac	tgtcaaggac	cgaatagcaa	caatcaacta	cactgtgttg	840
acatcagtg	tgaacccatt	tatctacagt	ttaagaaaca	aagacatgaa	acggggctta	900
cagaaattga	taaacaagat	taagtctcaa	atgagtaggt	tctctacaaa	g	951

&lt;210&gt; 961

&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g811 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 961

atgctgaata	caacctcagt	cactgaattt	ctccttttgg	gagtgacaga	cattcaagaa	60
ctgcagcctt	ttctcttcgt	tgttttcctt	accatctact	tcatcagtg	ggctgggaat	120
ggagccattc	tgatgattgt	catctctgat	cctagactcc	attcccctat	gtattttctt	180
ctgggaaacc	tgtcctgcct	ggacatctgc	tactccagcg	taacactgcc	aaaaatgctg	240
cagaacttcc	tctctgcaca	caaagcaatt	tctttcttgg	gatgcataag	ccaactccat	300
ttcttccact	tcctgggagc	cacagaggcc	atgttggttg	ccgtgatggc	atttgaccgc	360
tttgtggcta	tttgcaagcc	acttcgctac	actgtcatta	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	gatgattgg	tttttccatg	ccctgctgca	ctccctaatt	480
acctctcgct	tgaacttctg	tggttctaac	cgtatctatc	acttcttctg	tgatgtgaag	540
ccattgctaa	agctgagctt	aatcagtgcc	tgctcagtac	tgctcacagg	acaatcgcca	600
tgggcccctt	ctttctcaca	ttactctcct	atttctacat	tatcacccat	ctcttcttca	660
agactcattc	tttttagcatg	ctccgcaaag	cactgtccac	ttgtgcctcc	cacttcatgg	720
tagttattct	tttgtatgca	cctgttctct	tcacctatat	tcatcatgce	tcagggaacct	780
ccatggacca	ggaccggatc	actgccatca	tgtatactgt	ggtcactcca	gtactaaacc	840
cactgatcta	cactttgagg	aacaagggaag	tgaagggggc	ctttaataga	gcaatgaaaa	900
ggtggccttg	gcctaaagaa	atcttg				926

&lt;210&gt; 962

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g812 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 962

tcagtggacc	aagtaaata	ctctctggta	acagaatttg	tattacttgg	acttgcacaa	60
tccttggaaa	tgcagttttt	cctttttctc	ttcttctctt	tattctatgt	gggaattatc	120
ctgggaaacc	tcttcattgt	gttcacagtg	atctttgatc	ctcacttaca	ctcccccatg	180
tatattctgc	tggccaacct	atcgctcatt	gacttgagcc	tttcatctac	cacagttcct	240
agggtgatct	acgatctttt	tactgattgt	aaagtatttt	ccttccataa	ttgtatgata	300
caaaagttct	ttatccatgt	tacgggagga	gttgaaatgg	tgctgctgat	agtcattgaa	360
tatgataggt	acactgcat	ctgcaagcct	ctccactatc	caactattat	gaatcccaaa	420
atgtgcatgt	ttttggtagc	agcagcttgg	gtcattgggg	tgattcatgc	tatgtctcag	480
tttgtttttg	tcataaatta	accttctgtg	gccctaataa	tgtagggagc	ttttattgtg	540
attttctctg	ggttattaaa	cttgcattga	tggacactta	cgggctagaa	tttgtggtca	600
ctgccaacag	tggattcata	tcgatgggca	ccttcttttt	cttaattgta	tcatacatct	660
ttattctggt	cactgtccaa	cgacattcct	caaagtattt	atccaaagca	ttcttcactt	720
cgtaggctca	catcacgcta	gtggttttgt	tttttgctcc	atgcatgttt	ctctacgtgt	780
ggcctttccc	tactaagtca	ttggataaat	tttttgccat	catgaacttt	gttgtcacc	840
ctgtctttaa	tcctgccatc	tatactttta	ggaacaaaga	tatgaagttt	gcaatgagaa	900
ggctgaatca	acatatctta	aattctatgg	agacgacata	acacatttgg	ttgatgagag	960
cacaggataa	atgccatgga	cca				983

&lt;210&gt; 963

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g813 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 963

atgtggatca	acaatcaaag	ctcgctagat	gatttttatcc	tattgggatt	ttctgaccgt	60
ccctggctag	agacacccct	ctgtaatctt	tctgggtggcc	tacatctttt	ccctatttgg	120
aaatatctcc	attatcctag	tttcccatct	ggatccccag	cttgacagtc	ccatgtactt	180
ttttgtctct	aatctatcct	ttctggacct	ctgctatacc	accagcactg	tcccacagat	240
gctggtcaac	ctccggggac	cagaaaagac	cattagctat	gggggttggt	ttgcccact	300
ctatatattt	ttggccctgg	gttctactga	atgcatactt	ctagccatca	tggcctttga	360
ccgttacgct	gccatattga	agccccctca	ctaccagtc	atcatgaacc	atagacgctg	420
tatccacatg	gctgctggca	cttggatcag	tggttttgct	aactcccttg	tccagtccac	480
tctcacagtg	gtggccccc	gatgtggaca	gagggtgttg	gaccatttct	tctgtgaagt	540
tccagccctt	ttgaaactag	cctgtattga	tattcgtgtg	aatgaaatgg	agctcaatgt	600
actaggcgct	ttgcttctcc	tgatgccact	cacctcatc	ctgggcactt	atgtgttcat	660
tgctcaggca	gtaatgagaa	tctgctctgc	tgaaagtcgc	tggaaggctt	tcaatacctg	720
tgccctcat	ttgctggtgg	tctccctctt	ctacttcaca	gccatcagta	tgatgtcca	780
gcctccctct	agctattctc	atgaccgggg	gaagatc			817

&lt;210&gt; 964

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g814 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 964

atgaatgtct	ctgagccaaa	ttccagcttt	gcttttgtaa	atgaatttat	actccaaggt	60
ttctcttggt	agtggaaca	tcagatcttc	ctcttctcac	tctttactac	aacatattga	120
ctgactataa	cagggaatgg	agccattgct	tttgtcctgt	ggtgtgaccg	gcgacttcac	180
actcccattg	acatgttctt	gggaaatttc	tcctttttag	agatatggta	tgtctcttct	240
acagttccca	agatgttggt	caacttcctt	tcagagaaaa	aaaacatctc	ctttgctgga	300
tgttttctcc	agttttatct	cttcttctct	ttgggtacat	cagaatgctt	gcttttgact	360

gtgatggcct	ttgatcagta	ccttgetatc	tgccgtccct	tgtctatcc	taatatcatg	420
actgggcac	tctatgccaa	actggtcata	ctgtgctggg	tttgtggatt	tctgtggttc	480
ctgatcccca	ttgttctcat	ctctcagatg	cccttctgtg	gccccaaacat	tattgaccat	540
gttgtgtgtg	acccagggcc	acgatttgca	ttggattgtg	tttctgcccc	aagaatccaa	600
ctgttttgct	acactctaag	ctcattagtt	atthttggta	acttctctct	tattattgga	660
tcctatactc	ttgtcctgaa	agctatgttg	ggatgacctt	caagcactgg	gagacataag	720
gccttctcta	cctgtgggtc	tcatttggct	gtggatcac	tgtgctatag	ctctcttatg	780
gtcatgtatg	tgagcccagg	actcggacat	tctacaggga	tgcagaaaat	tgaaactttg	840
ttctatgcta	tggtgacccc	actcttcaat	ccccttatct	atagcctcca	gaataaggag	900
ataaaggcag	ccctgaggaa	agttctgggg	agttccaaca	taatc		945

&lt;210&gt; 965

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g815 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 965

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcaactc	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaaag	tcattctctt	caagggtcgc	ctgtttcaga	tatttctcct	tcacttcttt	300
gggtgggagtg	agatgggtgat	cctcatagcc	atgggctatg	acagatatat	agcaatatgc	360
aaaccactaa	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggt	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggctcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaattgac	catccagcat	660
cgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattcccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

&lt;210&gt; 966

&lt;211&gt; 953

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g816 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 966

atgacattac	ccagcgatga	ctccactgtc	ccagtctctg	aattcctcct	catctgettc	60
cccaactttc	agagttggca	gcacttgctg	tccttgcccc	tcagcctcat	ttcctcctgg	120
ccatggggac	caacacccac	ccccccatc	accatccacc	tgagggcctc	tctgcacctg	180
cccctgtact	acctgccag	cctcctctcc	ctgtgggaca	tcgtgctctg	cctcaccgtc	240
atccccaagg	tcctggccat	cttctggttt	gatcttaggt	cgatcggtt	ccctgcctgc	300
ttccttcaga	tgttcatcat	gaacagtctc	ctccccatgg	agtcctgcac	attcatggtc	360
aaggactatg	atcattatgt	ggccatctgc	caccactgtc	agtacctgtc	catcatcact	420
catcaatttg	tgcccaaagc	tagtgtcttc	attgtgggtc	agaatgcttt	gctgctttca	480
cctgttcccta	ttctctctgc	ccagctccat	tactgtagga	aaaatgtgat	tgagaactgc	540
atctgtgcca	acctgtctgt	gtccaggctc	tcctgtgata	atttcaccct	taacagactc	600
taccaatttg	tggtggttg	gaccttctctg	ggctcggatt	tcatectcat	cttctctctc	660
tacaccttca	ttctaagagc	tgtgcttaga	ttcaaggtgg	agggggtggc	agtgaaggcc	720
ctgagcacat	ctggctccca	ctttatctct	ctcctctctc	tcagcacctg	ctgggtgtgg	780
tggtgacaaa	tgtggccaga	aagaaggtcc	ccatggacat	cctgatcctg	tttaatgtcc	840
ttcatccctt	tagtctctct	gcattaaacc	ctatcatatg	tggaattcaa	actaaagagt	900

taaagaagga attttagaag ttgctgcaga ggggcctttg aaaacacgga agg 953

<210> 967

<211> 954

<212> DNA

<213> Unknown (H38g817 nucleotide)

<220>

<223> Synthetic construct

<400> 967

aaacacaatc	acacggcagt	gaccaagggt	actgaattta	ttctcatggg	gattacagac	60
aaccctgggc	tgcaggtcc	actgtttgga	ctcttctca	tcatatatct	ggtcacagt	120
ataggcaatc	tgggcattgt	tatctttgac	ctactttgga	ctccaagcta	cacaccccca	180
tgtacttttt	ccttaaacat	ttggcaatca	ctgatctttg	gttactccac	tgtcattggg	240
ccccaagat	gttttagtgaa	acctcatatg	tgcacaaaga	acacaatttc	ttttacaatt	300
ggtatgcaa	tcacagagca	cgctttgaga	ggaacatcat	ctctcaccgc	ggcattctat	360
cagcaacgaa	caatgagccc	tacaaacca	tcactaaaca	acttctgaac	ccgatcatca	420
tgccagagaa	aatacgggag	gagcaataaa	ccgttcccga	gctcgataaa	acgtgtgcgc	480
cactatttct	caaaagggaag	tgagtcaaaa	cagtctccac	caaccagac	acaaccaaca	540
attgtcacgg	tgaagggacc	gctaaaatgt	gaatactccg	ttctgaaaaa	aagaaaataa	600
caataataaa	ggcgatgacc	gcaggaaccg	aacatgctca	tctccctctc	aattgttctc	660
atatactaca	tgttttattct	agtggccaat	ctcagaatga	actcaaggaa	agggaggtac	720
aaagccttct	ccacctgtag	ctctcatctg	acagtgggtga	tcatgttcta	tgggacattg	780
ttattttatt	acttgcaacc	caagtccagt	catactttgg	ctattgataa	aatggcctca	840
gtgtttttata	ccctgttgat	tcctatgctg	aatccgttga	tctacagcct	aaggaacaaa	900
gaagtaaaag	atgctctaaa	gagaacttta	accaatcgat	tcaaaattcc	catt	954

<210> 968

<211> 660

<212> DNA

<213> Unknown (H38g818 nucleotide)

<220>

<223> Synthetic construct

<400> 968

tccaacctgt	gctgggctga	catcggttcc	acctcggcca	tggttcccaa	gatgattgtg	60
gacatgcagt	ctcatagcag	agtcattcct	tatgcgggct	gcctgacacg	gatgtctttc	120
ttggctcctt	ttgcatgtat	agaagacatg	ctcctgactg	tgatggccta	tgactgcttt	180
gtagccatct	gtcgccctct	gcactacca	gtcatcatga	atcctcacct	ctgtgtcttc	240
ttcgttttgg	tgctcctttt	ccttagcctg	ttggattccc	agctgcacag	ttagattgtg	300
ttacaattca	ctttcttcag	taatgtggaa	attgctaatt	ttgtctatga	gccatctcaa	360
cttctcaacc	ttgactgttc	tgacaccgtc	atcaatagca	tatttatata	tttcgatagt	420
actgtttggg	tttcttccca	tttcagggat	cctttgtctt	agtataaaat	tgtcccctcc	480
attctaagga	tgtcatcgtc	agatgggaag	tataaagcct	tcgccacctg	tggtctctcac	540
ctagcagttg	tttgctgatt	tgatggaaca	ggcattggca	tgtacctgac	ttcagctgtg	600
tcaccacccc	ccaggaatgg	tgtggcggcg	tcagtgatgt	acgtgtgggt	caccccatg	660

<210> 969

<211> 933

<212> DNA

<213> Unknown (H38g819 nucleotide)

<220>

<223> Synthetic construct

<400> 969

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgatttctat	cacgtgcacc	cagctcatte	accaacccat	gtatttcttc	180

```

ctcaattacc tctcactctc cgacctttgc tacacatcca cagtgacccc caaattaatg 240
gttgacttac tggcagaaaag aaagaccatt tcctataata actgtatgat acaactcttt 300
accaccattt tttttggagg catagagatc ttcattctca cagggatggc ctatgaccgc 360
tatgtggcca tttgcaagcc cctgcactac accattatta tgagcaggca aaagtgtaac 420
acaatcatca tagtttggtg tactggggga tttatacatt ctgccagtca gtttcttctc 480
accatctttg taccattttg tggcccaaat gagatagatc actacttctg tgatgtgtat 540
cctttgctga aattggcctg ttctaataa cecatgatag gtctcttagt cattgctaata 600
tcaggcttaa ttgctttggt gacatttgtt gtcttggtgt tgtcttatgt ttttatattg 660
tataccatca gagcatactc tgcagagaga cgcagcaaag ctcttgccac ttgtagtctt 720
catgtaattg ttgtggctct gttttttgct cctgcattgt tcatctacat tagaccggtc 780
acaacattct cagaagataa agtgtttgcc cttttttata ccatcattgc tcccattgtc 840
aaccctctca tatacacgct gagaaacaca gagatgaaga acgccatgag gaaagtgtgg 900
tggtgtcaaa tactcctgaa aagaaatcaa ctt 933

```

&lt;210&gt; 970

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g820 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 970

```

cggaacttct ctttcttaga aatctcattt acaaccgtat gcatccccag atttctgggg 60
gcaattatca ccaggaataa gactatttcc tataacaact gtgcagccca actcttttct 120
tttatcttca tgggggtgac tgaattttac attttaactg ccatgtccta tgaccgctat 180
gttgccatct cgaagcccct tcattacaca tccatcatga acaggaaact ctgcactcta 240
cttgtgctgt gtgcctggct aagtgggttt cgcaccattt tcccaccctt tatgcttctc 300
ctccagctgg actactgtgc ttccaacgtc attgatcact ttgcatgtga ctattttccc 360
ctcttacaac tatcttggtc agatacatgg ctccatagaag taattgggtt ttactttgct 420
ttggttactt tgctgttcac tttggcatta gtgattttat cttacatgta cattatcagg 480
accattttga gaatcccgtc tgccagtcaa agaaaaaagg ctttctccac ttgttcttct 540
cacatgattg tcatttccat ttcttatgga agctgtatat tcatgtatgc taatccatct 600
gcaaaaagaa aggcatcatt gacaaaagga atagctattc tcaatacatc tgttgcccc 660
atgctg 666

```

&lt;210&gt; 971

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g821 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 971

```

ataattttgt gttttttcat cataggtaac tctcaggata attcccaaact gactttgatg 60
gataacattt cagaagtgtc agaattcgtt ctctgtgggt taacagatgt cctagagctt 120
caggtccctt tatttatcat ctttactgtc atttatctca ccactctggt tgggaacttt 180
gggatgatca tggtgattct gttggactcc cggtccaca ttcccatgta ctttttcctt 240
ggcaaaactc ctctgggtga cagtgtttgt cctgctagtc actggtcctt acatctgtgg 300
actctttcaa tctccatcc atgttgcttt tactttccat ctctcttctt gtcattctaa 360
tgtggttaac cacttttttt gtgatattcc accactctta gctctttctt gctctgatat 420
ttacgcacat gagattgtgc tcttcatatt ggcagcattt aatatctttt tcaactctct 480
gattatcttg aactcttatg tttttatttt tattgctatc ctgaggatgc attcagctga 540
gggacaaaag aaggtctttt ccacctgtgc ctatcacctc actactgttt ccatcttcta 600
tgggacaatc acctttatgt acttacagcc aagttctggt cattccatgg acacagacaa 660
aatctcatct gtgttctaca ccatggtcat ccccatgctt aaccctctag tctatagcct 720
gaggaacaaa gaagtccaga gtgcattcaa ggtggttatt ggaaaagcaa agtcttcatt 780
gggcttagcc tactattta 799

```

&lt;210&gt; 972

<211> 946  
 <212> DNA  
 <213> Unknown (H38g822 nucleotide)

<220>  
 <223> Synthetic construct

<400> 972

tggtaacctg	tcttcaacca	gtctgcccc	ctgagtttgt	gttcctgtgt	ttcaccacag	60
tccctgaatt	tcagggttctt	ctcttctctc	tcttctctct	cttctacttg	atgatcctct	120
gtggcaacac	agccatcatc	tgggttgtgt	gcacatacag	cggtctccga	accccaatgt	180
atttcttctt	gtccaacctg	tcctttgtag	agatctgcta	caccaccgtt	gtggtgccct	240
tgatgctttc	caacattttt	ggggcccaga	agcccattcc	attggctgga	tgtggggccc	300
aaatgttctt	ctttctcaca	cttgggtggt	ctgactgttt	cctcttggcg	atcgtggcct	360
atgaccgcta	tgtggccatc	tgccaccctt	tgcactaccc	ctcatcatga	cctgcaatct	420
gtgcgtgcag	atgctgggcg	gcgctgtggg	cctggccctc	ttcctctccc	tgcagctcac	480
cgccttaatc	ttcaccttgc	ccttctgcgg	ctaccgccag	gaaattaacc	acttctctct	540
cgatgtacct	ccggtcctgc	gcctggcctg	cgctgccatc	cgtgttcacc	aggctgtcct	600
ctatgtcgtg	agcatcctcg	tgctgaccgt	ccccttcttg	ctcatctgcg	tctcctacgt	660
gttcatcacc	tgtgccatcc	tgagcatccg	ttctgctgag	ggccgccacc	aggccttctc	720
cacctgctcc	tcccacctca	ccgtggctct	gctgcagtat	ggctgctgtg	ccttggcata	780
cttgcacccc	cagtcagct	cctctgcaga	tgaggatcgc	cagtttgccc	ttgtttacac	840
ctttatcaca	ccattactca	accctttgat	ttacaccctt	aggaacaagg	atgtcaaagg	900
tgccttgtaa	aaaagtgtc	agtaccaaag	ggacacctga	gtcctt		946

<210> 973  
 <211> 936  
 <212> DNA  
 <213> Unknown (H38g823 nucleotide)

<220>  
 <223> Synthetic construct

<400> 973

atgtagaaca	gtagagaggc	gtcacagttc	atcttctctag	gactaagcaa	tgtcccagaa	60
ctgcagggtcc	ccttctttat	catgtttgtt	ctcatctatc	tcatcaatgt	agttggaaac	120
ttggggatga	tcattttgat	tctctggtac	tctcagctcc	acaatccaat	gtacttcttc	180
ttcagtaate	tgtctctggt	agactttttt	tactcttcag	ttgtcactcc	aaaggtcatg	240
actgggctcc	ttagagaaga	caaaatcatt	tcctatactg	tgtgggctac	tcagacattc	300
ttttctgatt	cctttgccag	tgtggtaaat	ttattattgg	ccttaatggc	ctctggccac	360
tatgcagcag	tgtgcaaacc	cctgcattac	accaccacca	tgatgacaag	tgtgtgtaca	420
tgtctggcca	taggttgata	cgttgggtgt	ttcctgaatg	cctccattca	cactggggaa	480
acattcagtc	tctttctgta	tgtccagtga	agtccatcac	tttttctgtg	aggttccagc	540
agtcatggct	ctgtcttgct	ctgatagaca	tgtgaatgta	gtggttcttg	tttatgtaac	600
cagctcaata	tcctctttgc	ccttctagtt	atcttgatat	cctacttatt	gatgtttatc	660
accatcctaa	agatgcactc	aactgcagga	taccagaagg	ccttggccat	ttgtgcctct	720
cacctcactg	cagttgccat	cttctatggg	actattatct	tcatgcatat	acagcccagc	780
tccagtcatt	ccattgacac	agacaaaatt	gcagctgtgt	tttatactat	tgtcttcccc	840
atgggtgaacc	atgtgtgcta	aagattgaag	aacaagggtga	agagtacatt	caagaaaatt	900
gttgagaagg	taaaattgtc	cctaggattg	tgagtt			936

<210> 974  
 <211> 954  
 <212> DNA  
 <213> Unknown (H38g824 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(954)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 974

atggctgggg	aaaaccatac	tacactgcct	gaattcctcc	ttctgggatt	ctctgacctc	60
aaggccctgc	agggcccccct	gttctgggtg	gtgcttctgg	tctacctggg	caccttgctg	120
ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctcgc	gccaaactctc	agtgggtggag	ctcttctaca	ccactgacat	cgtgcccagg	240
accctggcca	atctgggctc	cccgcatccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	tcttcattgt	cctgggcatac	tcgagtgct	gcctgctcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgctatt	ccaccctctt	gagcccacgg	420
gcctgcattg	ccatgggtggg	tacctcctgg	ctcacaggca	tcatacaggg	ccaccaccca	480
tgcctccctc	atcttctctc	tacctttctg	cagccaccgg	atcatcccgc	actttctctg	540
tgacatcctg	ccagtactga	ggctggcaag	tgctgggaag	cacaggagcg	agatctccgt	600
gatgacagcc	accatagtct	tcattatgat	cccccttctt	ctgattgtca	cctcttacat	660
ccgcatcctg	gggtccaatc	tagcaatggg	cctcacccag	agccgcccga	agtcttctcc	720
acctgctcct	cccataggct	cgtgggtctct	ctcttctttg	ggacagccag	catcacnnac	780
aaccggccgc	aggcaggctc	ctctgaaacc	acagaccgcg	tcatacagtct	cttcnacaca	840
gtcatcacac	ccatgctcaa	ccccatcata	aacacccacg	ggaacaagga	cgtgaggagg	900
gcctcgcggt	acttggtgaa	gaggcgccgc	ccctcgccgg	gaagggggctc	gggt	954

&lt;210&gt; 975

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g825 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 975

atggagacaa	agaattatag	cagcagcacc	tcaggcttca	tcctcctggg	cctctcttcc	60
aaccctaagc	tgcaaaaacc	tctctttgcc	atcttctcca	tcattgtacct	actcactgcg	120
gtggggaatg	tgctcatcat	cctggccatc	tactctgacc	ccaggctcca	cacccttatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagattatct	cttatgtggg	ctgcctgac	300
cagatgtact	tcttcattggc	atttgggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtgggttat	gaaaccatgg	420
cattgcctac	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacacccagc	ctgtgctaaa	gctctcctgc	tctgacacat	cctccagcca	gatgggtggg	600
atgactgaga	ccttagctgt	cattgtgacc	cccttcctgt	gtaccatctt	ctcctacctg	660
caaatcatcg	tactgtgct	cagaatcccc	tctgcagcca	ggaagtggaa	ggccttctct	720
acctgtggct	cccacctcac	tgtagtggc	ctgttctatg	ggagtgtcat	ctatgtctat	780
tttaggcctc	tgtccatgta	ctcagtgatg	aagggccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaaaagg	900
ggtttgaaga	aattaagaca	cagaatttac	tca			933

&lt;210&gt; 976

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g826 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 976

atgaaaaata	aaaccgtggt	aactgagttt	atccttctgg	gtctaacaga	tgtccctgaa	60
ctccagggtg	cagttttcac	ctttcttttc	cttgcgatt	tactcagcat	ccttggaat	120
ctgactatcc	tcacccctcac	cttgctggac	tcccaccttc	agactcccat	gtatttcttt	180
ctccggaact	tctccttctt	ggaaatttcc	ttcacaaca	tcttcattcc	aagggctcctg	240
attagcatca	caacagggaa	caagagtatc	agctttgctg	gctgcttcac	tcagtatttc	300
tttgccatgt	tccttggggc	tacagagttt	taccttctgc	tgccattcct	atgaccgcta	360

tgtgccatct gcaaactgat gactatgcac

390

&lt;210&gt; 977

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g827 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 977

atggagataa	agaactacag	cagcagcacc	tcaggcttca	tcctcctggg	cctctcttcc	60
aaccctcagc	tgcagaaaacc	tctcttttgc	atcttctcca	tcattgtacct	gctegctgcg	120
gtggggaatg	tgtcatcat	cccggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aaggttatct	cctatgtggg	ctgcctggcc	300
cagatgtact	tctttatggc	atgtgggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtggttat	gaaaccacgg	420
cattgcctgc	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacacccagc	ctgtgctaaa	gctctcctgc	tctgacacat	cctccagcca	gatggtggtg	600
atgactgaga	ccttagctgt	cattgtgacc	cccttctctg	gtatcatctt	ctcctacctg	660
cgaatcatgg	tcactgtgct	cagaatcccc	tctgcagccg	ggaagtggaa	ggccttctct	720
acctgtggct	cccacctcac	tgcagtagcc	cttttctatg	ggagtattat	ttatgtctat	780
tttaggcccc	tgtccatgta	ctcagtgggt	agggaccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaagagg	900
ggtttgaaga	aattacagga	cagaattttac	cgg			933

&lt;210&gt; 978

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g828 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(939)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 978

atgccaaata	agattgtggt	gactgagttc	ttcctcacia	ggcctgacgg	attacaaaag	60
agctttcagg	tggtgtttt	tctgtccct	gatgcttgc	ataccttggt	actgtctctg	120
ggaacctgaa	tcattcatcag	ccatgacctt	gctggacacc	cgcatgcaga	catctatgta	180
cttatttttc	cagaatctgt	cctgcttaga	aatttgttcc	agacagtcat	cgtgccaag	240
atgctgtca	acattgcca	ggggaccaag	accgttagct	ttgctgggtg	cattaccag	300
gactttttcc	acatcttctg	ggggccacag	agttcttctc	cctgacagcc	atggcctatg	360
accagtatat	tgccatctgc	aagcccttcc	actaccccat	gctcataagt	agtagagtct	420
gcacacagct	catcctcacc	tgtgtgttac	taggtttctc	cttcatcatc	atgcctgtca	480
tcctgaccag	tcagcttcca	ttctgtgata	cccacatcaa	gcatttcttc	tgtgactaca	540
cgccctctaat	ggaggtggtc	tgcagtgggc	caaagtgct	ggagatgggtg	gattttaccc	600
tgcccttagt	agcactgttt	ggcaccttgg	tactcatcac	cctgtcctat	gtccagatca	660
tcagacaat	tgtcagaatc	cccgtgttcc	aggagaggaa	gaaggctttc	tctacctgtt	720
cctctcatgt	cattatgggt	accatgtgtt	atgacagctg	cttctttatg	tatgtcaagc	780
cctctccagg	aaagtgggtt	gatgtcaaca	angggagtgt	ctctaataca	tacaattatt	840
gccccactgt	taaatccctt	catctgtact	ctgaggaacc	aacaagttaa	gcaggtaatg	900
aaagacctag	tcagaaaaat	gactttgtcc	gaaaataaa			939

&lt;210&gt; 979

&lt;211&gt; 951

&lt;212&gt; DNA



<213> Unknown (H38g829 nucleotide)

<220>

<223> Synthetic construct

<400> 979

atgaactcag	agaacctcac	ccgggcccgcg	gttgcccctg	ctgaattcgt	actcctgggc	60
atcacaaatc	gctgggacct	gcgtgtggcc	ctcttctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcattggatgc	ccggctccac	180
acacctatgt	acttcttctc	ggccaacctc	tccctgctgg	atgcctgcta	ttcctccgcc	240
atcggcccca	agatgctagt	ggacctgctg	ctgcccgcag	ccaccatccc	ttacacagcc	300
tgtgcccctc	agatgtttgt	ctttgcaggt	ctggctgata	ctgagtgttg	cttgctggca	360
gccatggcct	atgaccgcta	cgtggccatc	agaaaccac	ttctctatac	aacagctatg	420
tcgcagcgtc	tatgcctggc	cttgctggga	gcattcagcc	tgggtggggc	agtgagtgcc	480
tttgttcaca	caacctcac	cttcgcctg	agcttctgcc	gctcccggaa	gatcaatagc	540
ttcttctgcg	atatccctcc	actgctggcc	atctcgtgca	gtgacaccag	tctcaatgaa	600
ctccttctct	tcgccatctg	tggcttcac	cagacagcca	cgggtgttagc	tatcacggtg	660
tcttatggct	tcattcgtgg	ggctgtgatc	cacatgcgct	cggctcaggg	cagtcggcga	720
gcagcctcca	cgggtgggtc	ccacctcaca	gccgtggcca	tgatgtacgg	gacactcatt	780
ttcatgtacc	tgcgcccag	ctccagctat	gccctggaca	ctgacaagat	ggcctctgtg	840
ttctataccc	tggtcattcc	gtctctcaac	ccactcatct	acagcctccg	caataaggag	900
gtcaaggagg	ccctcaggca	gacctggagc	cgattccact	gtccagggca	g	951

<210> 980

<211> 948

<212> DNA

<213> Unknown (H38g830 nucleotide)

<220>

<223> Synthetic construct

<400> 980

atgggtgatc	tgtcctggga	aaaccaaacy	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttctct	tttatgataa	ttttagtgtt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagtgttag	tcagacatca	tctccacacc	180
cctatgtact	tctcctgggt	gaacttgtcc	tgtctggaga	tctggtatac	ctctaaccac	240
atccccaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaa	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcattcaggt	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcattct	tcttgcatgg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atcccatctt	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattgcc	780
acataccttg	tgcctcagc	caactcatcc	caactcttgt	gcaaaagggtc	ctctctgtct	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggtg	tttgcctt		948

<210> 981

<211> 925

<212> DNA

<213> Unknown (H38g831 nucleotide)

<220>

<223> Synthetic construct

<400> 981

gagtaaatgg	gaacaagtaa	taatgttaca	gaatttgtcc	tcccaggcct	ctctcaggat	60
cctgatgtgc	aaaaagcatt	atttgtaatg	tttttactca	catacaatgt	gactatgggtg	120
ggcaaccttc	tcattgtggg	gaccattatt	gccatgcctc	ccttggtgactc	cccagtgtcc	180

ttcttctctg	catgcctgtc	atattattgat	gctgtatatt	ccacttcctt	ttcccctaag	240
ttgatgatag	acttactctg	tgataaaaaa	gactgtttct	ttcctggctt	gcattgggcca	300
gctattttata	aactacccat	ttgggtggtat	tgagggtctt	cttttggtgg	gtatggcctg	360
tgatcactat	gtggacatct	gtaagctact	gcactatttg	accatcatga	actggcaggt	420
ttgcacctc	ctgtttatgg	tggtgtgtgac	tgagggtttt	tgacattctat	gtttcaaatt	480
gttgttgtgt	acagtctccc	ttctgtggc	cccaatgtca	ttgaccattt	tgtgacatgt	540
accattatt	ggaaatgggtg	tgactgaca	cttactttat	aggcctcact	gtgattgcca	600
atgggtggagc	agtctgtatg	gtcatcttca	tccttctact	aatctcctat	ggagtcaccc	660
taaactccct	taaaacttat	agtcaggaag	gcgggcataa	agccctgtct	acctgcagct	720
ccaacattac	tggtgtgtcc	ccttttttga	tcctgtatt	ttcatctatg	ttagacctga	780
ttcaaacttt	cctattgata	aattcatgac	tgtgttttat	acaattatca	cacctatgtt	840
gaatccatta	atatacacac	tgagaaattt	agagggtgaga	attgctgtga	aaaatctctg	900
gtgtaaaaac	taaactatag	taaga				925

&lt;210&gt; 982

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g832 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 982

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgaggagatgc	atccttttct	tttttggttc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcattgtgtt	cacagtaatt	attgactctc	atttaaattc	cccaggctact	180
gcctactggc	caacatttat	cttcttgatc	tggtctctct	cctacagtcc	tgactttttc	240
actaactgca	gcacatttcc	ttttccaaga	tgcatgatac	agatattttt	catttgtgtc	300
atgctgtaaaa	attgagatgg	tgctgctcat	aaccatggca	tagagcaggt	acactgcca	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tactttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagtaggt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagacac	ttacaaacta	gaggttgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttatttaata	atatcctata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttgttc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgagggttct	900
agcaggatgt	cataataaat	ggtgcataac	cagagtgcac	gatgattcag	tctcacca	958

&lt;210&gt; 983

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g833 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 983

atggaaggaa	taaataaaac	tgcaaagatg	cagtttttct	ttcgtccatt	ctcacctgac	60
cctgagggtcc	agatgctgat	ttttgtggtc	ttcctgatga	tgatctgac	cagcctcggt	120
ggaaatgcta	caattgcagt	cattgttcag	atcaatcatt	ccctccacac	ccccatgtac	180
tttttcttgg	ctaactctggc	agttctagaa	atcttctata	catcttccat	cacccatttg	240
gccttggtcaa	acctcctttc	aatgggcaaa	actcctgttt	ccatcacggg	atgtggcacc	300
cagatgtttt	tctttgtctt	cttgggtggg	gctgattgtg	tcctgtgggt	agtcattggct	360
tatgaccggt	ttatagcgat	ctgtcacctc	ctgcgataca	ggctcatcat	gagctgggtcc	420
ttgtgtgtgg	agctgctggg	aggctccttg	gtgctggggg	tcctgttggt	actgccactc	480
accattttta	tcttccatct	cccattctgc	cacaatgatg	agatctacca	cttctactgt	540
gacatgcctg	cagtcacgag	cctggcttgt	gcagacacac	gcgttcacaa	gactgctctg	600
tatatcatca	gcttcatcgt	ccttagcacc	cccctctcat	tgatctccat	ctcctatgtc	660
ttcatcgtgg	tagccatttt	acggatccgg	tcagcagaag	ggcgccagca	agcctactct	720

acctgctctt	ctcacatctt	agtggctctc	ctgcagtatg	gctgcaccag	ctttatatac	780
ttgtccccc	gttccagcta	ctctcctgag	atgggcccgg	tggtatctgt	ggcctacaca	840
tttatcactc	ccattttaaa	ccccttgatc	tatagtttga	ggaacaagga	actgaaagat	900
gccctaagga	aagcattgag	aaaattc				927

&lt;210&gt; 984

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g834 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 984

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctggga	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactccccc	180
atgtatattc	tgtggccaa	cctatcgctc	attgacttga	gcctttcacc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagttgaaa	tggtgctgct	gatagtcacg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tggtgcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagcttttat	540
tgtgattttc	ctcgggttat	taaacttgca	tgcatggaca	cttatgggct	agaattttgtg	600
gtcactggca	acagtggatt	catatcgatg	ggcaccttct	ttttcttaat	tgtatcatatc	660
atttttattc	tggtcactgt	ccaacgacat	tcctcaaatg	atztatccaa	agcattcttc	720
acttcgtagg	ctcacatcac	cgtagtgggt	ttgttttttg	ctccatgcat	gtttctctac	780
gtgtggcctt	tcctactaa	gtcattggat	aaattttttg	ccatcatgaa	ctttgttgtc	840
accctgtct	taaatcctgc	catctatact	ttaaggaaac	aagatatgaa	gtttgcaatg	900
agaaggctga	atcaacatat	tttaaattct	atggagatga	cataacacat	ttggttgatg	960
agagcacagg	ataaatgcca	tggacca				987

&lt;210&gt; 985

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g835 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 985

tccatgtact	tcttctgac	aaactttgca	ggctctggaga	tcttctactt	tttcaccatt	60
gcccctctga	ctctggccaa	tgctctaccc	atggggagaa	acctcatttc	cctgcccggc	120
tgtggaggcc	agatgttctt	cttcactctc	ctgggaaggg	ctgactgcat	cctgctggcc	180
gtcatggcct	ttgactgggt	tgtggccatc	tggtgtcctc	tctgttacgg	cctcatcatg	240
agctggaggt	tgtgtgtcca	gctgaccctg	gggtctctgc	tggtgggggt	cttcttagcc	300
atgcagctga	ccgtgcttat	cttccaactc	cctttatgca	gcagcaaaga	aatcagcacg	360
ttctactgtg	atgtcctccc	tgctatgaga	ctggcctgtg	cagataacctg	ggtccatgag	420
gccactatgt	ctatggtcag	caccaccttt	ctcaccgtcc	ccttctctgct	catcactctt	480
tcctatgtct	ccatcatggc	cgccatcttg	aagatttgct	ctgcagaggg	gaggcacaag	540
gccttctcca	cctttcctcc	cacctgactg	tggttctcct	ccaggactga	tgtacacgcc	600
tcgccttctt	gtgtcccagc	tctagctact	atcctgagag	gggccaggca	gtgtctgtgg	660
tttacacctt	cattaccctt	gtgctgaacc	ctttgatcta	cagcatgagg	aacacagaac	720
ttaaggatgc	tttgaagaga	gcaatgacga	gggtcccgtc	gctctaaaca		770

&lt;210&gt; 986

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g836 nucleotide)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 986

atggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgata	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggtctg	cttggttcaga	tatttctcct	tcacttcttt	300
ggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggtctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtctt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgtctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaatagac	catccagcat	660
tgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgtctacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcaccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

&lt;210&gt; 987

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g837 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 987

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atctttttct	tttttgggtc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacattttat	cttcttgatc	tgggtcttct	cctacagttc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcatgatac	agatattttt	catttgtgtc	300
atgcgtaaaa	attgagatgg	tgctgtcat	aaccatggca	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tcctttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagtaggt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagatac	ttacaaacta	gaggttgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atacctata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttgttc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgagggttct	900
agcaggatgt	cataataaat	ggtgcatatc	cagagtgcac	gatgattcag	tctcacca	958

&lt;210&gt; 988

&lt;211&gt; 982

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g838 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 988

ctttctattt	gcttctttct	ttgcatattt	tcagctgata	tttaatctat	gctagccatg	60
gaacaaaata	atggcactga	agtgactgaa	ttcattctcc	tgggatttgc	tggtcaacac	120
aagtcttggc	atatcctctc	catagcattt	ctagcaatct	atgtgggttac	cccagtaggt	180
aatattggaa	tgatcctact	tatcaaaatt	gatgcttctc	ttcatatccc	catgtaaatt	240
ttctcccaac	acttggcatt	tgttgatctc	tgttacacct	ctgctatcac	tcccaagatg	300
ttgaaaaact	ttgtagaaac	aaaaaaatct	atctcatgta	taggatgtat	ggtgcaatta	360

ctagtttatg	gtactttgca	acaagtgact	gctacatcct	ggctgctatg	gcagtagacc	420
gttatgtggc	cttctgtaac	ccactccatt	atccaggggt	tatgtcccag	agactctgca	480
ttaagctatt	agtttagttca	tatgtcatgg	gtttccctaaa	tgccctctata	aacataagtt	540
tcactttctc	attgaacttc	tgcaaatacca	aaacaattaa	tcactttttc	tgtgatgaac	600
ctccaattat	tgccctacca	tgctccaata	ttgacctcaa	catcatgtta	ttaacagtat	660
ttgtgggatt	aaatttgatg	tgcaactgtga	tggtgggtcat	catttcctgc	atatatgtcc	720
tggttgccat	cctgaggata	tcttctgctg	caggggaagaa	aaaagtctct	ctacatgtgc	780
ctcccacctg	acagcagtca	ccatttttcta	tgggggttctc	tcttacatgt	atctatgcca	840
tcgtattaat	gagtctcaaa	aacaagaaaa	agtggcctct	gtgttttatg	gcattattat	900
tcccatgtta	aacccttga	tttacagcca	gagaaaccaa	gatgtgattg	aagccataaa	960
actaacagaa	aaaaagtatt	tc				982

&lt;210&gt; 989

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g839 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 989

atgatttctt	tccttgtagc	aggtctaattg	gaagaggaaa	accagagggg	agtggtagac	60
ttccacttcc	acttcttttc	aacagacctg	gtgggtggctt	cctttataat	tgtggccttg	120
atgttgacc	agaagcctt	gttggaact	tcacctttgg	gcccacagtc	tggaagatc	180
ccttctcca	tattccaatg	tatttatttt	tatttttttg	gcattgacta	tgttggaat	240
tggtactacc	accaacattt	ctcctcaac	actggctacc	gtcctttaca	tggaagat	300
gcttatctcc	ctccctggct	atggaaactca	gatgctcttt	gtcatccttt	tgagaggatc	360
tgagtgtgtc	ttgcttgctg	tcattggctta	tgataggat	ataaccatct	gtcatccatt	420
caattacaat	ctcatcatga	gtgggtagct	ctgtgggcag	atgactttgg	gctctttgag	480
gctgggattc	ctgttgtagc	tggttttgac	tatgttgatc	tgacaccctc	cattctgtgg	540
cctaataaaa	cctaccactt	cttctgtgac	atgcccacag	caagtgcctg	gtctgtgcag	600
acaccacatg	catgagtcag	ctctctgact	tcctgtgggc	caccatcacc	atccctctcc	660
ttcctccttg	tctgcctccc	ctatggctgc	cttgacagcca	ccatcttgag	gatgcattca	720
gctaagagaa	agcactaggc	cttctctacc	agttcctccc	acctcattgt	ggttctcctg	780
aagtattggg	gttgcatcct	catctgcctt	tgccccagct	ctagttactc	cccagaggag	840
ggctgggagg	tatctcttgt	tcacatgttt	ttctccgggt	gtggaatccc	ttgatctata	900
gcgtatggaa	ccaagacgta	actgatgcag	tagagagact	tgtggcaaga	atgtccttgt	960
tctaacagcc	agaaatattc	cttcttaaaa	aatatattccc	taacta		1006

&lt;210&gt; 990

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g840 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 990

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgc	60
caatccttgg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactcccc	180
atgtatatcc	tgttgcccaa	cctatcgctc	attgaacttga	gcctttcacc	taccacagtt	240
cctagggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacagga	ggagttgaaa	tggtgctgct	gatagtcatg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaacccc	420
aaaaatgtgc	tgtttttggg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagctttttat	540
tgtgattttc	ctcgggttat	taaaacttgc	tgcatggaca	cttatgggct	agaattttgtg	600
gtcactgcca	acagtggatt	catatcgatg	ggcaccttct	ttttcttaat	tgtatcatac	660
atttttatcc	tggtcactgt	ccaacgacat	tctcaaatg	atttatccaa	agcattcttc	720
acttcgtagg	ctcacatcac	cgtagtgggt	ttgttttttg	ctccatgcat	gtttctctac	780

gtgtggcctt tccctactaa gtcattggat aaattttttg ccatcatgaa ctttgttgtc	840
accctgtct taaatcctgc catctatact ttaaggaaca aagatatgaa gtttgcaatg	900
agaaggctga atcaacatat tttaaattct atggagatga cataacacat ttggttgatg	960
agagcacagg ataatgcca tggacca	987

&lt;210&gt; 991

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g841 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 991

atgcaatcag aacaccttgc agaattttca gaattcctca ttttgagcct ctgaggagat	60
ccagaactgc agccccctct tgggctgttt ctgtccatga acctgggtcac agtgcttgga	120
aacctgctca ttatcctggc catcagttct gactcccacc tccacaagcc tatgtacttc	180
ttactctcca aattgtccat ggctgccatt tgttttgtct tcacatgat ccaaaagatg	240
atggtaaacc tcagggcaca gagcaaagac atctttactc agccaagtgg tagtccaatt	300
ccattctaaa tgtgtagtct tatcagattt cttctaattc agcagaaatc tgtgtttta	360
atcttcgaat actcactggg tctaattctc ctatttgaat ctgaagatgt aaactaatta	420
ttcttttgta tgagcctttc aaaataattg aagacagtta tgccttttc ttgataatca	480
ccatactttc ttcacactaa ttgatacaca attgttaata agtcatggat tttctactca	540
aacaaccttt attctatcat cttatgcttc tggttatgca acagttgact ctcaatgctt	600
tatttatttt ttaaactatga tgattactat taacctcttt gtaagattta aaaatatctt	660
tatgcacagt agtatctcaa taaattacaa ctattatttt aaaaaataaa ataaagggtgg	720
tatctatgag atatat	736

&lt;210&gt; 992

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g842 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 992

atggtgactg aattcatttt tctgggtctc tctgattctc aggaactcca gaccttcta	60
tttatgttgt tttttgtatt ctatggagga atcgtgtttg gaaaccttct tattgtcata	120
acatgggtat ctgactccca ccttcaactct cccatgtact tcctgctagc caacctctca	180
ctcattgac tgtctctgtc ttcagtcaca gcccccaaga tgattactga ctttttcagc	240
cagcgcaaag tcatctcttt caagggctgc cttgttcaga tatttctcct tcacttcttt	300
ggtgggagtg agatgggtgat cctcatagcc atgggctttg acagatatat agcaatatgc	360
aaacccctac actacactac aattatgtgt ggcaacgcat gtgtcggcat tatggctgtc	420
gcatggggaa ttggctttct ccattcgggt agccagttgg cctttgccgt gcacttacc	480
ttctgttggt ccaatgaggt cgatagtatt tatttggacc ttcctagggg aatcaaaactt	540
gcctgtacag atacctacag gctagatatt atggtcattg ctaacagtgg tgtgtctact	600
gtgtgttctt ttgtttctct aatcatctca tacactatca tcctaataac catccagcat	660
cgccctttag ataagtcgtc caaagctctg tccactttga ctgtcacat tacagtagtt	720
cttttgttct ttggaccatg tgtctttatt tatgcctggc cattcccat caagtcatta	780
gataaattcc ttgctgtatt ttattctgtg atcacccctc tcttgaacct aattatatac	840
acactgagga acaaagacat gaagacggc ataagacggc tgagaaaatg ggatgcacat	900
tctagtgtaa agttt	915

&lt;210&gt; 993

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g843 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 993

atggctgcag	gaaatcactc	tacagtgaca	gagttcattc	tcaagggttt	aacgaagaga	60
gcagacctcc	agctccccct	ctttctcttc	ttcctcggga	tctacttggg	caccatcgtg	120
gggaacctgg	gcatgatcac	tctaatttgt	ctgaactctc	agctgcacac	ccccatgtac	180
tactttctca	gcaatctgtc	actcatggat	ctctgctact	cctccgtcat	tacccttaag	240
atgctgggtga	actttgtgtc	agagaaaaac	atcatctcct	acgcaggggtg	catgtcacag	300
ctctacttct	tccttgtttt	tgtcattgct	gagtgttaca	tgctgacagt	gatggcctac	360
gaccgctatg	ttgccatctg	ccaccctttg	ctttacaaca	tcattatgtc	tcatacacacc	420
tgcttctgtc	tggtggctgt	gggtctacgcc	atcggactca	ttggctccac	aatagaaact	480
ggcctcatgt	taaaactgcc	ctattgtgag	cacctcatca	gtcactactt	ctgtgacatc	540
ctccctctca	tgaagctgtc	ctgctctagc	acctatgatg	ttgagatgac	agtcttcttt	600
tcggctggat	tcaacatcat	agtcacgagc	ttaacagttc	ttgtttctta	caccttcatt	660
ctctccagca	tcctcggcat	cagcaccaca	gaggggagat	ccaaagcctt	cagcacctgc	720
agctcccacc	ttgcagccgt	gggaatgttc	tatggatcaa	ctgcattcat	gtacttaaaa	780
ccctccacaa	tcagttcctt	gacccaggag	aatgtggcct	ctgtgttcta	caccacggta	840
atccccatgt	tgaatcccct	aatctacagc	ctgaggaaca	aggaagtaaa	ggctgccgtg	900
cagaaaacgc	tgaggggtaa	actgttt				927

&lt;210&gt; 994

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g844 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 994

atggcagcca	aaaactcttc	tgtgacagag	tttatcctcg	aaggcttaac	ccaccagccg	60
ggactgcgga	tccccctctt	cttcctgttt	ctgggtttct	acacggtcac	cgtgggtggg	120
aacctgggct	tgataaccct	gattgggctg	aactctcacc	tgacactcc	catgtacttc	180
ttccttttta	acctctcttt	aatagatttc	tgtttctcca	ctaccatcac	tcccaaaatg	240
ctgatgagtt	ttgtctcaag	gaagaacatc	atttccttca	cagggtgtat	gactcagctc	300
ttcttcttct	gcttctttgt	cgtctctgag	tccttcaccc	tgtcagcgat	ggcgtatgac	360
cgctacgtgg	ccatctgtaa	cccactgttg	tacacagtca	ccatgtcttg	ccagggtgtg	420
ttgtcctttt	tggtgggtgc	ctatgggatg	gggtttgctg	gggccatggc	ccacacagga	480
agcataatga	acctgacctt	ctgtgctgac	aaccttgtca	atcatttcat	gtgtgacatc	540
cttcctctcc	ttgagctctc	ctgcaacagc	tcttacatga	atgagctggg	ggtctttatt	600
gtgggtggctg	ttgacgttgg	aatgcccatt	gtcactgtct	ttatttctta	tgccctcatc	660
ctctccagca	ttctacacaa	cagttctaca	gaaggcagg	ccaaagcctt	tagtacttgc	720
agttccacaa	taattgtagt	ttctcttttc	tttgggtctg	gtgctttcat	gtatctcaaa	780
cccccttcca	tcctgcccct	cgagcaaggg	aaagtgtcct	ccctgttcta	taccataata	840
gtccccgtgt	taaacccatt	aatctatagc	ttgaggaaca	aggatgtcaa	agttgccctg	900
aggagaactt	tgggcagaaa	aatcttttct				930

&lt;210&gt; 995

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g845 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(473)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 995

atgggagaag	caaggaacag	gacagtagtc	caggaattta	tcctggaggg	atttctctgt	60
gtccagcatc	tggggaatgt	ccttttctctg	gtgcacctgc	tggcatacct	ggcctccatc	120
atggcaaaaca	tgctcataat	caccatcacc	tgggctgacc	atcacctcca	gacacctatg	180

tattttcttc	tcagcagttt	ttccttctgt	gaatgctgtt	ttatcaccac	agttattcct	240
aaacttcttg	tcattccttc	tttcaggcag	ggcaaataat	cccccttct	actaccttgt	300
ctcatgcagt	ccccctttca	tttttatntt	cttgggtcaa	cagtttttct	tcccttaatg	360
gctgtgatgt	ccccttggat	tgatactgg	ccatttgcaa	gcctctgcat	tactccacca	420
tcatgagcct	gaggactagc	ttccacaagg	tcactgctg	gctttgtcct	ggg	473

&lt;210&gt; 996

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g846 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 996

acagaccac	agaatctaac	aacagatgct	tcaatattcc	tcgtcctaga	actctcagag	60
gatccagaac	tacagccggt	cctcgctggg	ctgttcctgt	ccatgtgcct	ggcatgggtg	120
ctggggaacc	tgctcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgctt	gacatgggtt	cacctccacc	atgggtcccca	240
agatgattgt	ggacatccaa	tctcacagca	gtcatctcct	atgcgggctg	cctgactcag	300
atgtctcttt	ttgccatttt	tggaggcatg	gaagaaagac	atgctcctga	gtgtgatggc	360
cctatgaccg	gtttgtagcc	atctgtcacc	ctctatatta	ttcagccatc	atgaacccat	420
gtttctgtgg	ctttctagtt	ctgttgtctt	gttgtctcag	tcttttagac	tcccagctgc	480
acaatttgat	tgccttgcaa	attacctgct	tcaaggatgt	ggaaattcct	aatttcttct	540
gtgacccttc	tcaactcccc	caccatgcgt	gttgtgacac	cttcaccaat	aacatagtca	600
tgtatttccc	tgctgccata	tttggttttc	ttcccacctc	ggggatcctt	ttctcttact	660
ataaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggaactat	aaagccctct	720
ctgcctgtgg	gtctcacctg	tcagttgttt	gcttatttta	tggaaacaggc	gttggagggt	780
acctcagttc	agatgtgtca	tcttccccca	gaaagggtgc	agtggcctca	gtgatgtaca	840
cgggtgtcac	ccccatgctg	aacccttcca	tctacagcct	gagaaacagg	gatattaaaa	900
gtgtcctgcg	gcgcctgcac	ggcagaacag	tctaacttca	atatcttatt	atctgttcca	960
ttccttttgt	agtggtgggt	taaaaaggca	gcaaggctc			998

&lt;210&gt; 997

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g847 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 997

agtcaactgt	cccttatgga	cctcatgctc	atctgcacca	ctctacccaa	gatgatcttc	60
agctacttgt	ctgggaagaa	atctatctct	ctggcagggt	gtggaaactca	gatattcttc	120
tatgtgtccc	tgcttgagac	tgaatgtttc	ttgttggtcg	tcattggctta	tgaccgctat	180
gtggctatat	gtcaccctct	tcagtacacc	atcctcatga	atccggaact	ctgtgtcttc	240
atgactgttg	cttctctggac	cttgggggtct	cttgatggga	tcattagtgt	tgacagctgc	300
ctgtcatttt	cttactgcag	ctctctggaa	attcatcatt	ttttctgtga	tggtgtgtcc	360
cttttacctc	tatcctgcac	agaaacatct	gcatttgaaa	gactacttgt	catttgttgt	420
gtggtaaatgc	taatctttcc	agtttcagtt	atcatacttt	cctattccca	tgctcttcga	480
gccgtcatcc	acatgggctc	tggggaaagt	cgtcgcaagg	ccttcactac	ctgctcctcc	540
cacccgtctg	tggtcggact	ctactacggt	gctgctatgt	tcattgtacat	gagaccagct	600
tctaaacata	cgccagacca	ggacaagatg	gtgtcggcct	tctacactaa	tctcaccctc	660
atgctg						666

&lt;210&gt; 998

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g848 nucleotide)

&lt;220&gt;



## &lt;223&gt; Synthetic construct

## &lt;400&gt; 998

cttgccctgca	tagttggata	gaagtttgca	tttattattt	ctccaaacca	tcacttcatg	60
ataatgggtca	cattcatttt	agttaacatt	taaaaacatt	cttcaggaaa	cttatccagt	120
gctcttatca	ttttgttcat	tttcatccct	gttggtttctc	tatttttcac	tccatgcgta	180
gttctctatg	tttggcctac	tttgccacca	tcacttgata	aaaatatgtt	cattgttgac	240
tttggttgca	accctgtctt	gaagcctgcc	acctacatat	tacagaacaa	agacataaag	300
gtagcacttt	gaaatttgca	tgaaaagaga	acttattcca	gc		342

## &lt;210&gt; 999

## &lt;211&gt; 915

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g849 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 999

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaaag	tcattctctt	caagggctgc	cttgttcaga	tatttctcct	tcacttcttt	300
gggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcggtg	agccagttgg	cctttgcegt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggt	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaattgac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattcccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcaccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

## &lt;210&gt; 1000

## &lt;211&gt; 669

## &lt;212&gt; DNA

## &lt;213&gt; Unknown (H38g850 nucleotide)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1000

tccaacctgt	ccttgectga	catcggtttc	ccctcccca	cggccccaa	gatggttggtg	60
gacatccaat	ctcacagcag	tcattctcct	atgcaggctg	cctgactcag	atgtctctct	120
ttgccatttt	tggaggcatg	gaagagacac	atgctcctga	atgtgatggc	ctatgtccgg	180
tttgtagcca	tctgtcaccc	tctatatcat	tcagccatca	tgaaccctgt	tttctgtggc	240
ttcttacttt	tgttgtcttt	tttttttctc	agtcttttag	acgcccagct	gcacaacttg	300
attgccttac	aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctt	ctgtgacctt	360
tctccactcc	cccatcttgc	atgttggtgac	accttcacca	ataacataat	catgtatttc	420
cctgctgcc	tatttggttt	tcttccatc	tcggggaccc	ttttctctta	ctataaaatt	480
gtttcctcca	ttctgagggt	ttcatcatca	ggtggaagt	ataaggcctt	ctccacctgt	540
gggtctcacc	tgctgggtgt	ttgctgattt	tatggaacag	gcgttggagg	gtacctcggt	600
tcagatgtgt	catcttcccc	gagaaagagt	gcagtggcct	cagtgatgta	cacggtgggtc	660
acccccatg						669

## &lt;210&gt; 1001

## &lt;211&gt; 986

## &lt;212&gt; DNA

<213> Unknown (H38g851 nucleotide)

<220>

<223> Synthetic construct

<400> 1001

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttg	aaatgcagtt	tttccctttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctggga	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactcccc	180
atgtatattc	tgttgccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccctcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagtggaaa	tggtgctgct	gatagtcag	360
gaatatgata	ggtacactgc	gatctgcaag	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tggttcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	ttaaccttct	gtggccctaa	taatgtgggg	agcttttatt	540
gtgattttcc	tgggtttatt	aaacttgcat	gcattggacac	ttacgggcta	gaatttgtgg	600
tcactgcaa	cagtggtatc	atatcgatgg	gcaccttctt	tttcttaatt	gtatcataca	660
tttttattct	ggtcactgtc	caacgacatt	cctcaaatga	tttatccaaa	gcattcttca	720
cttcgtaggg	tcacatcacc	gtagtgggtt	tggtttttgc	tccatgcatg	tttctctacg	780
tgtggccctt	ccctactaag	tcattggata	aatgttttgc	catcatgaac	tttgtgtgca	840
cccctgtctt	aaatcctgcc	atctatactt	taaggaacaa	agatatgaag	tttgcaatga	900
gaaggctgaa	tcaacatatt	ttaaattcta	tgagagcgac	ataacacatt	tggttgatga	960
gagcacagga	taaatgccat	ggacca				986

<210> 1002

<211> 659

<212> DNA

<213> Unknown (H38g852 nucleotide)

<220>

<223> Synthetic construct

<400> 1002

agtgtgctgt	ctattttctga	gacctattat	accgtggcca	tcaacccccca	aatgctgtcc	60
ggtctcctca	gtcctcaaca	aaccatctcc	atcccaggct	gtgccgctca	gctctttttc	120
tatctcactt	ttggtgtcaa	taaagtcttc	ctgctcacag	ccatggggta	tgaccactat	180
gtggccatct	gcaaccctct	acagtattca	gtcatcatgg	gcaaaaaggc	ttgtatacaa	240
ctggtcagtg	gacccctgaa	cattggcctg	agcacagcta	tcattcagg	gtcttctgta	300
ttcagccttc	ccttctgtga	tgctaatttc	atctccact	tcttttgtga	tatccggccc	360
ataatgaagc	ttgcctgtgc	agacactact	atcaaggagt	ttattacttt	gctcatcagt	420
ctctgtgtcc	ttgttctgcc	catggtattg	atcttcatct	cctatgtcct	aattgtcacc	480
accatcctca	agattgcac	agctgagggc	ggagaaaggc	ctttgtact	tgtgcctcac	540
acctcacagt	ggtcattgtc	cactatggcc	gtacttcttt	catctaccta	aaacccaaat	600
cccaaaattc	cctgcaggac	agacttatct	ctgtgacata	cactgttatt	actcctctg	659

<210> 1003

<211> 939

<212> DNA

<213> Unknown (H38g853 nucleotide)

<220>

<223> Synthetic construct

<400> 1003

atgtctacgt	ctaatacac	ccagttccat	ccttcttcat	tcctactgct	gggtatccca	60
gggctagaag	atgtgcacat	ttggattgga	gtcccttttt	tctttgtgta	tcttgttgca	120
ctcctgggaa	acactgctct	cttgtttgtg	atccagactg	agcagagtct	ccatgagcct	180
atgtactact	tcctggccat	gttggtatcc	attgacctgg	gcttgtctac	agccaccatc	240
cccaaaatgt	tgggcattct	ctggttcaat	accaaagaaa	tatcttttgg	aggctgcctt	300
tctcacatgt	tttcttccat	gctatgggaa	gcattgtggt	gggtggcatg		360
gcctttgacc	gctacattgc	catttgcaaa	cctcttcggg	acaccatgat	cctcaccagc	420

aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcctgtacat	ggttgttcca	480
ctgggtgtttc	tccttctgag	gctgcccttc	tgtgggcatc	gtatcatccc	tcatacttat	540
tgtgagcaca	tgggcattgc	ccgtctggcc	tgtgccagca	tcaaagtcaa	cattagggtt	600
ggccttggca	acatatctct	cttgttactg	gatgttatcc	ttattattct	ctcctatgtc	660
aggatcctgt	atgctgtctt	ctgccctgcc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtgggt	ctcatattgg	tgttatctta	gcctttttta	caccagcatt	tttttcattc	780
ttgacacatc	gttttggcca	taatatccca	cagtatatac	atattatatt	agccaacctg	840
tatgtgggtg	tcccaccagc	cctcaatcct	gtaatctatg	gagtcaggac	aaagcagatt	900
cgagagagag	tgctgaggat	ttttctcaag	accaatcac			939

&lt;210&gt; 1004

&lt;211&gt; 877

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g854 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1004

tacatgataa	ccatcttatg	ggaaatatct	aagccagtaa	ataatatattt	tctaacactt	60
tctgtaagat	atcaaagtct	aatcactact	gtgtcataat	tgtaaatgaa	attataatat	120
aaatttactg	agtttttctg	agtaccta	gagttaaaaa	atatgggagc	atatgtagta	180
ctgtgcttgt	atcaatatgg	ataaggtatc	tggaagtctt	ttctgaacat	ctttcgggtgc	240
tgctgagatt	attccactga	tggggatggg	ccatggctgc	tatgtgacca	tctgactgc	300
atgaaaatca	tgactcaata	taggtgtggc	catcttgctg	gaatggcatg	cactggaaga	360
tttatccagg	cacagtttag	atcctctccc	cagcttgact	tcctttctat	aattccaatg	420
tcacaatatg	aatagcccat	tcatatgtga	cttaaacact	ttgttgaagc	tcctctgcat	480
aggtagtatg	atacacttgg	tctctttgtt	gctgccaatg	atgggttcaa	ctgcctgtta	540
aacatcatct	tcttgatggg	ttcttaagtg	gccatcctat	atactttgaa	atcccacagc	600
ttggaggaaa	gatacaaagc	tctctctacc	tggtgtctctc	acaccaccgt	ggccatctaa	660
ttctttgtgt	tctgtatact	tgtttatctg	tgcccagtga	cccttcccga	gtcagtaaag	720
cagtggctgt	gctttacacc	atgataacgc	ctacattaaa	ccctttagtc	taaccctcag	780
aatgacagag	gtgaaaagtg	ttgagaaact	tctgggtcaa	aagatgactt	gaagagagaa	840
ataatccaaa	cataagatga	ttttactctt	tcaatgg			877

&lt;210&gt; 1005

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g855 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1005

atggagaaga	aaaagaatgt	gactgaattc	atttttaatat	gtcttacaca	gaaccccata	60
atggagaaaag	tcacgtttgt	agtatttttg	gttcttttaca	tgataaacact	ttcaggcaac	120
ctgctcattg	tgggttaccat	taccaccagc	caggctctga	gtcccccat	gtacttcttc	180
ctgacccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtggattcct	ttcaagagaa	gaaaatcatc	tcctttaatg	ggtgtatggc	tcaagcctat	300
gcagaacaca	tttttggtgc	tactgagatc	atcctgctga	cagtgtatggc	ctgtgactgc	360
tatgtggcca	tctgcaaacc	tctgaactac	acaaccatta	tgagccacag	cctgtgcatt	420
ctcctgggtg	cagtggcctg	ggtgggagga	tttcttcatg	caactattca	gattctcttt	480
acagtatggc	tgcccttctg	tggccccaat	gtcataggcc	acttcatgtg	tgacttgtac	540
ccattgttaa	aacttgtttg	catagacact	catacccttg	gtctctttgt	tgctgtgaac	600
agtgggttta	tctgcttatt	aaacttcctt	atcttggtgg	tatcctatgt	gatcatcttg	660
agatctttta	agaacaatag	cttggagggg	agggtgaaag	ccctctccac	ctgtatttct	720
cacatcatag	tagttgtctt	attctttgtg	ccctgtatat	ttgtgtatct	gcgctcagtg	780
accactctgc	ccattgataa	agctgttgct	gtattttata	ctatgggtgg	cccaatgtta	840
aatcccgtgg	tctacacact	cagaaatgct	gaggtaaaaa	gtgcaataag	gaagctttgg	900
agaaaaaaag	tgacttcaga	taatgat				927

<210> 1006  
 <211> 738  
 <212> DNA  
 <213> Unknown (H38g856 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1006  
 tgtattcaac aacattgac tccactttgt ctctgcatgt tctcctttta ttttaatttg 60  
 taccattttt ttcccaaata aaagtacttg cactcactta gagatgctga aataaattga 120  
 ttggtataaa gtaaggatc tgattaacca aatttacact aaagccaatt ggccttttca 180  
 tggattataa cactatgcac aaccactcca tactcaaaca tgcatttctt tctccaatgt 240  
 tatatgatgc agcacctagc tctttacagg acattttttt cttgggtggg cacagatttt 300  
 ccttctgttg gtgatggcct aggccactat agggccatct gcaagtcctt gcagtatttg 360  
 gttgtcatga agcaatggct gtgtgttggt ctgctgggtg tgctcctggg tggaggattt 420  
 ttgcacatag taattcaact tggacttatt tatgggctcc catcttatga cccaatgctc 480  
 attggtcatt ttatttgtga catggacccc ttaatgaagc ttgtctgtga ctacacactc 540  
 aacagatttg cctatttttg aggtcatgat taaatactag gttttatgta ttctacttat 600  
 gctcagactg gactgtttcc ttttgggtgat tgcacctcat tattcttttg tcattttttc 660  
 cctagaggac ttggttctat aaatcttgct atacatagtt attatccctg tggcatctct 720  
 agagatacgg agcctacc 738

<210> 1007  
 <211> 786  
 <212> DNA  
 <213> Unknown (H38g857 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1007  
 ctaattgtag tcaccgtaac tgtcagtgag accctgggct caccaatgta cttcttttctt 60  
 gctggccttat catttataga tatcatttat tcttcatcca tttccacag attgatttca 120  
 gacttggtct ttgggaataa ttccatatcc tcccatctt gcttggccca gctctttaca 180  
 gagcaccttt ttggtgggtc agaggtcttt cttctgttgg tgatggccta tgaccttgca 240  
 ttacttggtt atcatgagac aatgggtgtg tgttttgctg ctggtagcgt cctgggttgg 300  
 aggatttctg cactcagtat ttcaacttag tgttatttat gggctcccat tctgtgacgt 360  
 caatgtcatt gatcattttt tctgtgatat gcacccttta ttgaaactgg tctgtactga 420  
 taccatgtt attggcctct tagtgggtgc caatggagga ctagggttga ctatttgtgt 480  
 tctgtcttta ctcatctct atgggtgcat ctgcactctc taaagaacct tagtcagaaa 540  
 gggaggtgaa aagccctctc aacctgcagt tccacataa ctgtgggtgt tttcttcttt 600  
 gttccctgta tttttatgta tgctagacct gctaggacct tccccattga caaatcagtg 660  
 agtgtgtttt atacagtcac aactccaatg ctgaaccctt taatctacac tctgagaaat 720  
 tctgagatga caagtgtat gaagaagctc tggagaagag acttcatatc aagtagtaca 780  
 taagtg 786

<210> 1008  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g858 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1008  
 atgagacaga ataataatat tacagaattt gtccctcttg gcttctctca ggatctggat 60  
 gtgcaaaaag cattatttgt catattttta ctcacatact tggtagacag ggtggggaac 120  
 ctgctcattg tggtagactat tattgccagc ccttcttgg gctcctcaat gtacttcttc 180  
 cttgcctgcc tgtcatttat agatgctgca tattccacta caatttctcc caaattgatt 240  
 gtagacttac tctgtgataa aaagactatt tctttcccag cttgcatggg ccagttattt 300

atagaccagc	ctggatggcg	gagctgaggt	cgtgcttctt	gtgggtgaagg	cctgtgatca	360
ccatgtggac	atctggaagc	cactgcgcta	tctcgactat	catgaatcga	cagggctgaa	420
tgggctgct	cgtggctgtc	gtcgactcg	aggtgttctg	cattcgctgt	ctcatattgt	480
gagtgtgat	acagtctcgc	ctactgtggc	cccaatgtca	ttgactactt	tgtctgtgac	540
atgtacccag	ttattggaac	tggtatgcac	tgacacctac	tttattggcc	ttactgtttt	600
tgtcaatggt	ggaacaatct	gtatagtcgt	cttcaccctt	ctactaatct	cctatggagt	660
catcctaaac	tcccttaaaa	cttacagtca	agaaggagg	cataaagtcc	tgtttacctg	720
cagctccac	attatcgtct	ttgccctctt	ttttgttccc	tgtattttca	tgtatgttag	780
acctgtttca	aacatccctt	tgataaatc	ctgacagtgt	tttatacagt	tatcacaccc	840
atgttgaatc	ctttaatata	cacattgaga	aattcagaga	tgagaaatc	tgtagaaaca	900
ctcttgtgta	aaaagttaac	tgtattagag				930

&lt;210&gt; 1009

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g859 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1009

atgcagagga	gcaatcacac	agtgactgag	tttatactgc	tgggcttcac	cacagaccca	60
gggatgcagc	tgggcctctt	cgtgggtgtc	ctgggcgtgt	actctctcac	tgtggttagga	120
aatagcacc	tcacgtgtt	gatctgtaat	gactcccacc	tccacacacc	catgtatttt	180
gtcgttgaa	atctgtcgtt	tctggatctc	tggtattctt	ctgtctacac	cccaaagatc	240
ctagtgatct	gcattctctga	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
ttcttctctg	cagggctggc	ctatagttag	tgctgcttac	tggctgccat	ggcttatgac	360
cgctacgtgg	ccatctccaa	gcccctgctt	tatgccagg	ccatgtccat	aaagctgtgt	420
gcattgctgg	tagcagtctc	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
aaaacgtttt	cctttaactt	ctgccgtgaa	aacatcattg	atgacttttt	ctgtgatattg	540
cttcccttgg	tggagctggc	ctgtggcgag	aaggggcggt	ataaaattat	gatgtacttc	600
ctgctggcct	ccaatgtcat	ctgccccgca	gtgctcatcc	tggcctccta	cctctttatc	660
atcacagtg	tcttgaggat	ctcctcctcc	aagggtacc	tcaaagcctt	ctccacatgc	720
tcttcccacc	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgtcttc	780
cccagatcta	gctattcttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttccccatgt	tgaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	tccca					915

&lt;210&gt; 1010

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g860 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1010

atgatctgtg	aaaatcacac	cagagtcact	gaatttatcc	ttcttggttt	tacaaacaac	60
cccagatgc	aagtttccct	ctttattttt	ttcttggcca	tttatcacagt	cactttgttg	120
ggcaactttc	ttattgtcac	agttaccagt	gtggatctcg	cacttcaaac	acccatgtac	180
ttctttcttc	aaaatctgtc	acttcttgaa	gtatgtttca	ccttggttat	ggtgccaaaa	240
atgctttag	atctagtgtc	cccaaggaaa	attatctctt	ttgtgggctg	tggtacccag	300
atgtacttct	tcttcttctt	tggcagttct	gaatgtttcc	ttctctccat	gatggcttat	360
gatcgctttg	tggccatctg	taacctcttc	cattattcag	tcataatgaa	caggtcccta	420
tgcttgtgga	tggccatagg	ctcttggatg	tccggtgttc	ctgtgtctat	gctacagaca	480
gcttggtatg	tggcccttcc	tttctgtgga	ccaaatgccg	tggaccactt	tttctgtgat	540
ggtccccccag	tgttaaaact	agtcacagtg	gatacaacca	tgtatgaaat	gcaagcactt	600
gcctccacac	tcctgtttat	catgtttccc	ttttgtctca	ttttggtttc	ctacaccctc	660
attatcataa	caattctgag	gatgtctctc	gccactggcc	gccagaaggc	attttctact	720
tgttctctac	acctcattgt	ggtgtccctc	ttctacggaa	cagccagtct	gacctacctg	780
cggcccaaat	caaaccagtc	ccctgagagc	aagaagctag	tgctattgtc	ctacactgtc	840

atcacaccta tgctaaaccc catcatctac ggcctgagga acaatgaagt gaaaggggct 900  
gtcaagagga caatcactca aaaagtctta cagaagttag atgtgttt 948

<210> 1011

<211> 927

<212> DNA

<213> Unknown (H38g861 nucleotide)

<220>

<223> Synthetic construct

<400> 1011

atggcgaata gaaacaatgt gacagagttt attctattgg ggcttacaga gaatccaaaa 60  
atgcagaaaa tcatatttgt tgtgttttct gtcactaca tcaacgccat gataggaaat 120  
gtgctcattg tggtcacat cactgccagc ccatcactga gatcccccatt gacttttttc 180  
ctggcctatc tctcctttat tgatgcctgc tattcctctg tcaatacccc taagctgac 240  
acagattcac tctatgaaaa caagactatc ttattcaatg gatgtatgac tcaagtcttt 300  
ggagaacatt ttttcagagg tgttgaggtc atcctactta ctgtaatggc ctatgaccac 360  
tatgtggcca tctgcaagcc cttgcactat accaccatca tgaagcagca tgtttgtagc 420  
ctgctagtgg gagtgtcatg ggtaggaggc tttcttcacg caaccataca gatcctcttc 480  
atctgtcaat tacctttctg tggtcctaat gtcataagac actttatgtg tgatctctac 540  
actttgatca atcttgctc cactaatacc cacactctag gactcttcat tgctgccaac 600  
agtgggttca tatgcctgtt aaactgtctc ttgctcctgg tctcctgcgt ggtcatactg 660  
tactccttaa agaccacag cttagaggca aggcatagaag cctctctac ctgtgtctcc 720  
cacatcacag ttgtcatctt atcctttata cctgcatat ttgtgtacat gagacctcca 780  
gctactttac ccattgataa agcagttgct gtattctaca ctatgataac ttctatgtta 840  
aacccttaa tctacacctt gaggaatgct caaatgaaaa atgccattag gaaatttgtg 900  
agtaggaaag ctatttcaag tgtcaaa 927

<210> 1012

<211> 488

<212> DNA

<213> Unknown (H38g862 nucleotide)

<220>

<223> Synthetic construct

<400> 1012

tggaaaaatc atttcacctc tgtgaattgt ggttttgcca tctgcagagc tgaatgttaa 60  
ccatagccca agatactaag tattatagga ttgaaatgaa atataaatga aactttgtaa 120  
atgttaaatt ataacacaaa tcatatggtc agtgtcgatg tcctaattgt tcctaactcc 180  
tcatcacact ctctacttcc ttcatgtgg ctgccatcct gatatccgct ctgcagaggg 240  
gaggcacaa gcttttccca cctgctcctt ccacctggtt taattctcct ccagcacaat 300  
gaacaagcct cacctatttg tgccccagct ccactctctc ttatgagagg ggcaaggtag 360  
tgtctacggt ttacacatgc atcactcctg tgccaaaccc cttgatctgc agcatgagga 420  
agaagggaact caagcatgct cttaaaaaaa aagaagaaat tgcaagggtc ttgctgctca 480  
gaacacat 488

<210> 1013

<211> 953

<212> DNA

<213> Unknown (H38g863 nucleotide)

<220>

<223> Synthetic construct

<400> 1013

atgttttagct ctgagccac catagatgga aatcagtcct tgtgtgcca attcacattt 60  
gtggcttttt cttctataga agaattacag cttgtactct tcattgtgtt cttaatcatc 120  
acttatgcac tataggagga aatatcatca tcatctccct gatctggatc acccctgccc 180  
tgcacactcc aatgtatttc ttcctggtga acctctcatt tctggagatg tgctatacca 240

ccagtgtggt	gcctcatgct	ggtgcacctg	ctggtggaga	ccaaaaccat	aagtgtgggt	300
ggctgtgcaa	cccagatgta	catatttgcc	atcttgggac	tgacagaatg	ctgcttgcta	360
gcagctatgg	cttacgacg	ctttgtagct	atttgttacc	cactgcatta	cactctcttc	420
atggggccctc	gtgtttgttt	gaaattggct	gcagcatctt	ggttcactgg	agtgggtgtg	480
gagtcagccc	agatcacccct	gatcttcaact	ttgcctttct	gtggaacagg	aaagattcaa	540
cacttttttg	tgacataatg	cctgtactga	aactggcttg	tattgatacc	tcccaaattg	600
aaattgtgat	gttttctctc	tccgtgctat	ttattgtgag	tccttgtttc	ctcattctgt	660
gctcccacat	gcacatccct	gtgaccatct	tgagaatccc	ttcagcagct	ggaagacaca	720
aagctttctc	cacttgttct	tctcatatct	tgggtgtttc	tctgttctat	ggcactgcct	780
tgttcactta	tctgcaacct	aagactgcac	acactccaga	aacagacaaa	gcaactgcac	840
tcattgtacac	aatgggtcac	cctgctttga	atcctgttat	ctataccttg	aggaacaagg	900
aagtaaagga	agcctttcaa	aggataaacc	aaaggaactc	tcttagacaa	acg	953

&lt;210&gt; 1014

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g864 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1014

tccatgtacc	tggtcacgat	gctgaggaac	ctgttcatca	tcctggctgg	cagctctgac	60
ccccacttcc	acaccccat	gtacttcttc	ctctccaacc	tgctctgggc	tgacattggt	120
ttcacctcgg	ccacagtcc	caagatgatt	gtggacatgc	agtcgcatag	cagagtcac	180
tcttatgcgg	gctgcctgac	acagatgtct	ttctttgtcc	tttttgcatt	tatagaagac	240
atgctcctga	ctctgatggc	ctatgaccga	tttgtggcca	tctgcccac	tgacacccac	300
tgactaccg	agtcacatg	aatcctcacc	tctgtgtctt	cttagttttg	gtgtcctttt	360
tccttagcct	gttggattcc	cagctgcaca	gctggattgt	gttacacaa	tcaccttctt	420
caagaatgtg	gaaatctata	atcttttttc	tgtagcccat	ctcaacttct	caaccttgcc	480
tgttctgaca	gcacatcaa	taacatatta	tgtattttag	atatccctat	atttggtttt	540
cttcccattt	cagggatcct	tttgtcttac	tataaaattg	tctcctccat	tccaagaatt	600
ccatcgtcag	atgggaagta	taaagccttc	tccactgtg	gctctcacct	ggcagttggt	660
tgcttatttt	atgaaacagg	cattggcgtg	tacctgactt	cagctgtgtc	atcatctccc	720
aggaatggag	tggtggcatc	agtgatgtac	gctgtgtgtc	tcccatgct	gaaccctttc	780
atctacagcc	tgagaaacag	ggacattcat	agtgcctgt	ggaggctgcg	cagcagaaca	840
gtcaaatctc	atgatctgtt	ccatccttcc	tct			873

&lt;210&gt; 1015

&lt;211&gt; 981

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g865 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1015

atggatgtct	ctatattcct	cctcctagaa	ccacagagga	tccagaacgg	cagccggtcc	60
tcaactgggt	gttccctgac	atgtgcctgg	tcacagtgtc	ggggaagctg	ctcatcatgt	120
tggtcctcag	ccctgactcc	caacctccca	cccacatgta	cttcttcttc	tccaacctgt	180
ccttgccctga	catcggtttc	acctccacca	tgtccccca	gatgattgag	gacatccagt	240
ctcacagcag	agtgatctcc	tatgcaggcc	gcctgactca	gatgtctctc	tttgccattt	300
ttggaggcat	ggaagacaga	catgtcctcg	agtgtgatgg	cctatgaccg	gtttgtagcc	360
atctgtcacc	ctctatatca	ttcagccatc	atgaatccgt	gtttctgtgg	cttccctactt	420
ttgtgtgtct	tttttttttc	tcagtctttt	agacaccacg	ctgcacaact	tgattgcttt	480
acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	ttctgtgacc	cttctcaact	540
cccccatctt	gcatgttgtg	acaccttcac	caataacatc	atcgtgtatt	tcctgtgtgt	600
catatttggt	ttccttccca	tctcggggac	ccttttctct	ttaaaactgt	ttcctccatt	660
ctgagggttt	catcatcagg	cgggaagtat	aaaaccttct	ccacctgtgg	gtctccactg	720
tcagttattt	gctgatttta	tggaacaggt	gttggagggt	acctcagttc	agatgtgtca	780
tcttccctga	gaaaggctgc	agtggcctca	gtgatgtaca	agatgggtcac	ccccatgctg	840

aacccttca tctacagcct gagaaacagg gatatgaaaa gtgtcctgcg gcggccgcac 900  
 ggcagcacgg tctaattctca atatcttctt atctgttcca ttccttttgt aggggtgggtt 960  
 aaaaaaggca gcaagggtcaa a 981

<210> 1016

<211> 762

<212> DNA

<213> Unknown (H38g866 nucleotide)

<220>

<223> Synthetic construct

<400> 1016

atgggtgaca aggggaacagg caaccattca gatgtaactg atttcattct tgaaggcttc 60  
 aggggtccgcc cagagttcta cattctcctc ttcttcctgt tctgctgat ctatagcatg 120  
 gttcttttgg ggaacattag tgtgatgaca atcattgtaa ctgattccca gctgaacaca 180  
 ccaatgtatt ttttctagg caacctctcc ttcattgacg tctcctactc cactgttatt 240  
 gctcctaag ccatggccca ctctctgtct gaaaaaaga cagtctcttt tgcaggttgt 300  
 gttgccaggt tattcctttt tgccctgttc attgtaacag aggggtttgt cctggcagcc 360  
 atggcctatg accgcttcag tgccatctgc aatcctcttc ttcatagtgt tcacatgtca 420  
 agacgcctct gcactcagtt gggtgctggg tcttatttct gtggctgggc cagttccatc 480  
 ctccaagtca gtgtaacatt ctcaagtgtc ttctgtgctt ccagagtcac tgctcacttc 540  
 tactgtgatt cttatcaaat tgaaaagatt tctgtttcta atctctttgt caataagatg 600  
 gtatctctga gtttgagtgt catcattatt ttgacctaca ttgttgttat tatagtatt 660  
 tacctgtata ttgtatctc agtcttgaag atcccccca gtgaaggagg aaagaaagac 720  
 tttccactt gcagctccca tcgggggtgt gtaagtttgc tc 762

<210> 1017

<211> 1008

<212> DNA

<213> Unknown (H38g867 nucleotide)

<220>

<223> Synthetic construct

<400> 1017

tatacagacc cacagaatct aacagatgct tcaaaatacc tcctcctaga actctcagag 60  
 gatccaaaac tgcagctggc cctcgagtggt gcgtgaaccg tgtacatgta cctagtcatt 120  
 ggtgctggag aatctgctca ttatcctggc cgtcagctct gacttccacc tccacacccc 180  
 catgtacttc ttctctcca acctgtcctt ggctgacatc ggtttcacct ccaacacgggt 240  
 ccccaagatg attgtggaca tccaatctca cagcagagtc atctcctatg caggctgcct 300  
 gactcagatg tctctctttg ctgtttttgg aggcattgga gaaagacatg ctctgagtg 360  
 tgagggccta tgaccgggtt gtagccatct gtcaccctct atattattca gccatcatga 420  
 acccatgttt ctgtggcttc ctagttttgt gttttttttt ttctcagctt tttagactcc 480  
 cagctgcaca atttgattgc cttacaaatg acctgcatca aggatgtgga aattcctaatt 540  
 ttcttctgtg accttctca actccacac cttgcgtgtt gtgacacctt caccaataac 600  
 atagtcattg atttcttgc tgccatattt gggtttcttc ctatctcacg gatcattttc 660  
 tcttactata aaattgtttc ctccatgctg agtgtttcat catcagggtg gaagtataaa 720  
 gccttctcca cctgtgggtc tcccctgtca gttgtttgct tattttatgg aaaagtcggt 780  
 ggggggtacc tgagttcaga tgtgtcatct tccccagaa aggggtgcagt ggcctcaatg 840  
 atgtacacgg tgatcacccc catgctgaac cccttcatct acagactgag aaacagggac 900  
 atcaaaaggg tcctgtgggt gttgcatggc agaacagttt aatctcatta ttttattatc 960  
 tgttccattc cttttgtagt gtgggttaaa aaaggcagca aggtcaaa 1008

<210> 1018

<211> 949

<212> DNA

<213> Unknown (H38g868 nucleotide)

<220>

<223> Synthetic construct



&lt;400&gt; 1018

acagggtgtct	gagaattcct	cctcctggga	ctctcagagg	atccagaact	gcagccggcc	60
ctcgctttgc	tgteccctgc	cctgtccatg	tatctgggtca	cgggtgctgag	gaacctgttc	120
agcatcctgg	ctgtcagctc	tgactgcccc	ctccacaccc	ccatgtactt	cttcctctcc	180
aacctgtgct	ggcctgacat	cggtttcacc	tcggccatgg	ttcccaagat	gattgtggac	240
acgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	tgacacagat	gtctttcctg	300
ctccttggtg	catgtataga	aggcatgctc	ctgactgtga	tggcctatga	ctgctttgta	360
gccatctgtc	gccctctgca	ctaccagtc	atcgtgaatc	ctcacctctg	tgtcttcttc	420
gttttggtgt	cctttttcct	tagcctgttg	gattcccagc	tgcacagttg	gattgtgtta	480
caattaacca	tcatcaagaa	tgtggaaatc	tctaatttgg	tctgtgaccc	ctctcaactt	540
ctcaaacttg	cctgtttctga	cagcgtcatc	aataacatat	tcatataatt	cgatagtact	600
atgtttggtt	ttcttcccat	ttcagggatc	tttttgcctt	actataaaat	tgtcccctcc	660
attctaagga	tttcatcgtc	agatgggaag	tataaagcct	tctccacctg	tggctgtcat	720
ctagcagttg	tttgctggtt	ttatggaaca	ggcattggca	tgtacctgac	ttcagctgtg	780
tcaccacccc	ccaggaatgg	tgtggtggca	tcagtgatgt	acgctgtggt	caccccatgc	840
tgaacctttt	catctgcagc	ctgagaaaca	gggacataca	aagtgccctg	cggaggctgg	900
gcagcagagc	attcgaatct	catgatctgt	tccatccttt	ttcttgtgt		949

&lt;210&gt; 1019

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g869 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1019

atgggtgaca	ggggaacaag	caatcactca	gaaatgactg	acttcattct	tgcaggcttc	60
agggtaacgc	cagagctcca	cattctcctc	ttcctgctat	ttttgtttgt	ttatgccatg	120
atccttctag	ggaatgttgg	gatgatgacc	attattatga	ctgatcctcg	gctgaacaca	180
ccaatgtatt	ttttcctagg	caatctctcc	ttcattgac	ttttctattc	atctgttatt	240
gaaccaagg	ctatgatcaa	cttctggctc	gaaaacaagt	ctatctcctt	tgcaggctgt	300
gtggcccagc	tctttctctt	tgccctcctc	attgtgactg	agggatttct	cctggcggcc	360
atggcttatg	accgctttat	tgccatctgc	aaccctctgc	tctactctgt	tcaaagtctc	420
acacgtctgt	gtactcagtt	ggtggctggg	tcctattttt	gtggctgcat	tagctcagtt	480
attcagacta	gcattgacatt	tactttatct	ttttgcgctt	ctcgggctgt	tgaccacttt	540
tactgtgatt	ctcgcccact	tcagagactg	tcttgttctg	atctctttat	ccatagaatg	600
atatcttttt	ccttatcatg	tattattatc	ttgcctacta	tcatagtcat	tatagtatct	660
tacatgtata	ttgtgtccac	agttctaaag	atacattcta	ctgagggaca	taagaaggcc	720
ttctccacct	gcagctctca	cctgggagtt	gtgagtgtgc	tgtatgggtg	tgtctttttt	780
atgtatctca	ctcctgacag	atttctctgag	ctgagtaaag	tggcatcctt	atgttactcc	840
ctagtccact	ccatgttgaa	tcctttgatt	tactctctga	ggaacaaaga	tgtccaagag	900
gctctaaaaa	aatttctaga	gaagaaaaat	attattctt			939

&lt;210&gt; 1020

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g870 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1020

cattcttttc	tcagatatat	tttcgctaag	ttgacagggtg	agccagagct	tcaaccctct	60
ctctactctg	tgttttgggc	accctaactg	ggatgaccac	accacacctc	catgtaccca	120
ctgccacacc	tccatgtacc	tttatatctt	tagcttttcc	ttcatagggt	tcttctattc	180
ctctgtcatt	tctcccaaaa	tgacaataag	ctttgtgaca	gaaaagaaca	tcataccta	240
tgtgacatca	aacactcagc	cttttccctc	ggcttctttg	tcattagtga	ttactccata	300
tttatcccac	tggccttgga	tcactatgag	gccatgaccc	tgccggctct	tttcataagt	360
ttcatttctg	tagatgggtc	ataagttata	gaatttgctg	atgctgtggg	ccatcaaggg	420

```

acatggacca attcctgttt tgtgatcaca gttgcatgag ccttaacttg tgtaacatag 480
gcccgcctca ggctgcctga atcagtagct atgtcagaag caggtggatt tgatttcatt 540
agaaccagca gtgtaccatg ctgtgttatc attttcatat ttgttttca ttcttttcaa 600
catttttcat taaccagtg gtccaaatct tcagccagat tccataaatc tgtttatttc 660
tttttttggg ttaggggacat tcatgtacct cagatctcca gaagctatgg gttagtgtaa 720
attacagtgt ccttcaccaa gatggggcca gtgatgaacg gtctgttcaa caccttgagg 780
aacaagacta tctaacttgc tgcaatgaaa cctttgtcat tttcttct 828

```

&lt;210&gt; 1021

&lt;211&gt; 1001

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g871 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1021

```

gatacagacc cacagagtct aacagatgtc tctatatctc ttctcctcga actctcagag 60
gatccagaac tgcagccggg cgtcgctggg ctgttcctgt ccatgtgcct gggtcacgggtg 120
ctgggaaacc tgctcatcat cctggccgtc agccctgact cccacctcca caccctcatgt 180
acttcttctc ctccaacctg tcttgccctg acatcggttt cacctccaca cgggtcccaa 240
gatgattgtg gacatccagt ctacacagcag agtcatctcc tatgcagggt gcctgactca 300
gatgtctctc tttgccattt ttggaggcag ggaagagaga catgctcctg agtgtgatgg 360
cctacgacca gttttagacc atctgtcacc ctccatctcg ttcagccatc ttgaaccctg 420
gtttctgtgg cttcctagat ttgttgtctc tgtttttttt tttttttttt ttttttccct 480
cagtctttta gactctcagc tgcacaactt gattgcctta caaatgacct gcttcaagga 540
tgtggaaatt cctaatttct tctgggaacc ttctgtgaca ccttcaccag gaacatcaac 600
atgtatttcc ctgtgcctgt atttggtttt cttcccatct cggggaccct tttctcttac 660
tgtaaaattg tttcctccat tctgagggtt tcatcatcag gtgggaagta taaaccttca 720
ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaaacaggc gttggagggt 780
acctcggttc agatgtgtca tcttccccga gaaagcgtgc agtggcctca gtgatgtaca 840
cgggtggtcac ccccatgctg aacccttcca tctacagcct gagaaacagg gatatgaaaa 900
gtgtctctcg gcggccgcac agcagcgcag tctaattctc atatcttctt atctgttcca 960
ttccttttgt aggatgggtt aaaaaaggca gcaagggtcaa a 1001

```

&lt;210&gt; 1022

&lt;211&gt; 1025

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g872 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1022

```

gatacagacc cacagagtct aacagatgtc tctatatctc ttctcctcga actctcagag 60
gatccagaac tgcagccggg cgtcgctggg ctgttcctgt ccatgtgcct gggtcacgggtg 120
ctggggaacc tgctcatcat cctggccgtc agccctgact cccacctccc caccctcatg 180
tacttcttcc tctccaacct gtcttgccct gacatcggtt tcacctccac caccgtcccc 240
aagatgagcg tggacatcca gtctcacagc agagtcattc cctatgcagg ctgcctgact 300
caaatgtctc tctttgccat ttttgagggc atggaaaaaa gacatgtctc tgaggtgatg 360
gcctatgacc tgtttgtacc catctgtcac cttctatata gttcaaccat cttgaaccctg 420
tttgtccgtg gcttctctaaa tttgttgtct ttgttgttgg tttttttttt ttttctctca 480
gtctttttaga ctcccagctg cacaacttga ttgccttaca aatgacctac ttcaaggatg 540
tggaaattcc taatttcttc tgggaacctt ctcaactccc ccatcttgca tgttgtgaca 600
ccttcaccag gaacaacaac atgtatttcc ctgtgcctgt atttggtttt cttcccatct 660
cggggaccct tttctcttac tgtaaaattg tttcctccat tctgagggtt tcatcatcag 720
gtgggaagta caaaccttct ccacctgtgg gtctcacctg tcagttgttt gctgatttta 780
tggagcaggc gttggagggt accttgggtc agatgtgtca tcttccccga gaaaggggtg 840
agtggcctca gtgacgtacg tacacgggtg tcacccccat gctgaactcc ttcatctaca 900
gcctgagaaa cggggatatt aaaagtgtcc tacggcggcc gcatggcagc acagtcta 960
ctcaatacgt tcttatctgt tccattcctt ttgtagggtg ggtaacaaa gacagcaagg 1020

```

tcaaa

1025

&lt;210&gt; 1023

&lt;211&gt; 1044

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g873 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1023

atggatctgg	ggaactcagg	gaatgattca	gttgtagacca	agtttgcct	gctgggcctc	60
acagagactg	cagctctaca	gcccatactc	tttgtcatct	tccttcttgc	ttacgtcact	120
accattggag	gcaccctcag	catactggcg	gccatactta	tggaaaccaa	actccacagc	180
cccattgtact	tcttctggg	gaacttgctc	ctgccagatg	tggggtgtgt	cagtgtcact	240
gtccctgccca	tgtctagcca	tttcatatcc	aacgacagaa	gcattcccta	taaggcctgc	300
ctctccgagc	tcttcttctt	ccacctctg	gctggggcag	actgcttctt	gctgaccatc	360
atggcctatg	accgctatct	ggccatctgc	cagtccctca	cctacagcag	ccgcatgagc	420
tggggaatcc	agcaagccct	ggtgggcatg	tcattgtgtc	tttccttcac	caatgcactg	480
acccaaactg	ttgccctgtc	tcctcttaac	ttctgtggcc	ccaatgtgat	caatcacttc	540
tactgtgacc	ttccacagcc	cttccagctc	tcctgcgcca	gtgttcatct	caatgggcag	600
ttgctgtttg	tagcagcagc	tttcatgggt	gtggccccct	tggctctcat	cactgtgtcc	660
tatgcccatg	tggcagctgc	agtcctgcga	atccgctctg	cagagggcaa	aaagaaagcc	720
ttctccacgt	gtagtctcca	cctcactgtg	gtgggcatct	tctatgggac	gggcgtcttc	780
agctacacaa	ggctgggttc	agtggagtct	tcggacaagg	acaagggcac	tggcatcctc	840
aacactgtca	tcagcccat	gctgaaccca	ctcatctact	ggacatctct	gctggacgtc	900
gggtgcatca	gtcactgttc	ctccgatgct	ggcgtgtctc	caggcccacc	agtgcagagt	960
tccttatgct	gcctgcagtt	cacagctctt	ctttccccac	ctcctggctg	gggtggactg	1020
tcacctctta	atagccatgg	ccta				1044

&lt;210&gt; 1024

&lt;211&gt; 688

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g874 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1024

atgctcatatc	ctagctccac	caggaaaaatg	gcagcagaaa	gtcactctac	ggtgacagag	60
ttcattctca	ggaaaaagcc	agcaagggtc	ccagctcccc	ctcttctagg	gatctgtttg	120
aaaaccgtag	tgggggccct	cactctgac	actctagttt	tccttaattc	tcagcttcac	180
cctcccatgt	actacgtcat	cagaaattta	tcattttatg	atcactgcaa	ttgctctatt	240
agtaccctca	aaatactggt	gaagttttg	ttagagaaga	ccatcatctc	ctatgaggac	300
ggcatgtcac	agctttgtag	tgcttcgtgt	ttatattgtc	atggccaagc	gtaacatgag	360
gaccagcaac	tgctgtcatc	acatttcac	aagtcagctc	cctgctggta	gttgtagtat	420
ttatatggag	ttgactggta	caacaataga	tattttgcct	tgtattaaaa	tagtactagt	480
gtgagttatt	catcagtcac	acttctctca	tgcactagca	tctatgatat	tgataggaca	540
attttctttt	ttacttgatg	caatattgta	gtcactagat	taacagttgt	ttcctactcc	600
ttttctctcc	agcctcctcc	acatcagctt	tacaaagggc	aagctctggg	tttttcccgt	660
aggtctgacg	cattcatgct	gttgccct				688

&lt;210&gt; 1025

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g875 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1025

cacacagagc	cacggaatct	cacaagtgtc	tgagaattcc	tctcctggg	actctcagag	60
gatccagaac	tcgagccgct	cctcgctttg	ctgtccctgt	ccctgtccat	gcattctggc	120
atggtgctga	ggaacctgct	caacatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccacgtact	tcttctcttc	caacctgtgc	tgggctgaca	tgggtttcac	ctcggccacg	240
gttcccaata	tgattgtgga	catgcagtcg	catagcagag	tcattctctca	tgcggactgc	300
ctgacacaga	tttctttctt	gtctcttttt	gcattgtatag	aaggcatgct	cctgactgtg	360
atgacctatg	actgctttgt	agccatctgt	tgcctctctg	actaccagc	catcgtgaat	420
cctcacctct	gtgtcttctt	cgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
ctgcacagtt	ggattgtgtt	acaattcacc	atcatcaaga	atgtggaaat	ctctaattct	540
gtctgtgacc	cctctcaact	tctcaaactt	gcttgttctg	acagcgctcat	caatagcata	600
ttcatgcatt	tccataatac	tatgtttggt	tttcttccca	tttcagggat	ccttgtgtct	660
tactataaaa	tcgtcccttc	cattcttagg	atttcatcgt	cagatgggaa	gtataaagcc	720
ttctccacct	gtggctctca	cctagcagtt	gtttgctgat	tttatggaac	aggcattggc	780
gtgtacttga	cttcagctct	gtcaccaccc	cccaggaatg	gtgtgggtggc	gtcagtgtatg	840
tacgctgtgg	tcaccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgtggaggct	gctcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttcttgtg	tgggtaaggg	caaccacatt	aaa			993

&lt;210&gt; 1026

&lt;211&gt; 965

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g876 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1026

cacagagagc	cacggaatct	cacaggtgtc	tgagaattcc	tctcctggg	actctcagag	60
gatccagaac	tcgagccgct	cctcgctttg	tggtccctgt	cctgtccatg	tattctggta	120
cgggtgctga	gaacctgtgc	agcatcctgg	ctgtccgctc	tgactcccc	ctccacaccc	180
ccataactt	cttctctctc	aacctgtgct	gggctgacat	cggtttcacc	tgcggccacag	240
ttcccaaat	gattgtggac	atgcagtcg	atagcagagt	catctctcat	gcaggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgctttgta	gccatctgtc	accctctgca	ctaccagtc	atcgtgaatc	420
ctcacctctg	tgtcttcttc	gttttggtgt	cctttttcct	tagcctgttg	gattcccagc	480
tgacacagttg	gattgtgtta	caattcacca	tcattcaagaa	tgtggaaatc	tctaattttg	540
tctgtgaccc	ctctcaactt	ctcaaatttg	cctgttctga	cagcatcatc	aatagcatat	600
tcataataat	ccatagtact	atgtttggtt	ttcttcccat	ttcagggatc	cttttgtctt	660
actataaaat	catccctccc	attctaagga	tttcatcatc	agatgggaag	tataaagcct	720
tctccacctg	tggctctcac	ctagcagttg	tttgctgatt	ttatggaaca	gacattggca	780
tgtacctgac	ttcagctgtg	tcaccacccc	ccaggaatgg	tgtgggtggc	tcagtgtatg	840
acgctgtggt	caccccatg	ttgaaccttt	tcattctacag	cctgagaaac	agggacatac	900
aaagtgcct	gtgggggctg	cacagcagaa	cagtcgaatc	tcattgatctg	ttccatcctt	960
tttct						965

&lt;210&gt; 1027

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g877 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1027

atgcagccag	aattctggggc	caatggaaca	gtcattgtctg	agttcatcct	gctgggcttg	60
ctggaggcgc	cagggctgca	gccagtgtgc	tttgtgtctt	tcctctttgc	ctacctgggc	120
acggctcagg	gcaacctcag	catcctggca	gctgtcttgg	tggagcccaa	actccacacc	180
cccatgtact	tcttctctgg	gaacctatca	gtgctggatg	ttgggtgcat	cagcgtcact	240
gttccatcaa	tgttgagtgc	tctctgttcc	cgcaagcgtg	cagttccctg	tggggcctgc	300
cttaccacgc	tcttcttctt	ccatctgttc	gttggagtgg	actgcttctt	gctgaccgcc	360
atggcctatg	accaattcct	ggccatctgc	cggccctcca	cctacagcac	ccgcatgagt	420

cagacagtc	agaggatgtt	ggtggctg	tcctgggctt	gtgctttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgctcaac	ttctgtggcc	ccaatgtgat	caatcacttc	540
tactgtgacc	ccccacagct	cttccagctc	tcctgtctca	gcacccaact	caatgagctg	600
ctgctttttg	ctgtggggtt	tataatggca	ggtaccccca	tggtctctcat	tgtcatctcc	660
tatatccacg	tggcagctgc	agtcctgcga	attcgctctg	tagagggcag	gaagaaagcc	720
ttctccacat	gtggctccca	cctcactgtg	gttgccatat	tctatgggtc	aggtatcttt	780
aactatatgc	gactgggttc	aaccaagctt	tcagacaagg	ataaagctgt	tggaattttc	840
aacactgtca	tcaatcccat	gctgaaccca	atcatctaca	gcttcagaaa	ccctgatgtg	900
cagagtgcc	tctggaggat	gctcacaggg	aggcgggtcac	tggt		945

&lt;210&gt; 1028

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g878 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1028

atgacagatt	acaatgaacc	aatggaacca	atggaagata	agaaccagac	agtagtgact	60
gaattttctt	tattgggcct	cacagatcat	ccctatcaga	agattgttct	cttcttcatg	120
tttctctttg	tttatcttat	caccctggga	ggtaacttgg	ggatgatcac	tctcatatgg	180
attgatccca	gactccacac	tcctatgtac	ttttttctta	ggcacttgtc	ctttgtagat	240
atttggtcct	cttcttctgt	tgtgcctaag	atgctgtgta	atatctttgc	agagaaaaaa	300
gacatcactt	ttctgggttg	tgctgcacag	atgtggttct	ttggtctctt	tgaggcagct	360
gagtgttttc	tcctggctgc	catggcatat	gaccggtagt	tggccatctg	caagcccttg	420
ttgtatacgc	tcattatgtc	tcagcaggtc	tgtatgcagc	tggtggtagg	gccttatgcc	480
atggctctta	taagcaccat	gactcataca	attttcactt	tttgcttacc	cttttggtgt	540
tcaaatatta	tcaatcactt	tttctgtgat	atttttccac	tgctttccct	agcatgtgca	600
gacacctggg	tgaataaatt	tgtgctgttt	gtcttggtcg	gagctatagg	agtactcagt	660
ggtctgatca	tcattgtctc	ctatatgtgc	atcctgatga	ccatcttgaa	gatccagact	720
gctgatggga	agcaaaaagc	tttcttcacc	tggttttctc	accttgcggc	tgtctccatc	780
ctgtatggga	ctcttttctt	gatttatgtt	cggccaagtt	caagttcttc	cctgggtatc	840
tataaagtga	tttctctatt	ttatactgtg	gtaatcccca	tggttaaccc	ccttatttac	900
agcttgagga	ataaggaggt	gaaagatgca	ttcagaagaa	aaattgagag	gaaaaaattt	960
attataggt						969

&lt;210&gt; 1029

&lt;211&gt; 687

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g879 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1029

ttcttttctt	tagacctcat	tagaagccaa	gcaaatacaa	tgtcaaagaa	acactggaca	60
gccatagctg	agttttattcc	cctgggaccg	acagatcaag	ccgagttgca	gcttgcctt	120
tttttctgtc	acgttcctgg	tcattttacct	tattatggta	atgggcaatt	tgagcatgat	180
tttgatcatt	agaagtgact	gaaaacttca	cattccaatg	tacttcttcc	tcagtcacct	240
ctcctttgca	gttctctgtt	atactctcaa	tgctactcct	cagatattgg	tttaatttct	300
atccaagaga	aaaaccattt	tcttcattgg	ttgtgtaagt	gttttataat	tctacttttt	360
cattgtcctg	ataatcagag	attatcatat	gcttacagtg	atggctaagt	actgctacat	420
ggccatttgc	aagcccttgt	tatatggtag	taaaatgtcc	agatttgtct	gcctctctct	480
ggcttctgtt	tcttaaatat	atggctttgc	aaactatctg	gcacagacca	tccggatgct	540
tcttctgtcc	ttctgaggat	ccaatgagat	caaccacttt	gactgtgcgg	acccccctct	600
gttagtcctc	ccttgccgag	gtacctgtgt	caataaatac	atcatgttga	tgagaccaca	660
ctgtcttttg	aaacctggat	atatttt				687

&lt;210&gt; 1030

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g880 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1030

atgtatctgg	tcacgggtgct	gaggaacctg	ctcagcatcc	tggctgtcag	ctctgactcc	60
cacccccaca	cacccatgta	cttcttcctc	tccaacctgt	gctgggctga	catcggtttc	120
accttggcca	cggttcccaa	gatgattgtg	gacatggggg	cgcatagcag	agtcactctc	180
tatggggggt	gcctgacaca	gatgtctttc	ttgggtactt	ttgcatgtat	agtagacatg	240
ttcctgactg	tgatggctta	tgactgcttt	gtagccatct	gtcgccctct	gcactaccca	300
gtcatcgtga	atcctcacct	ctgtgtcttc	ttcgttttgg	tgtccttttt	ccttagcctg	360
ttggattccc	agctgcacag	ttggattgtg	ttacaattca	ccttcttcaa	gaatgtggaa	420
atctctaatt	ttgtctgtga	gccatctcaa	cttctcaagc	ttgcctctta	tgacagcgtc	480
atcaatagca	tattcatata	ttttgataat	actatgtttg	gttttcttcc	catttcaggg	540
atccttttgt	cttactataa	aattgtcccc	tccattctaa	ggatttcata	atcagatggg	600
aagtacaaag	ccttctcagc	ctgtggctgt	cacctggcag	ttgtttgctt	attttatgga	660
acaggcattg	gctgtgtacc	tgacttcagc	tgtggcacca	cccctcagga	atgggtatgg	720
ggcgtcagtg	atgtacgctg	tggtcacccc	catgctgaac	cctttcatct	acagcctgag	780
aaacagggac	attcaaagtg	ccctgtggag	ggtgtgcaac	aaaacagtcg	aatctcatga	840
tctgttccat	cctttttct					859

&lt;210&gt; 1031

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g881 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1031

atggctaattg	aaaactacac	aaaggtcacc	taattcattt	tcacaggctt	gaattacaat	60
cctcagttgc	gggtcttctt	tttctactc	tttctgacaa	ctttctatgt	catcaatgta	120
actggaact	tgggaatgat	tgctctcacc	cgaattgatt	cccgcttca	cacacccatg	180
tactttttcc	tcagccacct	gtcctttgtg	gacacctgct	tctcctcagt	tgtgagcccc	240
aagatgctca	ctgacttctt	tgtgaagagg	aaagccattt	ctttccttgg	ctgtgctttg	300
cagcagtggg	tctttgggtt	ctttgtggca	gcagactggt	tctcttggga	gtccatggcc	360
tatgactgct	atgtggccat	ctgtaaccca	ttgttatact	cagttgctat	gtcccagagg	420
ctctgcaccc	agctagtggg	gggtccctat	gtcattggac	tcatgaatac	catgactcac	480
acaacaaatg	cattttgtct	ccctttttgt	ggccctaatt	tcatcaatcc	tttcttctgt	540
gatattgtccc	ccttactttc	ccttgatagt	gctgatacca	ggctcaataa	gttggcagtt	600
ttcatcgtgg	ctggagctgt	gggagtcttc	agtggctctga	ctatcctgat	ttcctacatt	660
tacatcctca	tggccatcct	gaggatccgc	tctgtctgat	ggagggtgcaa	aaccttttct	720
acttgcctct	ctcacctgac	agctgttttc	atctcgtatg	gtaccctttt	ccttatattat	780
gtacatccca	gtgcaacctt	ctccctggat	ctcaataaag	tagtgtctgt	gttttacaca	840
gcagtgatcc	ctatgttgaa	cccacttatc	tacagcttga	gaaacaagga	agtcaaagat	900
gccatccaca	ggactgtcac	tcagaggaag	ttttgcaagg	cctaaattct	tatccagaag	960
gaattagggg	ggaaa					975

&lt;210&gt; 1032

&lt;211&gt; 941

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g882 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1032

atggagactg	aaaacaatac	aacagtgaca	gagttcatta	ttttgggatt	aacagacaat	60
cctatgctat	gtgccatttt	cttcgtgttt	tttctagcag	tttatatagt	tactataccg	120

ggaaatatta	gcataatcct	cttaatccaa	agcagcccac	agcttcacac	gctaattgtac	180
ctttttctca	gccatttggc	ttctgtggac	attgggtatt	ccatatcagt	tacgccaatc	240
attctcatca	atttcttaag	agagaaaacg	actattcctg	tcacaggctg	tatagcacag	300
cttggctctg	atgtcatggt	tggaaccaca	gagtgtctcc	tgtgtgtcac	tatgtggcta	360
tctgtctctc	cctgctttac	tccatccaaa	tgccccagc	cgtctgtctc	ctcctactgg	420
gagcctccta	cctgggtgga	tgcctgaacg	cttctgtctt	tacaggctgt	ttgatgaacc	480
tgtccttctg	cggtcctaat	aaaatcaacc	actttttctg	tgacctcttc	ccactcttga	540
agctttcttg	tggccatggt	tacattgctg	aaatatcccc	tgccatctcc	tctgcatctg	600
tccttatcag	cacgtgtgtt	accataatcg	tgtctacat	ctacatcctt	cactccatcc	660
tgaagggtgtg	ctctactgag	ggaaggaaga	aggctttctc	cacctgcgct	tcccacctca	720
ctgcagtcac	tttgttctat	gggaccattt	tgtttgttta	tgtgatgccc	aagtcaagct	780
attcagcgga	tcagggtcaag	gtggcatttg	tgatctacac	ggtggtgatt	cccattgctga	840
acccctcat	ctacagtctc	aggaataagg	agggtgaaaga	ggccatgaga	aaattgatgg	900
caagaacaca	ttggttttcc	tgaattaaat	cagtataatc	c		941

&lt;210&gt; 1033

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g883 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1033

atctttgcc	tcttgaccac	cattgactgc	tgtgtatttg	tctgggaatt	cctggagtgc	60
acagtctttg	tgaataagag	ggcatgtgac	cagctggcgt	gtggtgcctt	ttgcattggc	120
ctgatcatga	cagtgggtcta	aataaccaca	gtgtcacaga	ggtacaaaag	gagcacatat	180
gctattttaga	ctgcttcttg	tttgacaccc	ttcttgtcat	gaaactctcc	tgcattgaca	240
atactatcta	tgaataaac	agtattttat	tcaccacaca	tgtgtgcagg	tgtccatggg	300
tttggtttgc	atttcttata	ttgacatccc	tgttacctcc	atcgtgctta	gaatttccta	360
atctgaggtc	tttgccacct	gtgtccccca	acccccacct	catcatggtc	attgtctata	420
tgtctgtgct	tgtactgctt	acctcaagca	caagccaatg	aattcaatag	aaaacaggtc	480
ttctataaga	gacctacatt	atcatcattc	attctgcctc	tggacactgt	tgtttacact	540
ctgaggtaca	tggaggccaa	ggataccatg	tacagagctg	tggacagaaa	tatttcttaa	600
cagatt						606

&lt;210&gt; 1034

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g884 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1034

atggagccag	aagctgggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgtctc	tcctctttgc	ctatctggtc	120
acaactgggg	gcaacctcag	catectggca	gccgtcttgg	tggagcccaa	actccagcc	180
cccattgtact	tcttctctgg	gaacctgtca	gtgctggatg	tcggatgtat	cactgtcact	240
gttctctgaa	tgttgggtcg	tctcttgtcc	cacaagtcca	caatttccta	tgacgcctgc	300
ctctcccagc	tcttcttctt	ccaccttctg	gctgggatgg	actgcttctt	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagcccccca	cctacagcac	ccgcatgagt	420
cagacagtcc	agaggatggt	ggtggctgcg	tccttggctt	gtgccttcac	caacgcactg	480
accacactcg	tggccatgtc	cacgtccaac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgtctca	gcacccaact	caatgagctg	600
ctgctctttg	ctgtgggttt	catcatggca	ggcacacctt	tggttctcat	catcactgcc	660
tacagccacg	tggcagctgc	agttctacga	atccgttcag	tggagggccg	aaagaaggcc	720
ttctccacgt	gtggctccca	cctcaccgtg	gtttgtcttt	tctttggaag	aggatatctc	780
aactacatga	gactgggttc	agaggaggct	tcagacaagg	ataaaggggg	tggagttttc	840
aacactgtta	tcaaccctat	gctgaaccct	cttatctaca	gcctcagaaa	ccctgatggt	900
cagggtgctc	tgtggcaaat	atttttgggg	aggagatcac	tgacc		945

<210> 1035  
 <211> 927  
 <212> DNA  
 <213> Unknown (H38g885 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1035  
 atgaagagaa agaacttcac agaagtgtca gaattcattt tcttgggatt ttctagcttt 60  
 ggaaagcatc agataaccct ctttgtgggt ttcttaactg tctacatttt aactctgggt 120  
 gctaaccatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180  
 ttcttctctaa gcatgctggc tagttcagag acgggtgtaca cactgggtcat tgtgccacga 240  
 atgcttttga gcctcatttt tcataaccaa cctatctcct tggcaggctg tgctacacaa 300  
 atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggtat 360  
 gaccgctatg tggccatctg cagacccctg agatacactg tcatcatgag caaggggacta 420  
 tgtgcccagc tgggtgtgtg gtcctttggc attgggtctga ctatggcagt tctccatgtg 480  
 acagccatgt tcaatttgcc gttctgtggc acagtggtag accacttctt ttgtgacatt 540  
 taccagtgca tgaactttc ttgcattgat accactatca atgagataat aaattatggt 600  
 gtaagttcat ttgtgatttt tgtgcccata ggctgatata ttatctccta tgtccttgtc 660  
 atctcttcca tcttcaaat tgcctcagct gagggccgga agaagacctt tgccacctgt 720  
 gtctcccacc tcaactgtgt tattgtccac tgtggctgtg cctccattgc ctacctcaag 780  
 ccgaagtcag aaagttcaat agaaaaagac cttgttctct cagtgcgta caccatcatc 840  
 actcccttgc tgaaccctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcccta 900  
 tgcagagttg tgggcagaaa tatttct 927

<210> 1036  
 <211> 958  
 <212> DNA  
 <213> Unknown (H38g886 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1036  
 atgttgacaga gagttgggga aatggatgga ggcaaccaga gtgaaggttc agagttcctt 60  
 ctcttgggga tctcagagag tcttgagcag cagcagatgc tgttttggat gttcctggtc 120  
 aggtacctgg tcacgggtgct gggaaatgtg ctcacatcc tggccatcag ctctgattcc 180  
 cgctgcaca ccccatgta cttcttctg gccaacctct ccttactga cctcttcttt 240  
 gtcaccaaca caatcccaa gatgctgggtg aacctccagt cccagaacaa agccatctcc 300  
 tacacagggt gtctgacaca gctctacttc ctggctctct tgggtggcct ggacaacctc 360  
 aacctggccg tgatggcgta tgatcgctat gtggccatct gccgtcccct ccactatgtc 420  
 acagccatga tccctgggct ctgtatcttg ctctctctct tgtgttgggt gttctctgcc 480  
 tctatggcc tcatccatat cctcctcatg accagtgag cttctgtggg tctcaaaaga 540  
 ctcactacct cttctgtgag atgtacttcc tgctaaggct ggcatgttcc aacatccacg 600  
 tcaaccacac agtactggtt gccacgggct gcttcatctt cctcatcccc ttaggtttca 660  
 tgatcacatc ctacgcccgc attgtcagag ccatectcca aataccctca gccactggga 720  
 agtacaaagc cttctccacc tgtgcttccc atttggctgt ggtctccctc ttctatggga 780  
 ctctgggtat ggtgtacctg cagccctcc aaacctactc catgaaggac tcagtagcca 840  
 cagtgatgta tgcgggtggg acgcatgat taacctttc atctacagcc tgaggaaaca 900  
 ggacatgcat ggggctctgg gaagacttcg ccaaggaaaa gccttcaga agttgaca 958

<210> 1037  
 <211> 828  
 <212> DNA  
 <213> Unknown (H38g887 nucleotide)

<220>  
 <223> Synthetic construct



&lt;400&gt; 1037

atgcgaagaa	agaacctcac	agaggtaaca	gagtttgttt	tcttgggatt	ctccagattc	60
cacaaacatc	acatcactct	ctttgtgggt	tttctcatcc	tgtacacatt	aactgtgggt	120
ggcaatgcc	tcatcatgac	catcatctgc	attgaccgtc	acctccacac	tcccatgtac	180
ttcttctga	gcatgctggc	tagctcaaag	acagtgtaca	caactgttcat	cattccacag	240
atgctctcca	gcttcgtaac	ccagaccag	ccaatctccc	tagccggttg	taccacccaa	300
acgttcttct	ttgttacctt	ggccatcaac	aattgcttct	tgctcacagt	gatgggctat	360
gaccactata	tggccatctg	caatcccttg	agatacaggg	tcattacgag	caagaagggtg	420
tgtgtccagc	tgggtgtgtg	agccttttag	attggcctgg	ccatggcagc	tgtccaggta	480
acatccat	ttaccttacc	ttttgtcac	acgggtggtg	gtcatttctt	ctgtgacatc	540
ctccctgtca	tgaactctc	ctgtattaat	accactatca	atgagataat	caattttgtt	600
gtcaggttat	ttgtcactct	ggccccatg	gggtcgtctc	tcattctcta	tgctctcatc	660
atctccactg	tctcaagat	tgccctcagc	gaggggtgga	agaagacctt	tgccacctgt	720
gccttccacc	tactgtgtg	cattgtccat	tatggctgtg	cttccattgc	ctacctcatg	780
cccaagtcag	aaaactctat	agaacaagac	ctccttctct	cagtgacc		828

&lt;210&gt; 1038

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g888 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1038

atggatggag	ataaccagag	tgagaactca	cagttccttc	tcttggggat	ctcagagagt	60
cctgagcagc	agcagatcct	gttttggatg	ttcctgtcca	tgtacctggg	cacgggtgctg	120
ggaaatgtgc	tcatcatcct	ggccatcagc	tctgattccc	acctgcacac	ccccatgtac	180
ttcttctctg	ccaacctctc	cttcactgac	ctcttctttg	tcaccaacac	aatccccaag	240
atgctggtga	acttccagtc	ccagaacaaa	gccatctcct	atgcagggtg	tctgacacag	300
ctctacttcc	tgggtctcct	gggtgacctg	gacaacctca	tcttggccgt	gatggcgctat	360
gatcgctatg	tggccatctg	ctgccccctc	cactatgtca	cagccatgag	ccctgggctc	420
tgtgtcttgc	tcctctcctt	gtgttggggg	ctgtctgttc	tctatggcct	cctcctcacc	480
ttcctcctga	ccagggtgac	cttctgtggg	cctcagagaga	tccactacct	cttctgtgac	540
atgtacatcc	tgtgtgtggc	ggcatgttcc	aacaccacac	tcattcacac	agcattgatt	600
gccactggct	gcttcatctt	cctcaccctc	ttaggggtca	tgaccacatc	ctatgtacgt	660
attgtcagaa	ccatccttca	aatgccctcg	gcctctaaga	aatacaaaac	tttctctacc	720
tgtgcctcgc	atttgggtgt	ggctctccctc	ttttatggga	cgcttgctat	gggtgacctg	780
cagccctctc	atacctactc	catgaaggac	tcagtagcca	cagtgtatga	tgctgtgctg	840
acacctatga	tgaacccttt	catctacagc	ctgaggaaca	aagacatgca	tgggggtccg	900
ggaagagtcc	tatggagacc	ctttcagagg	cctaaa			936

&lt;210&gt; 1039

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g889 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1039

atggctgatg	gaaatataaa	aggatcacag	aattcatttt	tgtaggctta	aggtatcatc	60
ttcagctgca	agtcctcctt	ttcttaccat	ttctaccttt	tttacctcat	tactatgaca	120
gaaaacttgg	gcatgatggg	tcgcatctgg	ctcgattcct	gctttcacac	acctatgtac	180
tttgtcctca	gctacctgtc	ctttgtggac	atctgcttct	catccgttgt	ggggccacaag	240
ttgtcactg	acttatattg	tgtaaggaaa	gccatctcct	tcctgggctg	tcccttgacg	300
cagtgggtct	ttgggttctt	cgtagtcaat	gagtatcttc	tcttggcttc	catggcctat	360
gacaattatg	tggccatctg	taaccatttg	ttgtactcag	tggccatgta	atagagactg	420
tgcatccagc	tgggtgttgt	acgttatgca	gctgatttct	tcaacaccat	aactcacaca	480
acggctgctt	ttcattttcc	cttttttcac	tccaacatta	tcaatcattt	cttctgtgac	540
atgtctctcc	ttctttctct	cgtgtgtgct	gacgcccggg	tcaataaatt	gtaggttttc	600

attgtggctg	gagctgtact	agttgtcagt	agcctgacca	ttataatctc	ctatTTTTac	660
atccttactg	acattctgag	gatctgctct	gctaattggg	aagaacaaaa	ctTTTTccac	720
ctgctcttca	cacttaacag	ctgtttccat	cttttatggg	tctctcttct	ttagctacgt	780
ttcgaccagg	tgcaactttt	taccgggaac	tcaataaaat	agtgttgggtg	ttctgtacat	840
ccccatgttg	aaacctctca	tctacagctt	gataaataaa	gaagtatcct	agccacta	898

&lt;210&gt; 1040

&lt;211&gt; 934

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g890 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1040

atggaaaaaa	taaacaacgt	aactgaattc	atTTTctggg	gtctttctca	gagcccagag	60
attgagaaag	tttgTTTTgt	gggtTTTTct	ttcttctaca	taatcattct	tctgggaaat	120
ctcctcatca	tgctgacagt	ttgcctgagc	aaacctgtta	agtcacccat	gtatttcttt	180
ctcagcttct	tgtcttttgt	ggacatttgt	tactcttcag	tcacagctcc	caagatgatt	240
gttgacctgt	tagcaaaagg	caaaaccatc	tcctatgtgg	gggtgcatgt	gcaactgctt	300
ggagtacatt	tctttggttg	cactgagatc	ttcatcctta	ctgtaatggc	ctatgatcgt	360
tatgtggcta	tctgtaaacc	cctacattat	atgaccatca	tgaaccggga	gacatgcaat	420
aaaatgttat	tagggacgtg	ggtaggtggg	ttcttacct	ccattatcca	agtggctctg	480
gtagtccaac	tacccttttg	tggacccaat	gagatagatc	actacttttg	tgatgttcac	540
cctgtgttga	aacttgcttg	cacagaaaca	tacattgttg	gtgtgtgtgt	gacagccaac	600
agtggtagca	ttgctctggg	gagttttgtt	atcttgctaa	tctcctacag	catcatccta	660
gtttccctga	gaaagcagtc	agcagaaggc	aggcgcaaa	ccctctccac	ctgtggctcc	720
cacattgcca	tggtcgttat	ctttttcgag	ccctgttact	tttatgtaca	tgcgccctga	780
tacgaccttt	tcagaggata	agatgggtgg	tgtattttac	accattatca	ctcccatggt	840
aaatcctctg	atTTTatacac	tgagaaatgc	agaagttaa	aatgcaatga	agaaactgtg	900
gggcagaaat	gttttcttgg	aggctaaagg	gaaa			934

&lt;210&gt; 1041

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g891 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1041

atggactata	gaaatcaaac	tttggttact	gaatTTTTtt	ccgtgggatt	aacaaatctc	60
tttcagcaca	agattgctct	ctttctggta	tttctctttg	tttatcttgt	cactgttccg	120
ggaaacttgg	gaatgatcac	tcttatttgg	atggattctc	gactccagac	ccccaagtac	180
ttttctctct	gccacttgtc	ctttgtggat	gtctgtcctt	cttctgccat	cggccccaa	240
atggtgactg	atatcttctg	ggagaaaaaa	gtaactctct	tggttggtgt	gccagtttat	300
ggTTTTtttg	ccatttttga	gtaactgaat	gtttcttctt	ggctgccatg	gcataatgac	360
ggtataggct	atctataagc	ctttgttcta	tacactcatt	atgtcccaac	aggtctgtgt	420
gcagctgggt	gtgggcctta	tgctgtgggc	cttataagca	ccatgaccca	tatgactttc	480
acctttcgcc	tactctactg	tggtccaaac	atcatcaatc	acttcttctg	tgaccttctc	540
cctgtcctct	ccctggcata	tgagataacc	catattaata	aatgtttact	ttttatcttg	600
gtgggtgccc	tgaggagtact	cagtgggtgt	atcatcttgg	tctcctacat	ttacattgtc	660
attgccatcc	tgagaattcg	ctctgctgac	gcgagacgca	aagacttctc	cacttgctct	720
tcacacctga	tggtgtgtct	catcctgtat	gggacactct	tctttatctg	tgtagtcca	780
agctctagtt	tctctatcaa	catcaataaa	gtgggttccc	tggtctacac	agcagtgatc	840
cccatgttga	atcccccttat	ctacagcctg	agaaacaagg	aggtaaaaga	ttcattcagc	900
aagaagtgtg	aaagaaagaa	gtttcttata	ggtaggtgaa	ctagaatacc	a	951

&lt;210&gt; 1042

&lt;211&gt; 930

&lt;212&gt; DNA

<213> Unknown (H38g892 nucleotide)

<220>

<223> Synthetic construct

<400> 1042

atggtgaatt ttacacatgt ctcagaatth gttctacttg ggttccaagg ggggtcccggg	60
atgcaggcta tgctatttct gatttttctg atcctgtatg gcatagctgt ggtgggaaac	120
cttggtcatga ttgtaattat ctgggtagat gcacacctcc acaccccaat gtatgccttc	180
ctgcaaagcc tttcattggt ggacatctgc tattcctcca caattgcacc cagggctctg	240
gcgaactcca tgcaagagga ccacacaatt tcctttggcg gatgtgctgc tcagttcttt	300
ttcttgtctc tctttggtat cacagaggct ttctctctgg ctgccatggc ctatgaccgc	360
ttcatcgcca tctgcaaccc tcttctgtac tctgtgagca tgtctcacca ggtctgtgtg	420
ctgttaatat caggatccta cttgtgggtg gtagtcaatg ccattgctca aacaaccatg	480
accttcaggt tgcctttctg tgggtccaat gagatcaacg actttttctg tgatgttccc	540
ccactcttgt ccctctcatg ttcagatacc tttataaacc aactggttct tcttggttta	600
tgtggctcca ttattgtcag tacctttttg attgtcctgg tctcatacat ttacatcatc	660
tcaacaattc tgaggatccc gaccatgcag ggacgctaga aagccttctc cacgtgcgct	720
tcccacctaa caggagtgtg cttgtttttt ggtactgttt tcttcattga tgcacaaccc	780
agtgccatct tcttcatgga gcaaagtata atagtgtcca tattctacac tatggtcac	840
cccatgctga atcccctgat atacagcctg aggaacaaag aggtcaagca ggctctgaga	900
cggagcatgc agaagctgtc tttgtgatca	930

<210> 1043

<211> 927

<212> DNA

<213> Unknown (H38g893 nucleotide)

<220>

<223> Synthetic construct

<400> 1043

atgagggaaa ataaccagtc ctctacactg gaattcatcc tcctgggagt tactgggtcag	60
caggaaacagg aagatttctt ctacatcctc ttctgtttca tttaccccat cacattgatt	120
ggaaacctgc tcattgtcct agccatttgc tctgatgttc gccttcacaa ccccatgtat	180
tttctccttg ccaacctctc cttggttgac atcttcttct catcggtaac catccctaag	240
atgctggcca accatctctt gggcagcaaa tccatctctt ttgggggatg cctaacgcag	300
atgtatttca tgatagcctt gggtaacaca gacagctata ttttggtgc aatggcatat	360
gatcgagctg tggccatcag ccaccactt cactacacaa caattatgag tccacggctc	420
tgtatctggc ttattgtctg gtcttgggtg attggaaatg ccaatgccct cccccacact	480
ctgctcacag ctagtctgtc cttctgtggc aaccaggaag tggccaactt ctactgtgac	540
attacccctt tgctgaagtt atcctgttct gacatccact ttcatgtgaa gatgatgtac	600
ctagggggtg gcattttctc tgtgccatta ctatgcatca ttgtctccta tattcgagtc	660
ttctccacag tcttccaggt tccttccacc aagggcgctg tcaaggcctt ctccacctgt	720
ggttcccacc tcacgggtgt ctctttgtat tatggtacag tcatgggcac gtatttccgc	780
cctttgacca attatagcct aaaagacgca gtgatcactg taatgtacac ggcagtgacc	840
ccaatgttaa atcctttcat ctacagtctg agaaatcggg acatgaaggc tgccctgcgg	900
aaactcttca acaagagaat ctcctcg	927

<210> 1044

<211> 927

<212> DNA

<213> Unknown (H38g894 nucleotide)

<220>

<223> Synthetic construct

<400> 1044

atgaagaaag aaaatcaatc ctttaacctg gattttattc tcctgggagt tactagtcag	60
caagaacaga ataatgtctt ctttgtgatt tttttgtgca tttaccccat cacactgact	120
ggaaatctgc tcatcatctt ggccatctgt gctgacattc gccttcacaa ccccatgtat	180

tttctccttg	ccaacctctc	cttggttgac	atcatcttct	catccgtaac	catccctaag	240
gtgctggcca	accatctctt	gggcagcaag	ttcatctcct	ttgggggatg	cctaatagcag	300
atgtattttca	tgatagcctt	ggccaaggca	gacagctata	ccttggtctg	aatggcatac	360
gacgagctg	tggccatcag	ctgcccactt	cattacacaa	caattatgag	tccacgggtct	420
tgtatcctgc	ttattgctgg	gtcttgggtg	attggaaaca	ccagtgtctt	ccccacact	480
ctgctcacag	ctagtttgtc	cttctgtggc	aaccaggaag	tagccaattt	ctactgtgac	540
attatgcctt	tgctgaagtt	gtcctgttct	gacgtccact	ttaatgtgaa	gatgatgtac	600
ctaggggtcg	gcgttttctc	tttgccatta	ctatgcatca	ttgtctccta	tggtcagggtc	660
ttttccacag	tcttccaagt	tccatctacc	aagagtctat	tcaaagcctt	ctgcacctgt	720
ggctcccacc	tcacagttgt	ttttttatat	tatggtacaa	cgatgggcat	gtatttccgc	780
cctctgacca	gttacagccc	caaagatgca	gtgataactg	tgatgtatgt	ggcagtgacc	840
ccagcattaa	atcctttcat	ctatagtctg	agaaattggg	atatgaaggc	agccctacag	900
aaactcttca	gcaagagaat	ctcctca				927

&lt;210&gt; 1045

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g895 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1045

gctcttcttt	tccattccta	caaacatccc	accagagga	gaatgactgt	caaaagtcac	60
tctatagtga	cagagttcag	tctcagggga	ttaacgaagc	agccagatct	ccagctcttt	120
cacttctctca	ttttccttga	tatccatatg	gtcaccaatgg	tggggaactt	gggcatgac	180
actctaattt	gtcttaactc	tcagcttcac	accccctatg	actacttctt	cagcaatctg	240
tcactcttgg	atctctgcta	ttcctccatt	actaacccta	agatgctggg	gaactttgtg	300
ttaaagaaga	gcattatctc	ttatgcaggg	tacatgtcat	agttctactt	tttcttggtt	360
tttgtcatag	ctaggtgtta	catgctgatg	gtgaaggcct	gtgaccacta	tggtgccatc	420
tgctgccctt	tgctttgcaa	cgctcatcatg	tctcatgtca	cctgctccct	gatggtggct	480
gtggtctaca	ccatgggact	cgttgtctcc	acaatagaga	ctgggctcat	attaaaactg	540
ccctatttgt	aactcctcac	cagtcgctgc	ttctgtgaca	tcctccctct	catgaaactc	600
tcctgatcta	gtgccttatg	atgttgagat	ggcagctctt	ttttttgcta	gattgcaacc	660
tgagaatcat	gatcttaaca	gttcttgttt	tcttacacct	tcattctctt	cagcatcctg	720
cacatcagca	ccactgaggg	caggtccaaa	gtcttcagca	cctgcagctt	ccaccttgca	780
gctataggga	tgttccatgg	atagactgca	ttcaggtact	taaaaccgcg	cataaccagt	840
tccttgcccc	aagagaatgt	ggcctctgtg	ttctacacta	cagtaatcta	cgtgccgaat	900
cccctaattg	acagcctgaa	aaacaaggat	gtaaaagctg	ccatgcagaa	aacactaagg	960
agtaagtttt	gttgccagatg	taattatctt				990

&lt;210&gt; 1046

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g896 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1046

ctcctggaag	gagggaaatca	gactagcacc	tttgagttcc	tcctctgggg	actctcagac	60
cagccacagc	agcaacacat	cttcttctctg	ctgtttctgt	ggatgtacgt	ggtcactgtg	120
gctgggaacc	tgctcattgt	cctggccatt	ggcactgaca	cacacctcca	cacctctatg	180
tacttcttcc	ttgccagctt	gtcgtgtgca	gatattcttt	ccacctccac	cactgtgccc	240
aaggccctgg	tgaatatcca	gacctagagc	aggtccattt	cctacgcagg	gtgtttggca	300
cagctctact	tcttcttgac	ttttggggac	atggacatct	ttctcccggc	tacaatggcc	360
tatgaccgct	atgtggccat	ttgccacctg	ctccactata	tgatgatcat	gagcctccac	420
cgctgtgcct	tcctgggtgac	agcctgctgg	accctcacaa	gtcttctcgc	catgactcgc	480
accttctctca	tattccggct	ttccttgtgc	tcttagatcc	ttcctggctt	cttctgtgat	540
ttgggaccgc	tgatgaaggt	gtcttgcctc	gacgccagg	tcaatgagct	tgtgctcctc	600
ttcctagggg	gagcagtcac	tttaatccct	tttatgtcga	tcctgggtctc	ttatatccgc	660

attgtttcag	ccatcctcag	ggccccctct	gccagggaa	ggcgcaaggc	cttctctacc	720
tgcgactctc	acctcggtgt	tggttgcttg	ttctttggga	cagtgatcag	ggcttatctg	780
tgccccctcat	cctcttctct	caactcagta	aaggaggata	cagcggctgc	tgatcatgtac	840
acagtgggtga	ctccccctgct	gaacccccctt	atttacagca	tgcggaacaa	ggacatgaag	900
gcggcggtgg	ttagacttct	caaggggcagg	gtctccttct	cacagggc		948

&lt;210&gt; 1047

&lt;211&gt; 1007

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g897 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1047

gatacagacc	cacagagtct	aacagatgtc	tctatattcc	tcctcctcaa	actctcagag	60
gatccagaac	tgcagcaggt	cgtcgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctgggggaacc	tactcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttggttc	tctccaacct	gtcccttgcc	tgacatcggt	ttcacctcca	ccacgggtccc	240
caagatgatt	gtggacatcc	agtctcacag	cagagtcac	tcctatgcag	gctgcctgac	300
tcagatgtct	ctctttgcca	tttttgagg	tatggaagag	agacatgctc	ctgagtgtga	360
tggcctatga	ccggtttgta	gccatctgtc	accctctata	ttgttcagcc	atctttaacc	420
cgtgtttctg	tggcttccta	gatttggtgt	cttttttttt	ttttttctca	gtctttcaga	480
ctcccagctg	cacaacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaattcc	540
taattttctt	tgggaacctt	ctcaactctc	ccatcttgca	tggttgtaga	ccttcaccag	600
gaacatcagt	atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gaccttttc	660
tcttactgta	aaattgtttc	ctccattctg	agggtttcat	catcaggtgg	gaagtataaa	720
ccttctccac	ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggcattg	780
gagggtagct	cggttcagat	gtgtcatctt	ccccgagaaa	gggtgcagtg	gcctcagtga	840
tgtacatggt	ggtcaccccc	atgctgaacc	ccttcattcta	cagcctgaga	aacagggata	900
tgaaaagtgt	cctgcggcgg	ccgcatggca	gcacagtcta	atctcaacat	cttcttatct	960
gttccattcc	ttttgtagg	tggtttaaaa	aaggcgccaa	ggtcaaa		1007

&lt;210&gt; 1048

&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g898 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1048

atgagacaga	ataataatat	tacagaattt	gtcctcctgg	gcttctctca	ggatctggat	60
gtgcaaaaag	cattatttgt	catattttta	ctcacatact	tggtgacagt	ggtggggaac	120
ctgctcattg	tggtgactat	tattaccagc	ccttcttgg	gctccccaat	gtacttcttc	180
cttgccctgcc	tgatatttat	agatgctgca	tattccacta	caatttctcc	caaattgatt	240
gtagacttac	tctgtgataa	aaagactatt	tctttccag	cttgcatggg	ccagttattt	300
atataccact	tggttggtgg	ttctgaggtc	ttccttcttg	tggtgatggc	ctgtgatcac	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgaatc	420
cttctgttgg	tggtggctgt	gactggaggt	tttctgcatt	ctgtgtttca	aattgttgtt	480
gtatacagtc	tcgctttctg	tgcccccaat	gtcattgact	actttgtctg	tgacatgtac	540
ccattattgg	aactggatg	cactgacacc	tactttattg	gccttactgt	ttttgtcaat	600
gggtggaacaa	tctgtatagt	cgtcttcacc	cttctactaa	tctcctatgg	agtcaccta	660
aactccctta	aaacttacag	tcaagaagg	aggcataaag	tctgttttac	ctgcagctcc	720
cacattatcg	tctttgccct	cttttttgtt	ccctgtatct	tcatgtatgt	tagacctgtt	780
tcaaacatcc	ttttgataaa	ttcctgacag	tgttttatac	agttatcaca	cccatgttga	840
atcctttaat	atacacattg	agaaattcag	agatgagaaa	ttctgtagaa	acactcttgt	900
gtaaaagtta	actgtattag	agtaag				926

&lt;210&gt; 1049

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g899 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1049

atggaaagaa tcaacagcac actgttgact gcgtttatcc tgacaggaat tccgtatcca	60
ctcaggctaa ggacactcct ttttgtgttc ttttttctaa tctacatcct gactcagctg	120
ggaaacctgc ttattttaat cactgtcttg gcagacccaa ggctccatgc ccgccccatg	180
tacatctttc ttgggtgttc ctcagtcatt gatatgagca tctcctccat cattgtccct	240
cgccctcatg tgaacttcac tttaggtgtc aaacccatcc catttggtgg ctgtgttgct	300
caactctatt tctatcactt cctgggcagc acccagtgct tcctctacac cctaattggc	360
tatgacaggt acctggcaat atgtcagccc ctgcgctacc ctgtgtcat gactgctaag	420
ctgagcgcct tgcttgtggc tggagcctgg atggcaggat ccatccatgg ggctctccag	480
gccatccata ccttccgcct gccctactgt gggcccaatc aggtggatta cttcttctgt	540
gacatccctg cagtgttgag actggcctgt gctgacacaa cagtcaacga gctggtgacg	600
tttgtagaca ttgggggtgt ggttgccagt tgcttctccc tgatcctcct ctctacata	660
cagatcattc aggccatcct gagaatccac acagctgatg ggcggcgccg ggctttttca	720
acttgtggag cccatgtaac cgtggtcacc gtgtactatg tgccctgtgc cttcatctac	780
ctgaggcctg aaaccaacag cccctgggat ggggcagctg ccctagtccc cacggccatc	840
actcctttcc tcaacccct tctctacact ctgcggaacc aagaggtgaa gctggccctg	900
aaaagaatgc tcagaagccc aagaactccg agtgaggtt	939

&lt;210&gt; 1050

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g900 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1050

atgggaaaga caaaaaacac atcgctggac actgtggtga gagatttcat tcttctgggt	60
ttgtctcacc cccgaatat aagaagcctc ctcttctctg tcttcttctg catttacatc	120
ctcactcagc tggggaacct gctcattctg ctaccctgtg gggctgaccc gaagctccgt	180
gctcgcccca tgtacattct tctgggagtg ctctcatctc tggacatgtg gctctcctca	240
gtcatcgctt cttgaattat tttaaacttc actcctgcca acaaggctat cccgttttgt	300
ggctgtgtgg ctcaactgta tttctttcac ttcttgggca gcaccagtg cttctcttac	360
accttgatgg cctatgacag gtacctggca atatgtcagc ccctgcgcta cccagtgtct	420
atgaatggga ggttatgcac agtccttctg gctggagctt gggctcgccg ctccatgcat	480
gggtctatcc aggccaccct gacctccgc ctgcccact gtgggcccac tcaggtagat	540
tactttatct gtgacatccc cgcagtattg agactggcct gtgctgacac aactgtcaat	600
gagcttgtga ctttgtgga catcggggta gtggccgcca gttgcttcat gttaattctg	660
ctctcgtatg ccaacatagt aaatgccatc ctgaagatac gcaccactga tgggaggcgc	720
cgggccttct ccacctgtgg ctcccaccta atcgtgggtca cagtctacta tgtcccctgt	780
atcttcatct accttagggc tggctccaaa ggccccctgg atggggcagc ggctgtgttt	840
tacactgttg tcaactcatt actgaacccc ctcatctata cactgaggaa ccaggaagtg	900
aagtctgccc tgaagaggat aacagcaggt caagggactg aatgaaaata agta	954

&lt;210&gt; 1051

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g901 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1051

atgggaaaga caaaaaacac atcgctggat gccgtggtga cagatttcat tcttctgggt	60
ttgtctcacc ccccaaatct aagaagcctc ctcttctctg tcttcttcat catttacatc	120

ctcactcagc	tggggaacct	gctcattctg	ctcaccatgt	gggctgacct	gaagctctgt	180
gctcgcccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctcctca	240
gtcaccgttc	ctcggcttat	tttggatttt	actccttcca	tcaaggctat	cccgtttggg	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagtg	cttcctctac	360
accttgatgg	cctatgacag	gtacctagca	atatgtcagc	ccctgcacta	cccagtgtct	420
atgaatggga	ggttatgcac	agtccttggt	gctggagctt	gggtcgccgg	ctccatgcat	480
gggtctatcc	aggccacctt	gaccttccgc	ctgccctact	gtggggccaa	tcagggtggat	540
tactttatct	gtgacatccg	cgcagtattg	agactggcct	gtgctgacac	aactgtcaat	600
gagcttggtg	cctttgtgga	cgtcagggtg	gtggccgcca	gttgcttcat	gttaattctg	660
ctctcctatg	ccaacatagt	ccatgccatc	ctgaagatac	gcaccgctga	tgggaggcgc	720
cgggccttct	ccacctgtgg	ctcccaccta	atcggtgtca	cagtctacta	tgtcccctgt	780
attttcatct	accttagggc	tggctccaaa	gacccctggg	atggggcagc	ggctgtgttt	840
tacactgttg	tcaactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt				930

&lt;210&gt; 1052

&lt;211&gt; 900

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g902 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1052

atgtttatat	tgacaggctt	cacagatgat	tttgagctgc	aagtcttctt	atttttacta	60
ttttttgcaa	tctatctctt	taccttgata	ggcaatttag	ggctgggtgt	gttggtcatt	120
gaggattcct	ggctccacaa	ccccatgtat	tattttctta	gtgttttata	attcttggat	180
gcttgctatt	ctacagttgt	cactccaaaa	atgttggtca	atttctctgg	aaaaaataaa	240
tccattttcat	ttatcggatg	tgaacacag	atgcttcttt	ttgttacttt	tggaaactaca	300
gaatgttttc	tcttggtctg	aatggcttat	gatcactatg	tagccatcta	caaccctctc	360
ctgtattcag	tgagcatgtc	acccagagtc	tatgtgccac	tcatactgtc	ttcctacgtt	420
gctggcattt	tacatgtac	tatacatata	gtggctacat	ttagcctgtc	cttctgtgga	480
tccaatgaaa	ttaggcattg	cttttgtgat	atgcctcctc	tccttgctat	ttcttgttct	540
gacactcaca	caaaccagct	tctactcttc	tactttgtgg	gttctattga	gatagtcact	600
atcctgattg	tcctcatttc	ctgtgatttc	attctgttgt	ccattctgaa	gatgcattct	660
gctaagggaa	ggcaaaaggc	cttctctaca	tgtggctctc	acctaactgg	agtgacaatt	720
tatcatggaa	caattctcgt	cagttatatg	agaccaagtt	ccagctatgc	ttcagaccat	780
gacatcatag	tgtcaatatt	ttacacaatt	gtgattccca	agttgaatcc	catcatctat	840
agtttgagga	acaaagaagt	aaaaaaggca	gtgaagaaaa	tgttgaaatt	ggtttacaaa	900

&lt;210&gt; 1053

&lt;211&gt; 974

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g903 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1053

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccagt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
acgggtgctga	ggaacttgct	gagcatcctg	gctgtccgct	ctgagtcccc	gtccacaca	180
accatgtact	tcttctcttc	catcctgtgc	tgggctgaca	tcggtttcac	ctcagccaca	240
gttcccaaga	tgattgtgga	catgcagtgg	tatagcaaag	tcattctctca	tgcgggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	aggcatctgt	cgccctctgc	actacccagt	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
ctgcacagtt	ggattgtgtt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaaact	gcctgttctg	acagcgtcat	caatagcatc	600
ttcatatatt	ttggtagtac	tatgtttggg	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	tcgtcccttc	cattctaagg	atttcatcgt	cagatgggaa	gtataaagcc	720

ttctccacct	atggctctca	cctagcagtt	ttttgctgat	ttgatggaac	aggcattggc	780
gtgtacctga	cttcagctgt	ggcaccaccc	ctcaaggaa	ggtgtggtgg	tgtcagtga	840
gtaagctgtg	gtcaccaccc	atgccgaacc	ttttcatcta	cagcctggag	aaacagggac	900
atacaaagt	ccctgcgagg	gctgcccac	aaaacagtcg	aatctcatga	tctgttccat	960
cctttttctg	gtgt					974

&lt;210&gt; 1054

&lt;211&gt; 1006

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g904 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1054

gatacagacc	cacagagtat	aacagatgtc	tctatattcc	tcctcctcga	actctcagag	60
gatccagaac	tgcaaccggg	cgctcgctgg	ctgttcctgt	ccatgtgcct	cgctcatggg	120
ctgggggaac	tgctcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgctc	gacatcggtt	tcacctccac	cacggteccc	240
aagatgattg	tggacatcca	gtctcacagc	aaagtcactc	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tggaggcatg	gaaaaaagac	atgtcctcga	gtgtgatggc	360
ctatgaccgg	tttgtaccca	tctgtcacc	tctatctcgc	tcagccatct	tgaacccgtg	420
tttctgtggc	ttcctaaatt	tgttgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctggga	accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	600
tcagcatgta	tttccctgct	gccgtatttg	gttttctttc	catctcgggg	acctttttct	660
cttactgtaa	aatggtttcc	tccattctga	gggtttcatc	atcagggtgg	aagtataaac	720
cttctccacc	tgagggtccc	acctgtcagt	tggttgctga	ttttatggaa	caggcggttg	780
agagtacctc	gggttcagatg	tgctcatctc	cccagaaaag	ggtgcagtgg	cctcagtgat	840
gtacacgggt	gtcaccacca	tgctgaaccc	cttcatctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcggcggc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	tttgtagggt	gggttaacaa	agacagcaag	gtcaaa		1006

&lt;210&gt; 1055

&lt;211&gt; 929

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g905 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1055

atggaaaata	ggaaaaattg	acttaattca	tcctcttggg	gctcacacag	aaccctgagg	60
gccaaaaagt	tttatttgtc	acattcttac	tcattctacat	tgtgacgata	atgggcaacc	120
tccttatcat	ggtgaccatc	atggccagcc	agtccttggg	ttcccccatg	tacttttttc	180
tggtctcttt	atcatttata	cataccgtct	attatactgc	cattgctccc	aaaatgattg	240
ttgacctgct	ctctgagaaa	aagaccattt	cttttcaggg	ttgtatggct	caacttttta	300
tggatcattt	atttgctggg	gctgaagtca	ttcttctggg	ggtaatggcc	tatgatcaat	360
atgtggccat	ctgtaagcct	cttcattatt	tgatcatcat	gaatcgctga	gtctgtgttc	420
tcattgctgt	ggtggcctgg	attggaggct	ttcttctactc	attggttcaa	tttctcttta	480
tttatcagct	ccctttctgt	ggacccaatg	tcattgacaa	cttcctgtgt	gatttgtatc	540
ccttattgaa	acttgcttgc	accaatacct	atgtcactgg	gctttctatg	atagctaattg	600
gtggagcgat	ttgtactgtc	accttcttcc	ctctcctgct	ttcctatggg	gtcatattac	660
cctctcttaa	gactcagagt	ttggaaggga	aatgcaaaag	tttctacacc	tgtgcatccc	720
acatcactgt	gatcacttta	ttctttgtcc	cctgcatctt	cctgttagca	aggcccaact	780
ccacctttcc	cattgataaa	tccatgactg	tggttttaac	ttgtataact	cccattgctga	840
aaccactaat	ctatgccctg	aggaatgcag	aaatgaaaag	tgccatgagg	aaactttgga	900
gtgaaaaagt	aagcttagct	ggaaaagg				929

&lt;210&gt; 1056

&lt;211&gt; 925



&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g906 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1056

cacatgcctc	ccaacaatgt	gactgaattc	attctcttgg	ggctcacaca	gaatccacac	60
ttgcagaaaa	tactctttat	tgtattttta	tttatttttc	tatttaccat	gctgggccaat	120
ctgttcattg	tcatacccat	ctcctgtagc	cccacacttt	catcacccat	gtacttcttt	180
ctcacttact	tatcctttat	agatgcctcc	tacacctctg	tcacaacccc	caaaatgatc	240
accgacctgc	tctaccagag	gagaactatt	tccttggctg	gctgcctgac	tcagctcttt	300
gtggagcact	tgtctggagg	ctcagagatc	atcctcctta	ttgtcatggc	ctatgaccgc	360
tacgtggcca	tctgcaagcc	cctgcactac	acaaccatta	tgcaacaagg	gatctgccac	420
cttctgggtg	tgatagcctg	gattggaggc	atcctgcatg	ccactgtgca	gattcttttc	480
atgaccgact	tgcccttctg	tggtccccaa	tgctcattgac	cactttatgt	gtgatctctt	540
cccattgttg	aaacttgcc	gcagagacac	ctacagactt	gggatgctgg	tggcagccaa	600
cagtggagcc	atgtgcttgc	tcattctttc	cctgctcgtc	atctcctaca	tagtcatcct	660
gagctccctg	aaatcctata	gctctgaagg	acagcacaaa	gccctctcca	cctgtggctc	720
ccactttact	gtcgttgtac	tcttttttgt	gccttgcata	ttcacctaca	tgcatcctgt	780
ggtcacctac	tctgtggaca	agttgggtgac	tgtgttcttt	gcaatcctca	ctcccatgtt	840
aaatcctata	atttacactg	tgagaaacac	agaggtaaaa	aatgccgtga	ggagtttgtt	900
gaggaaaaga	gtaacagttt	atgca				925

&lt;210&gt; 1057

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g907 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1057

atgtacacga	ctttactcat	ggcccagggt	gtgtctctgt	gcagacaatg	gatccacac	60
tctttctgtg	atatgtctgc	tctgctgaag	ctggccctct	ctgacactcg	agttaatgaa	120
tgagtgatat	ttatcatggg	agggtcatt	cttgtcatcc	catccatact	catccttggg	180
tcctatgcaa	gaattgtctc	ctccatctc	aaggctccct	cttctaagtg	tatctgcaag	240
gccttctcta	cttgtggctc	ccacctgtc	tgtggtgtca	ctgttctatg	gaaccgttat	300
tggtctctac	ttatgctcat	cagctaatag	ttctactcta	aaggacactg	tcattggctat	360
gatgtacact	gtggtgacct	ccatgctgaa	ccccttcac	tacagcctga	ggaacagaga	420
catgaaggga	gccctgagca	gagtcattca	tcagaagaaa	actttcttct	ctctctgatg	480
ataacacttg	gagctatta					499

&lt;210&gt; 1058

&lt;211&gt; 996

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g908 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1058

atgggaccaa	agaatctaac	tcgtgttttg	gaattcttcc	tcctccactt	cttagatgac	60
ttggaactgc	agcctttcct	cttcaggctg	tcctgaacc	atgcacctag	tcacagtgt	120
tgcgaaactg	ctcacatcct	tctgactgtc	agctttgccc	tcacctccac	aaccccatga	180
acttcaacct	gtccttagct	gacattgggt	tcacctctgc	cacaatttca	aagataactg	240
tagacctcca	aactcacagc	agaatcattt	tatacatgag	ctgcctgaaa	tagatgtctt	300
ttaaaattat	ttttggatgt	ttgcacaatc	tactcatgac	tgtgatggcc	tatgacctat	360
ttgtggcgac	ctgtcatctc	ttgtactaca	cagtgatcag	gaatcccccac	ctctgtggcc	420
tcctgtctct	gggtctctct	tctctctctc	tttttttttt	ttgatcagtc	ttttggaaac	480
ccagctgtac	agtttgatgg	tgtcacaagt	tctctcatgc	aatgtagac	attcctcatt	540

tcttctgtga	cccttctcag	tttctccacc	tttctgttc	tgacactgcc	accaataaca	600
cattaatgca	ttttattggt	gccatctctg	tggtccattc	tcagggatcc	tttactgtta	660
tactcaaatt	atgttctcca	tactcataac	cctataaaat	gtgggaagta	taaagcaaac	720
cttctccacc	catcgctctc	acctgtcagt	tgtttgctta	ttttatggaa	caggccttgg	780
agtatacctt	agtttggctg	gctcaccttc	cccaagaaca	ggtgtggtgg	cctcaatggt	840
atataccaca	gtcacctca	tgttgaaccc	tgcattcaca	gcctgaggaa	cagagacatc	900
aagaatacct	ggtggtggct	cctcagcata	actgcctggt	atcaatacct	gtgctatcct	960
ttatggagtg	tggttagaaa	aaacagcaaa	ctcaaa			996

&lt;210&gt; 1059

&lt;211&gt; 923

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g909 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1059

atggggactt	caaataatga	gactgaattc	attcttttgg	gcattacaaa	aaatccagaa	60
ctaaggaaaa	tattctctgc	tttgtttcta	gccatgtatg	tgaccacagt	gttgggaaat	120
ctattcattg	tggtgactct	ggctgcaagt	tgaggtctga	gatcacctat	gtacttttcc	180
cttacttctt	tgtctctcat	gggtgccacc	tactcttcca	tactgcccc	taagatgact	240
gtggactctt	tgagaacact	accatttccc	ttgaaggctg	catgaccag	ctctttgcag	300
agcattttct	tgatggtgta	gcgatcatcc	ttctcactgt	gatggtctgt	gactgctatg	360
aggccatcag	taagccccctg	catgacacaa	ccatcatgag	tccacgggtg	tgctgctgtt	420
ggtggttagaa	gcttgggtgg	ggggattaac	acatgccaca	atacagcttt	ttttttttca	480
tatatcaaat	acccttctgt	ggtcccaata	ttattgacca	ttttatatgt	gatttgtttc	540
cattgttaaa	acttgcttac	atggacaccc	acatgctggg	tctcttagtc	atcctcaaca	600
gtggggtgat	gtgtatggcc	atcttcttta	tctaattgc	atcctacatt	gtcacctgtt	660
actctctgaa	gtcttgacgc	tcggtaggtc	gacgcaacac	actttccacc	tggtgctccc	720
accacacagt	ggtcattctt	ttcttcgtgg	agtgtatttt	cttgtagata	agacctgtgg	780
tcacttacc	catagacaag	gatatggcta	tttcttttac	tattgttgca	cccattgttaa	840
atcctctgat	ctataccctg	aggggcatca	aggtaaaaaa	tgccataaga	aaaatgtgga	900
tgaacagggt	gacctaggt	ggt				923

&lt;210&gt; 1060

&lt;211&gt; 950

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g910 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1060

atggctccga	ccaacctcac	atctgcccc	gctgttcttc	ctctcggcc	tggtggacgg	60
aacagacgcc	caccgcctgc	tgttcctgct	ctgccttggg	tctatctgct	caacgccctg	120
agcaacctga	gcatggtggc	gctggtgaga	tccgacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcactgagc	ctcgtggacg	tctgctttac	caccgtcacg	gtccccaggc	240
tgctggccgg	cctgctccac	ccgggccagg	ccatatcctt	ccaggcgtgt	ctgccgagat	300
gtacttcttc	gtgactctgg	catcacccag	agctacctca	tgccggccat	gtcctagcga	360
gcccagacgc	gcgtgccggc	acctctgtac	ggcgcgctgg	tgacgccatc	ggcgtgcgcc	420
tgctgggtgc	tgcgctgtgg	gccgtgacgc	acctgcactc	gctgctgcac	acgctgctcc	480
tctccgcgct	ctcctacccc	taccccaccc	ccgtgcgccc	cttcttttgc	gacatgacgg	540
tgatgctgag	cttggcgacc	tcggacacgt	ccgcgcggga	gacggccatc	ttctccgagg	600
gcctggccgt	ggtgttggcc	ccgtgctccc	tcgtgttccc	tttctacgc	gcgcctcctg	660
gtcgcggtgc	tcggcttgcg	cggccgcgcc	gcgccttctc	cacctgcggg	gcccacctag	720
tgccggtggc	ggtggcgctt	ttctttggct	ctgtcctctc	cgtgtatttc	ccgcgcgtct	780
ctgcctactc	agcccgttac	gaccgcctgg	ccagcgtggt	ctacgctgtc	atcacgccga	840
ccttgaaccc	tttcatcaac	agccttcgca	acaaagaggt	caagggcgcc	ctgaaaaggg	900
ggctcagcat	ggagggctgc	accccaagag	gcgtgagggc	aaatctggct		950

<210> 1061  
 <211> 933  
 <212> DNA  
 <213> Unknown (H38g911 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1061  
 atgaaagggg caaacctgag ccaagggatg gagtttgagc tcttgggcct caccactgac 60  
 cccagctcc agaggctgct cttcgtgggtg ttcttgggca tgtacacagc cactctgctg 120  
 gggaacctgg tcatgttcct cctgatccat gtgagtggca ccctgcacac acccatgtac 180  
 tccctcctga agagcctctc cttcttggat ttctgctact cctccacggg tgtgccccag 240  
 accctgggtga acttcttggc caagaggaaa gtgatctctt attttggctg catgactcag 300  
 atgttcttct atgcgggttt tgccaccagt gagtgctatc tcatcgctgc catggcctat 360  
 gaccgctatg ccgctatttg taacccccctg ctctactcaa ccatcatgtc tcctgaggtc 420  
 tgtgcctcgc tgattgtggg ctccacagt gcaggattcc tcaattctct tatccacact 480  
 ggctgtatct ttagtctgaa attctgcggg gctcatgtcg tcaactactt cttctgtgat 540  
 gggccacca tcctgtcctt gtcttgtgta gacacctcac tgtgtgagat cctgctcttc 600  
 atttttgctg gtttcaacct tttagactgc accctcacca tcttgatctc ctacttctta 660  
 attctcaaca ccatcctgaa aatgagctcg gccaggggca ggtttaaggc attttccacc 720  
 tgtgcatccc acctcactgc catctgcctc ttcttgggca caacactttt tatgtacctg 780  
 cgccccaggt ccagctactc cttgacctag gaccgcacag ttgctgtcat ctacacagtg 840  
 gtgatccag tgctgaacct cctcatgtac tctttgagaa acaaggatgt gaagaaagct 900  
 ttaataaagg tttggggtag gaaaacaatg gaa 933

<210> 1062  
 <211> 948  
 <212> DNA  
 <213> Unknown (H38g912 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1062  
 atgcaaaacc aaagctttgt aactgagttt gtcctcctgg gactttcaca gaatccaaat 60  
 gttcaggaaa tagtatttgt tgtatttttg tttgtctaca ttgcaactgt tgggggcaac 120  
 atgctaattg tagtaacctt tctcagcagc cctgctcttc tgggtgtctcc tatgtacttc 180  
 ttcttggggt tcctgtcctt cctggatgcg tgcttctcat ctgtcatcac cccaaagatg 240  
 attgtagact ccctctatgt gacaaaaacc atctcttttg aaggctgcat gatgcagctc 300  
 tttgtgaac acttctttgc tgggggtggag gtgattgtcc tcacagccat ggcctatgat 360  
 cgttatgtgg ccatttgcaa gcccttgcat tactcttcta tcatgaacag gaggctctgt 420  
 ggcattctga tgggggtagc ctggacaggg ggcctcttgc attccatgat acaaattctt 480  
 tttactttcc agcttccctt ttgtggcccc aatgtcatca atcactttat gtgtgacttg 540  
 taccggttac tggagcttgc ctgcaactgt actcacatct ttggcctcat ggtggtcatc 600  
 aacagtgggt ttatctgcat cataaacttc tccttgttgc ttgtctccta tgcgtcatc 660  
 ttgctctctc tgagaacaca cagttctgaa gggcgctgga aagctctctc cacctgtgga 720  
 tctcacattg ctgttgtgat tttgttcttt gtcccatgca tatttgtata tacacgacct 780  
 ccatctgctt tttcccttga caaaatggcg gcaatatttt atatcatctt aaatcccttg 840  
 ctcaatcctt tgatttacac tttcaggaat aaggaaagta aacaggccat gaggagaata 900  
 tggaacagac tgatggtggt ttctgatgag aaagaaaata ttaactt 948

<210> 1063  
 <211> 930  
 <212> DNA  
 <213> Unknown (H38g913 nucleotide)

<220>  
 <223> Synthetic construct

<400> 1063

atgcaactga	ataataatgt	gactgagttc	attctgcttg	gattgacaca	ggatcctttt	60
tggaagaaaa	tagtgtttgt	tatttttttg	cgtctctact	tggaacact	gttgggtaat	120
ttgctaata	ttattagtg	caaggccagc	caggcactta	agaacccaat	gttcctcttc	180
cttttctact	tatecttate	tgatacttgc	ctctctactt	ccatagcccc	tagaatgatt	240
gtggatgccc	ttttgaagaa	gacaactatc	tccttcagcg	agtgcattgat	ccaagtcttt	300
tcaccccatg	tctttggctg	cctggagatc	ttcatcctca	tcctcacggc	tgttgaccgc	360
tatgtggaca	tctgtaagcc	cctgcactac	atgaccatca	taagccagtg	ggctctgtgt	420
gttttgatgg	ctgtggcctg	gggtgggacc	tgtgtgcatt	ctttagttca	gatttttctt	480
gccctgagtt	tgccattctg	tgcccccaat	gtgatcaatc	actgtttctg	tgacttgcag	540
cccttggtga	aacaagcctg	ttcagaaacc	tatgtggtta	acctactcct	ggtttccaat	600
agtggggcca	tttgtgcagt	gagttatgtc	atgctaatat	tctcctatgt	catcttcttg	660
cattctctga	gaaaccacag	tgctgaagtg	ataaagaaag	cactttccac	atgtgtctcc	720
cacatcattg	tggtcatctt	gttcttttga	ccttgcatat	ttatgtacac	atgccctgca	780
accgtattcc	ccatggataa	gatgatagct	gtattttata	cagttggaac	atcttttctc	840
aaccctgtga	tttacacgct	gaagaatata	gaagtgaata	gtgccatgag	gaagcttttg	900
agcaagaaat	tgatcacaga	tgacaaaaga				930

&lt;210&gt; 1064

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g914 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1064

atggagacaa	caaatacttc	tgccgtgact	gaattctttc	tggtggggct	ttcccaatat	60
ccagagctcc	agctttttct	gttcctgttc	tgccatcatc	tgtacatgat	aatcctcctg	120
ggaaatagct	tcctcattat	catcaccatc	ttggattctc	gcctccatac	ccccatgtat	180
ttctttcttg	gaaacctctc	attcttgggc	atctgttaca	catcatcatc	cattcctcca	240
atgcttatta	tatttgtatc	tgagagaaaa	tccatctcct	tcattggctg	tgctctgcag	300
atggttgtgt	cccttggctt	gggtccatt	gagtgatccc	tcctggctgt	gatggcctat	360
gaccgctatg	tggccatctg	caaccactg	aggtaactcc	tcacatgaa	cagagtgtctg	420
tatgtgcaaa	tggtgtcatg	gtcctggatc	ataggctgtc	tgacctccct	attgcgaaca	480
gttctgacaa	tgatgttgcc	tttctgtggg	aataatatca	ttgatcatct	tacctgtgag	540
atcctggctc	ttcttaaagt	catatgtctc	gatattccca	taaatgtgtt	tataatgaca	600
gtgtcaagta	ttgttttatt	gggtgattcct	cttaattttt	atctcctatg	tgtttattct	660
ctcttccatc	ttgagaatta	attctgtctg	gggaagaaag	aaagcctttt	ttacctgttc	720
agcgcaattg	actgtgtgca	tcttattcta	tggttcagtt	cttttcatgc	acatgaagcc	780
caaatcaaa	ttgcacaacag	catctgatga	aatcattgga	ttgtcttatg	aagtgtatcac	840
cccaatgaac	cccatcatct	acagcctgag	gaataaggag	ataaaagaag	ctgtgaagaa	900
aatcctcagc	agacacgtgc	atctatggaa	aatatgaaag	gccttgaggc	atgtgacgtt	960
ctca						964

&lt;210&gt; 1065

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g915 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(620)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1065

gatgcatgct	cgagcgcccc	cagtgatgat	gatattctga	gaattcgccc	ttccaatgta	60
ctttttcctg	aagaacctct	ctgttttggg	tctgtgctac	atctcagtca	ctgtgcctaa	120
atccatccgt	aactccctga	ctcgagaag	ctccatctct	tatcttggct	gtgtggctca	180
agcctatttt	ttctctgcct	ttgcatctgc	tgagctggcc	ttccttactg	tcattgtctta	240

tgaccgetat	gttgccattt	gccacccct	ccaatacaga	gccgtgatga	catcaggagg	300
gtgctatcag	atggcagtc	ccacctggct	aagctgcttt	tcctacgcag	ccgtccacac	360
tggcaacatg	tttcgggagc	acgtttgcag	atccaatgtg	atccaccagt	tcttccgtga	420
catccctcag	gtgttgccc	tggtttctg	ngagggtttc	tttgtagagc	tttgacceng	480
ccctgagcct	caatgcttgg	ntctgggatg	ctttattccc	atgatgatct	ccnattttcc	540
anatcttctn	aanggggctc	nagaatccct	tnaggaccag	antcnagcta	aaagcctttn	600
cccnnctgct	tccccccacg					620

&lt;210&gt; 1066

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g916 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(611)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1066

gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	cttccaatgt	60
atattttct	ctctgacctc	tccttcttgg	acctctgctt	taccacaagt	tgtgtccccc	120
agatgctggt	caacctctgg	ggcccaaaga	agaccatcag	cttcctggga	tgtctgttcc	180
agctcttcat	cttctgttcc	ctggggacca	ctgagtgcac	cctcctgaca	gtgatggcct	240
ttgaccgata	cgtggctgtc	tgccagcccc	tccactatgc	caccatcatc	cacccccgcc	300
tgtgctggca	gctggcatct	gtggcctggg	ttatgagtct	ggttcaatcg	atagtccaga	360
catcatccac	cctccacttg	cccttctgtc	cccaccagca	gatagatgac	tttttatgtg	420
aggtcccatc	tctgattcga	ctctcctgng	gagatacctc	ctacaatgaa	atccagttgn	480
ctgtgtccag	tgtcatcttt	ggtggntgtg	cctctcagcc	tcacccctgc	ctcttatgga	540
gccactgccc	aggcnggggc	tgaggattaa	ctttgccnna	gccatggaag	aaaggtcttt	600
nggacctngn	n					611

&lt;210&gt; 1067

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g917 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(619)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1067

gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	ctttctttat	60
ttcgaagagt	atacactagt	ggattgaaga	gaaacaaata	cataggaagg	gcgaattcca	120
gcacactggc	ggccgttact	agtggatccg	agctcggtag	caagcttgat	gcatagcttg	180
agtattctaa	cgcgctacct	aaatagcttg	gcgtaatcat	ggatcatagct	gtttcctgtg	240
tgaattgtt	atccgctcac	aattccacac	aacatacgag	ccggaagcat	aaagtgtaaa	300
gcctggggtg	cctaattgag	gagctaactc	acattaattg	cgttgcgctc	actgtccgct	360
ttccagtcgg	gaaacctgtc	gtgccagctg	cattaatgaa	tcggccaacg	cgcggnnaga	420
ggccggnttg	cgtattgggc	gctcttccgc	ttctcgtcga	ctgactcgct	gcgctcggga	480
cgtccggctg	cggcgagcgg	tatcagctta	ctcaanggcc	gtantacggt	tattcncagg	540
aatnnggggt	taacgcncng	naaagaacat	tgtgngccan	angncaagcn	taatgcccag	600
gaaccgntan	aacgntccc					619

&lt;210&gt; 1068

&lt;211&gt; 621

&lt;212&gt; DNA

<213> Unknown (H38g918 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(621)

<223> n = A,T,C or G

<400> 1068

```

gnnnnttntt cantccattg ggccctctag atgcatgctc gagcggccgc cagtgtgatg      60
gatatctgca gaattcgccc ttattccgga gggatatacat gaagggattg gtaactagac      120
gtaaactcga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa      180
gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag      240
actctgaaag aggtggaagg gattgaatac aatcaaaagt atggtgactg ctagtccaa      300
gatggtggcg taggggcaag ctggctttgc ttacccccct ggcagaaaac caaaaacaaa      360
tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc      420
cagggcccag agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt      480
tctaaggag acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc      540
cataaaacaa agattggaag atgttggaatt ttgcaaccag gagcaaatat tgggaaaggc      600
gaattccagc cacttgcnge c                                     621

```

<210> 1069

<211> 615

<212> DNA

<213> Unknown (H38g919 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1069

```

gnnnnttnan tcantgccct ngggccctct agatgcatgc tcgagcggcc gccagtgtga      60
tgatattctg cagaattcgc ccttggttgc caaggtgtaa atgaaaggtt ttgcgaggga      120
gtaaattgaag ggattacgca ggagtaaatg aagggattac gcaggagtaa atgaaggat      180
tacgcaggag taaatgaagg gattacgcag gagtaaatga agggattacg caggagtaaa      240
tgaagggatt acgcaggagt aaatgaaggg attacgcagg agtaaatgaa gggattacgc      300
aggagtaaat gaagggatta cgcaggagta aatgaaggga ttacgcagga gtaaattgaag      360
ggattacgca ggagcaaata cataggaagg gcgaattcca gcacactggc ggccgttact      420
agtggatccg agctcggtac caagcttgat gcatagcttg agtattctaa cgcgctcacct      480
aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg tgaaattgtt atccgctcac      540
aattccacac aacatacgag cccggaagca taaagtgtaa agnctggggg gcctaattgag      600
tgacttactc catta                                     615

```

<210> 1070

<211> 614

<212> DNA

<213> Unknown (H38g920 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 1070

```

ggnnnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatatt      60

```

```

tgcagaattc gcccttccga tgtattttct tctacgttaa ggtattttta attgttacta 120
atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat 180
gatgctgtta cctcaciaat atgtatgtgt ggatgtatat atatctattc aatatatgta 240
actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct 300
agtgtctcag ataagttggc tagttttttg ttccacataa aggaacaaac atttatagat 360
ttatatgtat attaaaaatg gtaaaaaattg gctgggtgca gtgggtcatg cctataatac 420
cagcactttg ggaagccgag gtgggaggat tacttgaggt aaggagccca gcctgaccaa 480
caaggtgaaa ccccatccct actaaaaata caagaattag cccggggatg gtgggtggcca 540
cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng 600
aggttcgagg ngag 614

```

<210> 1071

<211> 857

<212> DNA

<213> Unknown (H38g921 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(857)

<223> n = A,T,C or G

<400> 1071

```

atggnnnnnn nntttnnnaa anttttnccc antttgggcc gnccccccct tctttaaggn 60
aatgggcccc ttgggccctt cccggaaggc cggggggcnc cggcccccaa aggtttgggt 120
tggaagtgg ggggaattta aattcctttg ggccaaggna aaaattttcc ngccccctt 180
ttttccctt tttggttttt anccggggga angggggggt tgattaatta atcgggaagn 240
tnggggggaa nttttttaa aaaaacctg ggggaagggt ccaaccaaac aaggttggtt 300
ttccanggga ccgttgggac caggcttttn gaatcaagaa tcccaaaggg cattcttttg 360
gattaaggaa nggtgccggg accggtgaaa gggaaaaaac tgggtggacc cataccaaaa 420
tgagaaccac ggtgagatgc cgaggagcac gtggagaaag gctttgcttc cggccactgg 480
cagaggggat cctgaggatg gtgcttgatg atgtacacat agggagacaa gggtgatgag 540
gcatgaactc aggataacca caacagcnat cacaagggcc acaaagctct actgcctgtg 600
tgttgggtgc aggccagggc aatccagggg tgcaatgtca caagaaagaa agtggttgat 660
ggcacgggng ggccacagaa ggacaggcca cttgatgaag ggcttggtgg cactgcaatg 720
gccacgaaac caccagaccc aggaaccan ggccaagctt gcgctgaag agcaaggcta 780
ctcatgaatg gcttccgtag tngtaaagga tagcaagatg gcaaaggcaa gccggtcatn 840
aagccatggc ttgccng 857

```

<210> 1072

<211> 593

<212> DNA

<213> Unknown (H38g922 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 1072

```

aacgcagagt accgccact acgtaatctg tacatgaaag ggtttaaaag agactgggaa 60
gagaggaatt ggcaagatca agcagaggca actccttcta gtccttctag taccgcaagg 120
ggcagataaa tggaatgggt aacacctaga ggaaagtata cttgccaaaa gcaaatncat 180
aggggggagt acattatcgg gttgaaaaaa gtattccatg cagataaaaa ccaaaagcaa 240
atacatcggg gccgtacttc tgcgtcttt gagcgtactg atggtacca gcttttgnct 300
ctttagttag ggttaattgc gcgcttgccg taatcatggt catagctggt ttctgtgtga 360
aattgttate ccgtcacaa ttcacacaac atacgagccc gggagcataa agtgtaaagc 420
ctggggtgcc taatgagtg agcttactta cattaaattg cgttgcgctc actggccgct 480

```

tttccaagtc gggaaacctg tcgtgncagc ttcantaatg aatcggccaa cgccgcgggg 540  
agaggcggtg tgcgtattgg gcgctcttcc gcttcttngt tnactgactt cgg 593

<210> 1073

<211> 624

<212> DNA

<213> Unknown (H38g923 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 1073

gnnntttaac nccgnggctn cnagcagtgg aacaacgcag agtacgcccc cgatgtactt 60  
tctttttcag tctcaagtct tctcttctc caaagatttt gtcttttcta ctacctgagc 120  
taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcatt caacttcaaa 180  
cgtgtcatct cagaacaagc ttcatgttac ttccaatttt atccttcttg tttgctgatt 240  
ccaagaattc cagtcccatc taggccccga atgcattgtt cctgccaccc ttttcataatc 300  
ctcaattccc ttgtatcatc acttttcttt tatatagcac agattccatg attcataaca 360  
ataaattatgt ttttttttgc atgtgctctt aatttctttt cttgctccta ttatcttcta 420  
tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcactta 480  
tgctcagtcg gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540  
tttatagtcg tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600  
tctgcgcttg agcgtccggt gggg 624

<210> 1074

<211> 637

<212> DNA

<213> Unknown (H38g924 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(637)

<223> n = A,T,C or G

<400> 1074

ttatnnccat tggagctcca aagcagtggg aacaaccgca gagtacgccc cccatgtatt 60  
ttctttttct tggggnagct gnatgcttcc tncgtggctac catgggnatat gaccggctat 120  
gnggncatct gcagtcctct gnnctcccag tcattatgaa ccaaaggaca cgggccaac 180  
tggtggtgtn ttctgggtc ccaagcttct ctgnagctac tngcaagac cacaatggct 240  
cttnagnntt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc 300  
tgtgctgaaa gctggtctgn tgcaagacac agcactgttt gagatctacg ccatcgctcg 360  
aaccattctg gtggtcaatg aacccttctg tgctgatctt gngttcctat actcgnattg 420  
gtgctgctat ccctcaagaa cccatcaagc taaangggaa gcaataaagn cttttctcta 480  
cgtgctcctt aacacctccc ttggtggcct ctcttttcta atataatcnt ctaagcctca 540  
acctacttct tgggcctnaa ntcaataaaa ttcttctgga gaggcaagaa ggtggtattc 600  
atztatncta cactggtngn gactccatgn tggaaact 637

<210> 1075

<211> 621

<212> DNA

<213> Unknown (H38g925 nucleotide)

<220>

<223> Synthetic construct



<221> misc\_feature  
 <222> (1)...(621)  
 <223> n = A,T,C or G

<400> 1075  
 gtnatnccnt ttaatnccnt tggagctcca agcagtggtta acaacgcaga gtacgcccgt 60  
 tcctcagaca gtatatgaat ggggttaaaaa tgggccagag cagatgcagg aagatcaaatt 120  
 aggaggctac tgcagtagag tcaaatctag ggctgatggt ttcttgggat gcatagtaat 180  
 aggtagatag agaaagtctt taggaggttag aatggacagg acttcacaat gcattaaatg 240  
 tagggagaaa aaaaatgatt cctgggtttc tagcttgagc tagtagggat agtggtagaa 300  
 ttacttgata tggaaaactg gaggaaaaag agtttggaag agaaagatgg caagttaaatt 360  
 acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag 420  
 ccatgggcta ggaacataca gtgggattcc ctggcatgctc attggttact gaagtcagag 480  
 tgtatgagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg 540  
 gctggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttgngaa 600  
 aaggagagaaa nggttgaaat t 621

<210> 1076  
 <211> 631  
 <212> DNA  
 <213> Unknown (H38g926 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(631)  
 <223> n = A,T,C or G

<400> 1076  
 ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag 60  
 cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt 120  
 gtccctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aaggggtgcat 180  
 agtagaaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttcctccctt 240  
 ctgcagagtg catgtggttag acagcaagga gaatccggcc ataggaacat gcaatacaaa 300  
 tgaagggaaa cacaagaaaa atgggtggtgc tcaaaaacac cgtgcactca tagaccagg 360  
 tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc 420  
 tggacttgca atatgggata cggagtgcac ataccgtgtg agcacaagag ttgatggagc 480  
 ctatcatcca agatcctgtt atcatcagtg cacacactct ttttctcata cggatgagat 540  
 agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg 600  
 cttctgcacc tgctaaagtc aggaagaaga t 631

<210> 1077  
 <211> 620  
 <212> DNA  
 <213> Unknown (H38g927 nucleotide)

<220>  
 <223> Synthetic construct

<221> misc\_feature  
 <222> (1)...(620)  
 <223> n = A,T,C or G

<400> 1077  
 tgttantccn ntttctncc attggagctc ccaagcagtg gtaacaacgc agagtacgcc 60  
 ctcttgtgtt ctgagagtgt agatgaaggg gttataggag ataaagatca gggcaatatg 120  
 taggacaagg acacagacac tgacaacaaa gttgattatc tcattgacag tgggtgtctgt 180  
 gcaggccagc ttcagcaggg gtctcacatc acagaagaag tgggagatga caaagtcac 240  
 acaaaagggc aggccaaaca tagatgttac ttggacaata gccatgccca ggccaatcct 300  
 cagtgaacca gatcccgatc agacacaagc cctcttacct atgaataccg taagggtgtg 360

cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcc	420
aaagtcacat	agaagagctg	agtgcacacag	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcagggtctc	agagatagac	540
agcaatgctt	agggaaaaagt	acatggggccg	tactttctgtc	gtcttgagcg	tactgatggt	600
accagctttt	tggtcccttt					620

&lt;210&gt; 1078

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g928 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(627)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1078

tgtagctcca	aagcagtgg	aacaacgcag	agtacgccct	cttggttacg	taagggaata	60
gatgatggg	ttcagcatgg	gggtgactac	agtgtacatg	acagtggcca	cacgggtcca	120
ctctgctcg	gtcgggacgt	ggcctggaag	tagactgcaa	tgactgtcct	atagaaagag	180
gctcaccaca	nccaggtggg	agccacaggt	gggncacaag	tcccggagcc	tcccagaggc	240
ttgagggcag	ctggagcacg	ggnaagcttg	ntatggncct	acaaggaggc	gaggatgagc	300
agnaagggag	tgaccaccac	ttgengcgcc	ctnggtgaag	atgagcagct	tgatgtggt	360
ggntgtcaga	gcacgagagc	ctttaagaga	ggcttggtgg	gtcacagaag	aagtgggngc	420
actttgtggg	aaagcacaga	aaggacaagc	gagccatgag	caggatatac	aggagggagt	480
tgctcgtggg	acaccagcca	tgccattcca	accagggctg	cgcacatngc	cggggacatt	540
ctcgtgggat	aagggaaggg	gtgccggatn	ggcacgtatc	agtcataggc	cttggnccgc	600
agaagacagc	tttnaattta	ccccagg				627

&lt;210&gt; 1079

&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g929 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1079

gcagtggtaa	caacgcagag	taccgcccc	tatgtacttt	ttcttgggaa	acttgtctgt	60
gtttgacatg	ggtttctcct	cagtgcattg	tcccaaaatg	ctgctctacc	ttatggggct	120
gggccgactc	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttcctcgg	180
gagcattgag	tgcttcttgt	ttacgggtgat	ggcctatgac	cgcttcactg	ccatctgtta	240
tcctctgcga	tacacagtca	tcatgaacct	aaggatctgt	gtggccctgg	ctgtgggcac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtgtgtccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggt	gagcttcacc	aacgttgggc	tcatatctct	480
ggctgcttcc	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

&lt;210&gt; 1080

&lt;211&gt; 616

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g930 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(616)

<223> n = A,T,C or G

<400> 1080

gnnnnnnnnt	tcattccatt	gggccctcta	gatgcatgct	cgagcggccg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttggtgctt	agagtgtaaa	taaaagggtt	aacattggct	120
tagagggtgaa	gagtaaatac	ataggaagg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcgggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttctgtgt	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgcct	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaacgc	gcggggagag	gcgggttgcg	tattgggcgc	480
tcttcgcgtt	cctcgctcac	tgactcgctg	cgctcggtcg	ntcggctgcg	gcgagcggta	540
tcaagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcagggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

<210> 1081

<211> 615

<212> DNA

<213> Unknown (H38g931 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1081

ngnnnnnttna	ntcnangccn	ngngccctct	agatgcatgc	tcgagcggcc	gccagtgtga	60
tggatatctg	cagaattcgc	ccttccaatg	tatttacttc	tcagccagct	ctcccttatg	120
gacctgatgt	acatctccac	caccgtcccc	aagatggcgt	acaacttcct	gtccggccag	180
aaaggcatct	ccttcctggg	atgtggtgtg	caaagcttct	tcttcctgac	catggcgtgt	240
tctgaaggct	tactcctgac	ctccatggcc	tacgaccgtt	atttggccat	ctgccactct	300
ctctattatc	ctatccgcat	gagtaaaatg	atgtgtgtga	agatgattgg	aggctcttgg	360
acactggggg	ccatcaactc	cttggcacac	acagtctttg	cccttcatat	tccctactgc	420
aggtctaggg	ctattgacca	tttcttctgc	gatgtcccag	ccatgttgc	tcttgctgta	480
cagatacttg	ggtctatgaa	tatatggttt	ttgtaaggac	aaagcctctt	tcttcttttn	540
cctttcattg	gcatacttc	ttctgngggc	cgagtcctaa	ttgctggcta	tataatgcac	600
tcaaaggagg	ggagg					615

<210> 1082

<211> 628

<212> DNA

<213> Unknown (H38g932 nucleotide)

<220>

<223> Synthetic construct

<221> misc\_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 1082

gnnnnnnnat	ttnatgccnt	tnttgattcc	cnttnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttccac	acttctctat	taagaagcat	gtgagatact	180
tgttacaac	ataacatcct	ggtcccaccc	caaagccact	caatcaaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tggtggagaa	300
tctaggcaac	aatgaattaa	ggaaagctct	ctaccatttg	gtactggtag	cagggttgag	360
gatcacaggg	aagagggtaa	gcatacaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccattgtcca	tgtaagtagc	aaacaaccct	ctcatgtaca	480

ctctgaggaa	caagggggcg	tactttctgtc	gtcttgagcg	tactgatggg	accagccttt	540
tgccccctta	gtgagggtta	attgcgcgct	tggcgtaatc	atgggtcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

&lt;210&gt; 1083

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g933 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(613)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1083

annncentng	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttttgttaag	tccaacctcc	atcctccttg	gccttttgat	tcaattgac	actccttct	120
cctcaaaaaca	ccttggtcac	tcatecttcc	tcagtctcct	ttgtggattc	ttcctcattt	180
atctgacctc	ttgctgggta	accctttcat	atacactctc	cgtaacaaaag	agggcgctact	240
tctgtcgtct	tgagcgnact	gatggnaccc	agcttttggt	cccttttagtg	agggntaatt	300
gcgcgcttgg	cgnaatcatg	gncatagctg	nttncctgng	gaaantgnta	tttcgntnac	360
aattncacac	aacatacnag	ccgggagcat	aaaggggnnaa	gncctggggg	gcctaattgag	420
ggagcttact	cacaataatt	gggggtngcc	cactggcccc	ttttcaggcg	ggaaaacctn	480
gcggggccag	ctggaataaa	tgaatcgggc	cacgcgcgcg	ggaggagggc	gggttnngga	540
attgggcgct	ttttccnttt	ctnggttaat	ggactnggtn	ggcnngtcc	gttcgggttg	600
gggggancgg	nnt					613

&lt;210&gt; 1084

&lt;211&gt; 886

&lt;212&gt; DNA

&lt;213&gt; Unknown (H38g934 nucleotide)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(886)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1084

ggteccentcg	ngtatnctt	naccctctga	tgtctctga	gcggccggca	gggtgatgga	60
tatctgcaga	attcgccctt	ctgttacgca	ggaatatata	aaggggttac	tgaggataaa	120
ataaatgggt	tactgaggaa	taaataaatg	ggttactgag	gaacaaatac	atagggttga	180
aagaactgta	aaatagaaaa	aggaccttnt	gctgctctc	aggatggcgg	nacttagggg	240
ccatgtacat	gacgatgnng	ctgccnntna	agagtccac	tntcancng	cctcagcccg	300
ncttttttct	cacnnccnt	ntttntctnc	cctcttnnnc	tcttttcttc	ctattccccc	360
cccttccnct	cctccctttt	gentnaccat	tgncctnat	ccctttaatt	cnntcnntcn	420
tctccctctc	attccttcnn	tnttcgntt	cantctctnc	ctctttctcc	ccnctttct	480
ctctctctct	cttctctng	tcatectngt	tentctctt	ncctanttcc	ctctancctt	540
ntcttattnc	tcctctatnc	cctctcatct	caentctent	cctctentcn	tacttnnctc	600
nnctcttcen	ctccgtctnc	cnctttctct	tentnacgcc	acccctcnnn	cntnctctct	660
ntctentcct	cactctctcc	tctccctnnc	cntcaenttt	ctccnctctc	acntcctatn	720
ctcncntctc	nncttnactt	tgtaacgctc	tctctctctc	ctctacgcac	nttttatctc	780
ttatctcncn	catcncctc	ntttctncac	nctattnact	cttttctcnc	atactntatn	840
ctcctntcnn	cttanatcnc	ctcccttctn	tnanccnntc	actgcn		886

&lt;210&gt; 1085

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g1 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1085

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
 1          5          10          15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
          20          25          30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
          35          40          45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
          50          55          60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
          65          70          75          80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
          85          90          95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
          100          105          110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
          115          120          125

```

&lt;210&gt; 1086

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g2 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1086

```

His Thr Glu Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20          25          30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Met Arg Asn Leu Leu Ser
          35          40          45
Ile Leu Thr Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
          50          55          60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
          65          70          75          80
Val Pro Thr Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Val Phe Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
          145          150          155          160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Phe Asp Ser Thr Met

```

```

      195              200              205
Phe Ala Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210              215              220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ser
 225              230              235              240
Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly
      245              250              255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260              265              270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
 275              280              285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu
 290              295              300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg
 305              310              315              320
Phe Ser

```

&lt;210&gt; 1087

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g3 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1087

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1              5              10              15
Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
      20              25              30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35              40              45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50              55              60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65              70              75              80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
      85              90              95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
      100              105              110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Cys
      115              120              125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
      130              135              140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
      145              150              155              160
Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
      165              170              175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
      180              185              190
His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
      195              200              205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
      210              215              220
Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
      225              230              235              240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
      245              250              255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
      260              265              270

```

Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu  
 290 295 300  
 Trp Arg Pro Phe Gln Arg Pro Lys  
 305 310

<210> 1088

<211> 305

<212> PRT

<213> Unknown (H38g4 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(305)

<223> Xaa = Any Amino Acid

<400> 1088

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro  
 1 5 10 15  
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile  
 20 25 30  
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe  
 35 40 45  
 Leu His Thr Pro Met Tyr Phe Leu Gly Arg Leu Ser Thr Phe Asp  
 50 55 60  
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser  
 65 70 75 80  
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe  
 85 90 95  
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met  
 100 105 110  
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu  
 115 120 125  
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu  
 130 135 140  
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu  
 145 150 155 160  
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro  
 165 170 175  
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val  
 180 185 190  
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val  
 195 200 205  
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser  
 210 215 220  
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val  
 225 230 235 240  
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Ile Tyr Leu Lys Ser  
 245 250 255  
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val  
 260 265 270  
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu  
 275 280 285  
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val  
 290 295 300  
 Cys  
 305

<210> 1089  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g5 protein)

<220>  
 <223> Synthetic construct

<400> 1089

```

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
          20           25           30
Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
          35           40           45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50           55           60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
65           70           75           80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
          85           90           95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
          100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
          115          120          125
Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
          130          135          140
Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
          145          150          155          160
Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
          165          170          175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
          180          185          190
Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
          195          200          205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
          210          215          220
Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
          225          230          235          240
Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
          245          250          255
Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
          260          265          270
Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
          290          295          300
Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
          305          310          315

```

<210> 1090  
 <211> 342  
 <212> PRT  
 <213> Unknown (H38g6 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(342)  
 <223> Xaa = Any Amino Acid



&lt;400&gt; 1090

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Ile Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Glu Lys Leu Leu Ile Ile Met
          35          40          45
Ala Val Ser Pro Asp Phe His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
          115          120          125
Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
 130          135          140
Phe Gln Asp Leu Leu Ser Leu Phe Phe Phe Ser Phe Phe Phe Phe
 145          150          155          160
Leu Arg Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
          165          170          175
Thr Cys Phe Lys Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser
          180          185          190
Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
          195          200          205
Leu Tyr Phe Pro Ala Ala Val Leu Gly Phe Leu Pro Ile Ser Gly Thr
 210          215          220
Leu Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser
 225          230          235          240
Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser
          245          250          255
Ala Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser
          260          265          270
Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
          275          280          285
Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn
          290          295          300
Arg Asp Met Lys Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Xaa
 305          310          315          320
Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Lys
          325          330          335
Lys Gly Ser Lys Val Lys
          340

```

&lt;210&gt; 1091

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g7 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1091

```

Met Val Lys Gly Asn His Ser Thr Val Thr Glu Phe Asn Leu Ala Gly

```

```

1           5           10           15
Leu Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20           25           30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Ser Met Ile Thr Leu
35           40           45
Ile Gly Phe Ser Ser His Leu His Thr Pro Met Tyr His Phe Leu Ser
50           55           60
Ser Leu Ser Phe Ile Asp Leu Cys Gln Ser Ser Val Ile Thr Pro Lys
65           70           75           80
Met Leu Val Asn Phe Val Ser Glu Arg Asn Ile Ile Ser Tyr Pro Ala
85           90           95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Leu Val Ile Ser Glu Cys
100          105          110
His Met Leu Ala Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Asn
115          120          125
Pro Leu Leu Tyr His Val Ala Met Ser Tyr Gln Val Cys Ser Trp Met
130          135          140
Val Val Glu Val Tyr Phe Met Gly Phe Ile Gly Ala Ser Ala His Thr
145          150          155          160
Val Cys Met Leu Arg Val Leu Phe Cys Lys Ala Asp Val Ile Asn His
165          170          175
Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu Ser Arg Ser Ser Ile
180          185          190
Ser Ile Asn Glu Ile Val Val Cys Ala Cys Ser Ala Phe Asn Ile Leu
195          200          205
Phe Arg Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Val Ala Ser
210          215          220
Ile Leu Cys Ile Arg Ser Thr Glu Gly Arg Ser Lys Thr Phe Ser Thr
225          230          235          240
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
245          250          255
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
260          265          270
Val Ser Ser Val Phe Tyr Ala Thr Val Val Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Ile Lys Phe
290          295          300
Leu Glu Lys Arg Ser Phe Leu Xaa Lys
305          310

```

&lt;210&gt; 1092

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g8 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1092

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
1           5           10           15
Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
20           25           30
Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
35           40           45
Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
50           55           60

```

```

Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
65          70          75          80
Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
          85          90          95
Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser
          100          105          110
Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
          115          120          125
Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
          130          135          140
Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
145          150          155          160
Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
          165          170          175
Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
          180          185          190
Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
          195          200          205
Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
          210          215          220
Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
225          230          235          240
Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
          245          250          255
Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
          260          265          270
Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
          290          295          300
Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
305          310          315          320
Leu Ser Ser Lys Pro Lys Arg Arg
          325

```

&lt;210&gt; 1093

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g9 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1093

```

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
1          5          10          15
Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
          20          25          30
Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
          35          40          45
Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
          50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
65          70          75          80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
          85          90          95
Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
          100          105          110
Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
          115          120          125
Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

```

```

      130              135              140
Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys
145              150              155              160
Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His
      165              170              175
Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr
      180              185              190
Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu
      195              200              205
Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala
      210              215              220
Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr
      225              230              235              240
Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile
      245              250              255
Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys
      260              265              270
Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu
      290              295              300
Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys
      305              310              315

```

&lt;210&gt; 1094

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g10 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1094

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Thr Tyr Leu Ala Thr Val Leu Arg Asn Val Leu Asn
      35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
      50      55      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Ser Tyr Ser Arg Val Ile Ser
      85      90      95
His Glu Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
      165      170      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu Ala Cys
      180      185      190

```

Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Phe Ser Xaa Phe Lys Ile  
 210 215 220  
 Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser  
 305 310 315 320  
 Phe Phe Leu Cys

&lt;210&gt; 1095

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g11 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1095

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu  
 20 25 30  
 Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Leu Leu  
 35 40 45  
 Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys  
 65 70 75 80  
 Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu  
 85 90 95  
 Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys  
 100 105 110  
 Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu  
 130 135 140  
 Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile  
 145 150 155 160  
 Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met  
 180 185 190  
 Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu  
 195 200 205  
 Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr  
 210 215 220  
 Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Leu Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met  
 245 250 255  
 Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile

260 265 270  
 Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr  
 290 295 300  
 Cys Gln Ala Ser Arg Ser Asp  
 305 310

<210> 1096  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g12 protein)

<220>  
 <223> Synthetic construct

<400> 1096  
 Met Glu Gln Val Asn Lys Thr Val Val Arg Glu Phe Val Val Leu Gly  
 1 5 10 15  
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu  
 20 25 30  
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr  
 35 40 45  
 Ile Val Leu Asp Arg Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Val Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Phe Gly Ser Ser His Ser  
 100 105 110  
 Phe Leu Leu Ala Ala Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu  
 130 135 140  
 Met Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr  
 145 150 155 160  
 Ser Leu Val Phe His Leu Pro Phe His Ser Ser Asn Gln Leu His His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser  
 180 185 190  
 Gly Phe Ser Gln Leu Val Ile Phe Met Leu Gly Val Phe Ala Leu Val  
 195 200 205  
 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala  
 210 215 220  
 Ile Leu Lys Ile Pro Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ile Val Val Thr Val His Tyr Ser Cys Ala Ser  
 245 250 255  
 Phe Ile Tyr Leu Arg Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr  
 260 265 270  
 Leu Ile Ser Val Ser Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr  
 290 295 300  
 Ile Gly Gln Thr Phe Tyr Pro Leu Ser  
 305 310

<210> 1097  
 <211> 318  
 <212> PRT

&lt;213&gt; Unknown (H38g13 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1097

Cys	Val	Asp	Ser	Ser	Leu	Lys	Xaa	Glu	Ile	Thr	Gln	Xaa	Cys	Leu	Ser
1				5					10					15	
Leu	Leu	Leu	Xaa	Met	Ala	Glu	Gly	Trp	Arg	Leu	Tyr	Phe	Ile	Ile	Leu
			20					25					30		
Ile	Ile	Ser	Tyr	Lys	Phe	Cys	Thr	Leu	Leu	Gly	Asn	Val	Ile	Phe	Arg
		35					40					45			
Thr	Leu	Val	Cys	Ser	Leu	Gly	Phe	His	Thr	Ser	Cys	Met	Tyr	Phe	Phe
		50				55					60				
Pro	Xaa	Lys	Ile	Ser	Leu	Xaa	Leu	Ala	Xaa	Val	Cys	His	Ser	Ile	Ile
65					70					75					80
Ala	Leu	Pro	Ser	Thr	Gln	Lys	Xaa	Ala	Ile	Asn	Val	Gln	Gly	Ala	Ala
			85						90					95	
Val	His	Val	Phe	Ser	Phe	Pro	Cys	Leu	Tyr	Cys	Pro	Glu	Ile	Phe	Leu
			100					105					110		
His	Ser	Leu	Thr	Gln	Cys	His	Pro	Phe	Ile	Ala	Ile	Gly	Tyr	Pro	Leu
		115					120					125			
Gln	Gly	Met	His	Thr	Ile	Thr	His	Lys	Leu	Tyr	Ile	Leu	Leu	Thr	Thr
		130				135					140				
Gly	Pro	Trp	Arg	Gly	Cys	Xaa	Leu	His	Val	Asn	Leu	Leu	Thr	Ala	Ile
145					150					155					160
Leu	Gly	Ser	Tyr	Pro	Asn	Pro	Val	Pro	Thr	Lys	Leu	Trp	Leu	Ser	Phe
			165						170					175	
Pro	Ser	Ile	Pro	Glu	Val	Lys	Leu	Xaa	Pro	Met	Gln	Ala	Tyr	Thr	Lys
			180					185					190		
Pro	Tyr	Ala	Gly	Leu	Ser	Leu	Cys	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser
		195					200					205			
Phe	Ser	Leu	Phe	Ser	Ile	Ile	Ser	Ile	Ser	Tyr	Ile	Cys	Asn	Glu	Ile
		210				215					220				
Asp	Ile	Pro	Lys	Ile	Ile	Ser	Ala	Asp	Ser	Val	His	Gly	Ala	Phe	Ser
225					230					235					240
Thr	Cys	Leu	Ala	His	Leu	Phe	Ala	Phe	Ser	Thr	Cys	Ile	Ala	Gln	Pro
			245							250				255	
Ala	Val	Cys	Asn	Ser	Leu	Trp	Pro	Trp	Thr	Glu	Ala	Gln	Thr	Glu	Ser
			260					265					270		
Ser	Arg	Asp	Ser	Val	Ile	Gln	Arg	Pro	Asn	Leu	Cys	Val	Thr	Ile	Ser
		275					280					285			
Leu	Asn	Ser	Leu	Ile	Ser	Ser	Leu	Arg	Asn	Glu	Ser	Val	Lys	Gln	Ala
		290				295					300				
Ser	His	Lys	Ile	Phe	Lys	Glu	Gln	Thr	Leu	Phe	Met	Lys	Ile		
305					310					315					

&lt;210&gt; 1098

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g14 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1098

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1          5          10          15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
          20          25          30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35          40          45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
          130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
145          150          155          160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
          195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
          210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225          230          235          240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
          245          250          255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
          275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
          290          295          300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
305          310          315          320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
          325          330

```

<210> 1099

<211> 322

<212> PRT

<213> Unknown (H38g15 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1099

```

His Thr Gly Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15

```



Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Thr Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr L u Val Thr Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Il Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Xaa Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Val Cys Leu Ile Gln Met Ser Leu Leu Val Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Leu Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu  
 165 170 175  
 Ile Ser Asn Ser Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg  
 305 310 315 320  
 Phe Ser

&lt;210&gt; 1100

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g16 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1100

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile  
 1 5 10 15  
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn  
 20 25 30  
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu  
 35 40 45  
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu  
 50 55 60  
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu  
 65 70 75 80  
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu

```
<210> 1101
<211> 257
<212> PRT
<213> Unknown (H38q17 protein)
```

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(257)
<223> Xaa = Any Amino Acid
```

<div> <div>&lt;400&gt;</div> <div>1101</div> </div>															
Phe	Ile	Leu	Trp	Gly	Phe	Phe	Asp	His	Pro	Xaa	Pro	Glu	Met	Phe	Leu
1				5					10				15		
Phe	Ile	Met	Gly	Leu	Val	Gly	Leu	Ser	Leu	His	Thr	Gly	Gly	Gln	His
			20					25					30		
Leu	Asn	Tyr	Cys	Gly	Thr	Gln	Gly	Ile	Phe	Xaa	Gly	Ser	Thr	Lys	Cys
	35						40					45			
Ile	Ile	Leu	Ala	Val	Thr	Ser	Leu	Asp	Pro	Tyr	Ile	Ala	Ile	Cys	Lys
	50					55					60				
His	Leu	Arg	Tyr	Pro	Ala	Ile	Met	His	Gln	Gln	Leu	Cys	Val	Leu	Leu
65					70					75				80	
Val	Ala	Met	Ala	Trp	Leu	Ser	Ser	Leu	Ala	Asn	Ser	Leu	Gln	Ser	Ser
			85						90					95	
Leu	Ala	Val	Gln	Leu	Pro	Leu	Gly	Gly	Asn	Lys	Val	Asp	Asp	Phe	Leu
			100					105					110		
Cys	Glu	Val	Ser	Ala	Met	Ile	Lys	Ile	Ser	Arg	Phe	Asp	Thr	Thr	Phe
	115						120					125			
Asn	Val	Ser	Met	Leu	Ser	Ile	Val	Arg	Ile	Phe	Xaa	Ser	Leu	Val	Leu
	130					135					140				
Xaa	Ser	Ile	Ile	Phe	Ala	Tyr	Cys	Gly	Phe	Ile	Val	Ala	Thr	Val	Leu
145					150					155				160	
Arg	Ile	Gln	Ser	Ser	Gly	Gly	Lys	Lys	Glu	Val	Phe	Asn	Thr	Cys	Gly
				165					170					175	

Ser His Ile Val Ser Leu Leu Tyr Gly Pro Val Ile Ser Met Tyr Val  
                   180                  185                  190  
 Gln Pro Ser Ala Asn Ser Gln Asp Lys Asn Lys Phe Met Ser Leu Phe  
                   195                  200                  205  
 Tyr Ser Leu Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Ser  
                   210                  215                  220  
 Asn Arg Asp Ile Lys Gly Ala Met Arg Arg Leu Leu Val Phe Leu Tyr  
 225                  230                  235                  240  
 His Gln Glu Glu Asn Lys Ser Asn Tyr Cys Leu Tyr Ser Thr Phe Phe  
                   245                  250                  255  
 Ile

<210> 1102

<211> 334

<212> PRT

<213> Unknown (H38g18 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1102

Ser Thr Asp Pro Gln Asn Val Thr Asp Val Ser Arg Phe Leu Leu Leu  
 1                  5                  10                  15  
 Lys Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
                   20                  25                  30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
                   35                  40                  45  
 Ala Val Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro  
 65                  70                  75                  80  
 Lys Met Val Val Asp Ile Gln Ser His Arg Val Ile Ser Tyr Ala Gly  
                   85                  90                  95  
 Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu  
                   100                  105                  110  
 Asn Met Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys  
                   115                  120                  125  
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe  
                   130                  135                  140  
 Leu Leu Leu Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu  
 145                  150                  155                  160  
 His Asn Met Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile  
                   165                  170                  175  
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys  
                   180                  185                  190  
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Val Phe  
                   195                  200                  205  
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val  
                   210                  215                  220  
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Pro Cys  
 225                  230                  235                  240  
 Ser Thr Cys Gly Ser His Leu Ser Val Phe Cys Xaa Phe Tyr Gly Thr  
                   245                  250                  255  
 Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys  
                   260                  265                  270  
 Ala Ala Val Ala Ser Leu Met Tyr Lys Met Val Thr Pro Met Leu Asn

```

      275              280              285
Pro Ser Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg
  290              295              300
Gln Pro His Gly Ser Thr Val Xaa Ser Gln Asp Leu Leu Ile Cys Ser
  305              310              315              320
Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
      325              330

```

&lt;210&gt; 1103

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g19 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1103

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
  1              5              10              15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
      20              25              30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
      35              40              45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
      50              55              60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
      65              70              75              80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
      85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100              105              110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
      115              120              125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
      130              135              140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
      145              150              155              160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
      165              170              175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
      180              185              190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
      195              200              205
Gly Thr Phe Phe Ile Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
      210              215              220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
      225              230              235              240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
      245              250              255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
      260              265              270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
      275              280              285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
      290              295              300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
      305              310              315              320

```



<210> 1105  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g21 protein)

<220>  
 <223> Synthetic construct

<400> 1105  
 Met Glu Thr Arg Lys Tyr Ser Ala Met Thr Glu Phe Phe Leu Val Gly  
 1 5 10 15  
 Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu  
 20 25 30  
 Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Leu Leu Ile Ile Ile  
 35 40 45  
 Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Pro  
 65 70 75 80  
 Met Leu Ile Ile Phe Met Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Thr Glu Cys  
 100 105 110  
 Val Leu Leu Ala Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Ile Ile Met Asn Gly Val Leu Tyr Val Gln Met  
 130 135 140  
 Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Gln Thr  
 145 150 155 160  
 Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Val Ile Asp His  
 165 170 175  
 Ile Thr Cys Glu Ile Leu Ala Leu Leu Lys Leu Val Cys Ser Asp Ile  
 180 185 190  
 Thr Ile Asn Val Leu Ile Met Thr Val Thr Asn Ile Val Ser Leu Val  
 195 200 205  
 Ile Leu Leu Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser  
 210 215 220  
 Ile Leu Arg Ile Asn Cys Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Ser Ile Val Val Ile Leu Phe Tyr Gly Ser Ala Leu  
 245 250 255  
 Phe Met Tyr Met Lys Pro Lys Ser Lys Asn Thr Asn Thr Ser Asp Glu  
 260 265 270  
 Ile Ile Gly Leu Ser Tyr Gly Val Val Ser Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Val Lys Lys Val  
 290 295 300  
 Leu Ser Arg His Leu His Leu Leu Lys Met  
 305 310

<210> 1106  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g22 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1106

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
1      5      10      15
Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
20      25      30
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Val Val Thr Ile Thr
35      40      45
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
50      55      60
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
65      70      75      80
Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
85      90      95
Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
100     105     110
Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
115     120     125
His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
130     135     140
Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
145     150     155     160
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
165     170     175
Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
180     185     190
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
195     200     205
Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
210     215     220
Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
225     230     235     240
His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
245     250     255
Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe
260     265     270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275     280     285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
290     295     300
Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
305     310     315

```

&lt;210&gt; 1107

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g23 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1107

```

Met Arg Asn Phe Ser Val Val Ser Glu Phe Ile Leu Leu Gly Ile Pro
1      5      10      15
His Thr Glu Gly Leu Glu Thr Ile Leu Leu Val Leu Phe Leu Ser Phe
20      25      30
Tyr Ile Phe Thr Leu Met Gly Asn Leu Leu Ile Leu Leu Ala Ile Val

```

```

      35              40              45
Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Lys Leu
  50              55              60
Ser Val Phe Asp Leu Phe Phe Pro Ser Val Ser Ser Pro Lys Met Leu
  65              70              75              80
Cys Tyr Leu Ser Gly Asn Ser Arg Ala Ile Ser Tyr Ala Gly Cys Ala
      85              90              95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu
      100              105              110
Tyr Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
      115              120              125
Arg Tyr Thr Ile Ile Met Ser His Arg Ala Cys Ile Ile Leu Ala Met
      130              135              140
Gly Thr Ser Phe Phe Gly Cys Ile Gln Ala Thr Phe Leu Thr Thr Leu
      145              150              155              160
Thr Phe Gln Leu Pro Tyr Cys Val Pro Asn Glu Val Asp Tyr Tyr Phe
      165              170              175
Cys Asp Ile Pro Val Met Leu Lys Leu Ala Cys Ala Asp Thr Ser Ala
      180              185              190
Leu Glu Met Val Gly Phe Ile Ser Val Gly Leu Met Pro Leu Ser Cys
      195              200              205
Phe Leu Leu Ile Leu Thr Ser Tyr Ser Gly Ile Val Phe Ser Ile Leu
      210              215              220
Xaa Ile Cys Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser
      225              230              235              240
Ala His Leu Thr Ala Ile Leu Leu Phe Tyr Met Pro Val Val Leu Ile
      245              250              255
Tyr Leu Arg Pro Thr His Ser Leu Trp Leu Asp Ala Thr Val Gln Ile
      260              265              270
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
      275              280              285
Arg Asn Lys Glu Val Lys Leu Ser Leu Arg Lys Val Leu Tyr Gln Leu
      290              295              300
Gly Phe Leu Pro Glu Gln Leu
      305              310

```

&lt;210&gt; 1108

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g24 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1108

```

Met Asp Ile Pro Gln Asn Ile Thr Glu Phe Phe Met Leu Gly Leu Ser
  1              5              10              15
Gln Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile
      20              25              30
Tyr Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr
      35              40              45
Ser Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu
      50              55              60
Ser Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile
      65              70              75              80
Ala Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met
      85              90              95
Ala Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu
      100              105              110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115              120              125

```



```

His Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly
  130                135                140
Val Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu
 145                150                155                160
Val Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala
                165                170                175
Cys Asp Leu Tyr Pro Leu Leu Glu Val Ala Cys Thr Asn Thr Tyr Val
                180                185                190
Ile Gly Leu Leu Val Val Ala Asn Ser Gly Leu Ile Cys Leu Leu Asn
                195                200                205
Phe Leu Met Leu Ala Ala Ser Tyr Ile Val Ile Leu Tyr Ser Leu Arg
 210                215                220
Ser His Ser Ala Asp Gly Arg Cys Lys Ala Leu Ser Thr Cys Gly Ala
 225                230                235                240
His Phe Ile Val Val Ala Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
                245                250                255
Val His Pro Phe Ser Thr Leu Pro Ile Asp Lys Asn Met Ala Leu Phe
                260                265                270
Tyr Gly Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
                275                280                285
Asn Glu Glu Val Lys Asn Ala Met Arg Lys Leu Phe Thr Trp
 290                295                300

```

&lt;210&gt; 1109

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g25 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1109

```

Met Ile Thr Leu Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr
  1                5                10                15
Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val
                20                25                30
Ile Thr Pro Lys Met Leu Val Asn Phe Ala Thr Glu Lys Asn Ile Ile
  35                40                45
Ser Tyr Pro Glu Cys Met Ala Gln Leu Tyr Leu Phe Ser Ile Phe Ala
  50                55                60
Ile Ala Glu Cys His Met Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val
  65                70                75                80
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His
                85                90                95
Cys Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser
                100                105                110
Thr Ile His Thr Ser Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn
                115                120                125
Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser
                130                135                140
Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala
 145                150                155                160
Phe Asn Ile Leu Met Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe
                165                170                175
Ile Ile Ala Ser Ile Leu Arg Ile His Ser Thr Glu Gly Arg Ser Lys
                180                185                190
Ala Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe
                195                200                205
Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met
 210                215                220
Asp Gln Arg Lys Val Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met

```

225		230		235		240									
Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala
		245		250		255									
Val	Lys	Lys	Ile	Leu	His	Gln	Thr	Ala	Cys						
		260		265											

&lt;210&gt; 1110

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g26 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1110

Met	Gly	Asn	Ser	Asn	Gln	Ser	Phe	Met	Thr	Glu	Phe	Val	Leu	Leu	Gly
1				5					10					15	
Leu	Ser	Gly	Tyr	Pro	Glu	Leu	Glu	Ala	Ile	Tyr	Phe	Val	Leu	Val	Leu
		20					25					30			
Cys	Met	Tyr	Leu	Val	Ile	Leu	Leu	Gly	Asn	Gly	Val	Ile	Ile	Ile	Val
	35					40					45				
Ser	Val	Tyr	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50				55					60					
Asn	Leu	Ser	Phe	Leu	Asp	Ile	Cys	Tyr	Thr	Ser	Ser	Ser	Ile	Pro	Leu
65				70					75					80	
Phe	Leu	Ser	Ser	Phe	Leu	Thr	Ser	Lys	Lys	Thr	Ile	Ser	Phe	Ser	Gly
			85					90					95		
Cys	Gly	Val	Gln	Met	Phe	Leu	Ser	Phe	Ala	Met	Gly	Ala	Thr	Glu	Cys
		100					105					110			
Val	Leu	Leu	Ser	Met	Met	Ala	Phe	Asp	Cys	Tyr	Val	Ala	Ile	Cys	Asn
	115					120					125				
Pro	Leu	Xaa	Tyr	Pro	Ile	Ile	Met	Ser	Lys	Ala	Ser	Tyr	Met	Ser	Met
	130				135					140					
Ala	Ala	Gly	Ser	Trp	Ile	Gly	Gly	Gly	Ile	Asn	Ser	Val	Leu	Gln	Thr
145				150					155					160	
Ser	Leu	Ala	Met	Arg	Leu	Pro	Phe	Cys	Gly	Asp	Asn	Val	Ile	Asn	His
			165					170					175		
Phe	Thr	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	Ala	Cys	Ala	Asn	Ile
		180					185				190				
Ser	Ile	Asn	Ile	Ile	Ser	Met	Val	Val	Ala	Ser	Met	Ile	Phe	Leu	Val
	195				200						205				
Gly	Pro	Val	Leu	Phe	Ile	Phe	Val	Thr	Tyr	Val	Phe	Ile	Leu	Ser	Thr
	210				215						220				
Ile	Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Ser	Ser	Thr
225				230					235					240	
Cys	Ser	Ala	His	Leu	Thr	Val	Val	Ile	Ile	Phe	Tyr	Arg	Thr	Ile	Leu
			245					250					255		
Phe	Met	Tyr	Ala	Lys	Pro	Lys	Ala	Lys	Asp	Ser	Ser	Gly	Ala	Asp	Lys
		260					265					270			
Glu	Gln	Val	Thr	Asp	Lys	Ile	Ile	Ser	Leu	Phe	Tyr	Gly	Val	Val	Thr
	275					280					285				
Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys
	290				295						300				
Ala	Ala	Val	Lys	Ser	Ile	Leu	Xaa	Gln	Lys	Cys	Phe	Leu	Glu		
305				310					315						

&lt;210&gt; 1111

<211> 329  
 <212> PRT  
 <213> Unknown (H38g27 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(329)  
 <223> Xaa = Any Amino Acid

<400> 1111

Lys	Ser	Met	Lys	Lys	Met	Asn	Asn	Val	Ile	Glu	Phe	Ile	Leu	Leu	Gly	1	5	10	15
Leu	Thr	His	Asn	Pro	Glu	Leu	Gln	Lys	Phe	Leu	Phe	Val	Met	Phe	Leu	20	25	30	
Ile	Thr	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Phe	Ile	Ser	Val	Ile	35	40	45	
Ile	Phe	Ile	Ser	Pro	Ala	Leu	Gly	Ser	Pro	Met	Tyr	Ser	Phe	Pro	Ser	50	55	60	
Tyr	Leu	Phe	Ile	Ile	Asp	Ile	Phe	Cys	Ser	Ser	Ser	Ile	Ala	Pro	Lys	65	70	75	80
Met	Asn	Phe	Asp	Leu	Ile	Ser	Glu	Lys	Asn	Thr	Ile	Ser	Phe	Asn	Gly	85	90	95	
Cys	Met	Thr	Gln	Leu	Phe	Thr	Glu	His	Phe	Phe	Thr	Glu	His	Phe	Phe	100	105	110	
Glu	Ala	Ala	Glu	Ile	Ile	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	His	Tyr	115	120	125	
Val	Ala	Ile	Arg	Lys	Pro	Leu	His	Tyr	Ala	Thr	Ile	Met	Ser	Gln	Pro	130	135	140	
Met	Cys	Gly	Phe	Leu	Met	Val	Val	Ala	Gly	Ile	Leu	Gly	Phe	Val	His	145	150	155	160
Gly	Gly	Ile	Gln	Thr	Leu	Phe	Ile	Ala	Gln	Leu	Pro	Phe	Cys	Gly	Pro	165	170	175	
Asn	Val	Ile	Asn	His	Phe	Met	Cys	Asp	Leu	Val	Pro	Leu	Leu	Glu	Leu	180	185	190	
Ala	Cys	Thr	Asp	Thr	His	Thr	Leu	Gly	Pro	Leu	Ile	Ala	Ala	Asn	Ser	195	200	205	
Gly	Ser	Leu	Cys	Phe	Leu	Ile	Phe	Ser	Met	Leu	Val	Ala	Ser	Tyr	Val	210	215	220	
Ile	Ile	Leu	Cys	Phe	Leu	Arg	Thr	His	Ser	Ser	Glu	Gly	Arg	Arg	Lys	225	230	235	240
Ala	Leu	Ser	Ser	Cys	Ala	Ser	His	Ile	Phe	Ile	Val	Ile	Leu	Phe	Phe	245	250	255	
Val	Pro	Phe	Ser	Tyr	Leu	Tyr	Leu	Arg	Pro	Ile	His	Ser	Phe	Pro	Thr	260	265	270	
Asp	Lys	Ala	Val	Thr	Val	Phe	Cys	Thr	Leu	Phe	Thr	Pro	Met	Leu	Asn	275	280	285	
Pro	Leu	Ile	Tyr	Thr	Leu	Lys	Asn	Lys	Glu	Val	Lys	Asn	Val	Ile	Lys	290	295	300	
Lys	Leu	Trp	Lys	Gln	Ile	Met	Thr	Thr	Asp	Asp	Lys	Xaa	Val	Leu	Xaa	305	310	315	320
His	Lys	His	Leu	Gly	Lys	Asn	Ile	Trp								325			

<210> 1112  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g28 protein)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1112

```

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1      5      10      15
Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20      25      30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35      40      45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50      55      60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65      70      75      80
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
 85      90      95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
100      105      110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
115      120      125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
130      135      140
Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Ser
145      150      155      160
Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
165      170      175
Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
180      185      190
Ser Asp Asn Glu Phe Ile Met Leu Val Ala Thr Thr Leu Phe Ile Leu
195      200      205
Thr Pro Leu Leu Leu Ile Ile Val Ser Tyr Thr Leu Ile Ile Val Ser
210      215      220
Ile Phe Lys Ile Ser Ser Ser Glu Gly Arg Ser Lys Ala Ser Ser Thr
225      230      235      240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
245      250      255
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
260      265      270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
275      280      285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
290      295      300
Glu Ala Val Lys His Leu Leu Asn Arg Arg Phe Phe Ser Lys
305      310      315

```

&lt;210&gt; 1113

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g29 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1113

```

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala
 1      5      10      15
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp
 20      25      30
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Ile Phe Asp Leu Leu
 35      40      45
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe
 50      55      60

```

Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met  
 65 70 75 80  
 Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile  
 85 90 95  
 Thr Met Asn Arg Gln Val Cys Gly Leu Leu Val Ala Met Ala Trp Val  
 100 105 110  
 Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu  
 115 120 125  
 Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe  
 130 135 140  
 Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe  
 145 150 155 160  
 Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu  
 165 170 175  
 Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser  
 180 185 190  
 Thr Cys Ala Phe His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys  
 195 200 205  
 Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala  
 210 215 220  
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile  
 225 230 235 240  
 Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp  
 245 250 255  
 Ser Gln Ile Ile Trp Gly Asn Asn  
 260

&lt;210&gt; 1114

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g30 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1114

Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro  
 1 5 10 15  
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val  
 20 25 30  
 Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys  
 35 40 45  
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu  
 50 55 60  
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met  
 65 70 75 80  
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe  
 85 90 95  
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser  
 100 105 110  
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu  
 115 120 125  
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val  
 130 135 140  
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg  
 145 150 155 160  
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe  
 165 170 175  
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe  
 180 185 190  
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp

```

      195              200              205
Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
  210              215              220
Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile
  225              230              235
Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu
      245              250              255
Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile
      260              265              270
Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val
      275              280              285
Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
      290              295              300
Leu Ser Lys His Arg Phe Ser Arg
  305              310

```

&lt;210&gt; 1115

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g31 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(285)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1115

```

Asp Thr Glu Pro Gln Asn Leu Thr Ala Val Ser Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Phe
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Ile Gly Ser Asp Ser His Leu Asp Thr Pro Met Tyr Phe Phe Leu
      50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65              70              75              80
Lys Met Ile Glu Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly
      85              90              95
Asp Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp
      100              105              110
Asp Met Ile Leu Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys
      115              120              125
His Pro Leu Asn Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu
      130              135              140
Leu Val Leu Val Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145              150              155              160
Asn Leu Ile Val Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser
      165              170              175
Asn Phe Phe Cys Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp
      180              185              190
Ser Asp Ile Asn Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly
      195              200              205
Phe Leu Arg Ile Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe
      210              215              220
Pro Ile Leu Arg Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser
      225              230              235              240
Thr Xaa Gly Ser Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255

```

Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp  
                   260                  265                  270  
 Val Val Ala Ser Val Met Tyr Ala Val Val Val Thr Pro  
                   275                  280                  285

<210> 1116  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g32 protein)

<220>  
 <223> Synthetic construct

<400> 1116  
 Met Gly Glu Ile Asn Gln Thr Leu Val Ser Glu Phe Leu Leu Leu Gly  
   1                  5                  10                  15  
 Leu Ser Gly Tyr Pro Lys Ile Glu Ile Val Tyr Phe Ala Leu Ile Leu  
                   20                  25                  30  
 Val Met Tyr Leu Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala  
                   35                  40                  45  
 Ser Ile Phe Asp Ser His Phe His Thr Pro Met Tyr Phe Phe Leu Gly  
   50                  55                  60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Val Pro Ser  
  65                  70                  75                  80  
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly  
                   85                  90                  95  
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys  
                   100                  105                  110  
 Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
                   115                  120                  125  
 Pro Leu Arg Tyr Pro Ile Ile Leu Ser Lys Val Ala Tyr Val Leu Met  
  130                  135                  140  
 Ala Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Ala Val Gln Thr  
  145                  150                  155                  160  
 Leu Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn Ile Ile Asn His  
                   165                  170                  175  
 Phe Ala Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile  
                   180                  185                  190  
 Ser Leu Asn Ile Ile Thr Met Val Ile Ser Asn Met Ala Phe Leu Val  
                   195                  200                  205  
 Leu Pro Leu Met Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr  
  210                  215                  220  
 Ile Leu Gln Met Asn Ser Ala Thr Gly Arg Arg Lys Ala Phe Ser Thr  
  225                  230                  235                  240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe  
                   245                  250                  255  
 Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Ile Gly Glu Glu Lys  
                   260                  265                  270  
 Leu Gln Ala Leu Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr  
                   275                  280                  285  
 Pro Met Leu Asn Pro Ile Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys  
  290                  295                  300  
 Ala Ala Val Lys Tyr Leu Leu Asn Lys Lys Pro Ile His  
  305                  310                  315

<210> 1117  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g33 protein)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1117

```

M t Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
 1      5      10      15
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
 20      25      30
His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
 35      40      45
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
 50      55      60
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
 65      70      75      80
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
 85      90      95
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
 100     105     110
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
 115     120     125
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
 130     135     140
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
 145     150     155     160
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
 165     170     175
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
 180     185     190
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
 195     200     205
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
 210     215     220
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
 225     230     235     240
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
 245     250     255
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
 260     265     270
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275     280     285
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg
 290     295     300
Ser Leu Gly Glu Lys
305

```

&lt;210&gt; 1118

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g34 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1118

```

Ala Thr Cys His Leu Xaa Thr His Asn Ala Ala Pro Phe Leu Leu Pro
 1      5      10      15
Gly Phe Ser Val Leu Glu Ala Thr Tyr His Ser Ile Ser Ile Pro Phe
 20      25      30

```



Phe Ala Val Tyr Val Cys Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr  
           35                          40                          45  
 Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Cys Phe Leu  
       50                          55                          60  
 Ala Thr Leu Arg Gln Asp Leu Met Val Lys Leu Thr Met Met Pro Thr  
 65                          70                          75                          80  
 Val Met Gly Val Leu Trp Met Asn His Lys Glu Val Ile His Gly Ala  
                           85                          90                          95  
 Cys Phe Leu Gln Val Tyr Ile Ile His Ser His Tyr Pro Leu Ala Glu  
                           100                          105                          110  
 Ser Gly Ile Leu Leu Ser Met Ala Tyr Asp Arg Phe Ile Ile Ile His  
                           115                          120                          125  
 Met Leu Leu Arg Tyr Asn Ser Ile Ser Thr Lys Ser Trp Val Lys Ile  
 130                          135                          140  
 Glu Leu Trp Leu Phe Met Arg Asp Phe Leu Ser Leu Val Pro Pro Ile  
 145                          150                          155                          160  
 Leu Pro Leu His Cys Phe Pro Tyr Cys His Ser His Val Leu Phe His  
                           165                          170                          175  
 Thr Phe Phe Leu His Gln Asp Val Leu Lys Leu Ala Cys Ala Asp Ile  
                           180                          185                          190  
 Thr Phe Asn His Leu Tyr Pro Ala Ile Leu Val Ala Leu Ile Phe Phe  
                           195                          200                          205  
 Leu Asp Ala Leu Ile Ile Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr  
 210                          215                          220  
 Val Ile Gly Ile Ala Ser Arg Lys Glu Gln Ala Lys Ala Leu Asn Met  
 225                          230                          235                          240  
 Cys Val Ser His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Ile  
                           245                          250                          255  
 Ser Glu Thr Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val  
                           260                          265                          270  
 His Ile Thr Val Ser Tyr Asp Ser Phe Leu Phe Pro Pro Phe Met Asn  
                           275                          280                          285  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Val  
 290                          295                          300  
 Arg Leu Phe Ser Gly His Arg Met Ala Xaa Ala Leu Phe Ser Glu Phe  
 305                          310                          315                          320  
 Cys Asp Leu His Asp Phe Trp Ala Phe  
                           325

&lt;210&gt; 1119

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g35 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1119

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met  
   1                          5                          10                          15  
 Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His  
                           20                          25                          30  
 Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu  
                           35                          40                          45  
 Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg  
                           50                          55                          60  
 Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr  
 65                          70                          75                          80  
 Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Thr Val Met Ser Tyr  
                           85                          90                          95  
 Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met

```

      100      105      110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
      115      120      125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
      130      135      140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
145      150      155      160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
      165      170      175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
      180      185      190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
      195      200      205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
      210      215      220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
225      230      235      240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
      245      250      255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
      260      265      270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
      275      280      285
Glu Lys Arg Met Arg Ala Val Leu
      290      295

```

&lt;210&gt; 1120

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g36 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1120

```

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
 1      5      10      15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
      20      25      30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
      35      40      45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
      50      55      60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
      65      70      75      80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
      85      90      95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu
      100      105      110
Leu Val Leu Ala Tyr Asp Cys Phe Ile Ala Ile Arg Thr Pro Leu Arg
      115      120      125
Tyr Asn Cys Ile Leu Thr Asn Ser Arg Val Met Asn Ile Gly Leu Gly
      130      135      140
Val Leu Met Arg Gly Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu
145      150      155      160
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys
      165      170      175
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn
      180      185      190
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala
      195      200      205

```

```

Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly
 210                215                220
Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser Leu Asn Thr Cys Val Ser
225                230                235                240
His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser
                245                250                255
Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr
                260                265                270
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile
                275                280                285
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe
                290                295                300
Ser Gly Gln Ser Arg Ala
305                310

```

&lt;210&gt; 1121

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g37 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(332)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1121

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1                5                10                15
Gly Leu Pro Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
                20                25                30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile
                35                40                45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
                50                55                60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65                70                75                80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ala Ile Ser
                85                90                95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Phe Leu Phe Ala Cys
                100                105                110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
                115                120                125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys
                130                135                140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145                150                155                160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Phe Lys Asn Val Glu
                165                170                175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
                180                185                190
Ser Asp Gly Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
                195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
                210                215                220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ser Thr Cys Gly Ser His Gln Ala Val Val Cys Xaa Phe Tyr Arg
                245                250                255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg

```

						260		265				270			
Asn	Gly	Val	Val	Ala	Ser	Leu	Ile	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu
						275		280				285			
Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu
						290		295				300			
Arg	Arg	Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro
						305		310				315			
Phe	Ser	Trp	Trp	Val	Arg	Lys	Gly	Asn	His	Ile	Lys				
						325		330							

**<210> 1122**

**<211> 310**

<212> PRT

<213> Unknown (H38g38 protein)

**<220>**

<223> Synthetic construct

**<400> 1122**

[illegible]

**<210> 1123**

<211> 323  
 <212> PRT  
 <213> Unknown (H38g39 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(323)  
 <223> Xaa = Any Amino Acid

<400> 1123

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Thr
      20           25           30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
      35           40           45
Ala Val Ser Ser Asp Ser His Leu His Thr Ser Met Tyr Phe Val Leu
      50           55           60
Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85           90           95
Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe Phe Ala Cys Ile Glu
      100          105          110
Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln Phe Leu Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys Val Phe
      130          135          140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145          150          155          160
Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
      165          170          175
Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
      180          185          190
Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Gly
      195          200          205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
      210          215          220
Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys Tyr Lys Ala Phe Ser
      225          230          235          240
Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu Phe Tyr Gly Ala Gly
      245          250          255
Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Ser Gly Asn Gly
      260          265          270
Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Pro Trp Arg
      290          295          300
Leu Arg Ser Thr Thr Val Glu Ser Pro Xaa Ser Leu Pro Ser Phe Phe
      305          310          315          320
Leu Cys Leu

```

<210> 1124  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g40 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1124

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20          25          30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35          40          45
Ala Val Ser Ser Asp Pro His Leu His Thr Pro Met Cys Phe Phe Leu
 50          55          60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Met Gln Ser His Thr Arg Val Ile Ser Tyr Glu
 85          90          95
Gly Cys Leu Thr Arg Ile Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
100          105          110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
115          120          125
Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
130          135          140
Phe Leu Leu Val Tyr Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
145          150          155          160
Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile Ser
165          170          175
Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp
180          185          190
Ser Val Ile Asn Ser Ile Phe Met Tyr Phe His Ser Thr Met Phe Gly
195          200          205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
210          215          220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
225          230          235          240
Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr Gly
245          250          255
Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly
260          265          270
Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu
275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg
290          295          300
Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
305          310          315          320

```

<210> 1125

<211> 327

<212> PRT

<213> Unknown (H38g41 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1125

```

Ser Thr Asp Xaa Gln Ser Leu Thr Gly Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Lys Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn
145          150          155          160
Leu Ile Ala Leu Lys Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn
          165          170          175
Phe Leu Cys Asp Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr
          180          185          190
Phe Thr Asn His Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
195          200          205
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser
210          215          220
Ile Leu Arg Val Ser Ser Ser Arg Gly Arg Cys Lys Ala Phe Ser His
225          230          235          240
Leu Xaa Val Val Cys Xaa Tyr Tyr Gly Thr Gly Phe Gly Gly Tyr Leu
          245          250          255
Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val
260          265          270
Met Tyr Met Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu
275          280          285
Arg Asn Arg Asp Ile Lys Ser Val Val Gln Arg Pro His Gly Ser Thr
290          295          300
Val Xaa Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp
305          310          315          320
Val Lys Lys Gly Ser Lys Val
          325

```

&lt;210&gt; 1126

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g42 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1126

```

Met Gly Asn Trp Ser Thr Val Thr Glu Ile Thr Leu Ile Ala Phe Pro
 1          5          10          15
Ala Leu Leu Glu Ile Arg Ile Ser Leu Phe Val Val Leu Val Val Thr
          20          25          30
Tyr Thr Leu Thr Ala Thr Gly Asn Ile Thr Ile Ile Ser Leu Ile Trp
          35          40          45
Ile Asp His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
          50          55          60
Ser Phe Leu Asp Ile Leu Tyr Thr Thr Val Ile Thr Pro Lys Leu Leu

```

```

65      70      75      80
Ala Cys Leu Leu Gly Glu Glu Lys Thr Ile Ser Phe Ala Gly Cys Met
      85      90      95
Ile Gln Thr Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Ile Leu
      100      105      110
Leu Ala Val Met Ser Phe Asp Arg Tyr Met Ala Ile Cys Asp Pro Leu
      115      120      125
His Tyr Thr Val Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val Leu
      130      135      140
Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Phe Pro Thr Ile Val
      145      150      155
Val Thr Arg Leu Pro Tyr Cys Arg Lys Glu Ile Asn His Phe Phe Cys
      165      170      175
Asp Ile Ala Pro Leu Leu Gln Val Ala Cys Ile Asn Thr His Leu Ile
      180      185      190
Glu Lys Ile Asn Phe Leu Leu Ser Ala Leu Val Ile Leu Ser Ser Leu
      195      200      205
Ala Phe Thr Thr Gly Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg
      210      215      220
Ile Pro Ser Thr Gln Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala Ser
      225      230      235
His Ile Thr Val Val Ser Ile Ala His Gly Ser Asn Ile Phe Val Tyr
      245      250      255
Val Arg Pro Asn Gln Asn Ser Ser Leu Asp Tyr Asp Lys Val Ala Ala
      260      265      270
Val Leu Ile Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser
      275      280      285
Leu Arg Asn Glu Lys Val Gln Glu Val Leu Arg Glu Thr Val Asn Arg
      290      295      300
Ile Met Thr Leu Ile Gln Arg Lys Thr
305      310

```

&lt;210&gt; 1127

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g43 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(247)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1127

```

Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly
1      5      10      15
Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu
      20      25      30
Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu
      35      40      45
Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe
      50      55      60
Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn
      65      70      75      80
Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln
      85      90      95
Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val
      100      105      110
Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr
      115      120      125

```



```

Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
 130                      135                      140
Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
145                      150                      155                      160
Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
                      165                      170                      175
Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
                      180                      185                      190
Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
                      195                      200                      205
Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
210                      215                      220
Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
225                      230                      235                      240
Arg Pro Ile Leu Gly Asn Ser
                      245

```

&lt;210&gt; 1128

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g44 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid.

&lt;400&gt; 1128

```

Asp Ile Gln Asn Gln Thr Thr Val Thr Glu Phe Thr Leu Thr Ala Phe
 1                      5                      10                      15
Pro Val Leu Gln Gln Leu Gln Ile Ser Leu Leu Ala Val Leu Trp Phe
                      20                      25                      30
Thr Tyr Met Leu Thr Leu Thr Gly Asn Val Ala Ile Ile Ser Leu Thr
                      35                      40                      45
Trp Ala Asn His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
50                      55                      60
Trp Ser Ile Trp Asp Ile Phe Phe Thr Thr Ser Val Ile Pro Lys Leu
65                      70                      75                      80
Leu Ala Cys Leu Leu Gln Asp Lys Lys Thr Ile Ser Leu Ala Gly Cys
                      85                      90                      95
Ile Thr Gln Thr Tyr Phe Leu Gly Phe Leu Gly Thr Val Glu Phe Ile
                      100                      105                      110
Leu Trp Ala Val Met Ser Phe Asp Cys Tyr Val Ala Ile Cys Asp Pro
115                      120                      125
Leu His Tyr Thr Ile Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val
130                      135                      140
Leu Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Cys Pro Thr Ile
145                      150                      155                      160
Val Val Ser Arg Leu Pro Phe Cys Tyr Lys Glu Ile Ser His Phe Phe
                      165                      170                      175
Cys Asp Ile Thr Pro Leu Leu His Val Ser Cys Ile Asp Thr His Phe
180                      185                      190
Ile Glu Met Ile Asn Phe Leu Leu Ser Ser Leu Ile Leu Leu Thr Ser
195                      200                      205
Leu Val Leu Thr Thr Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
210                      215                      220
His Ile Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala
225                      230                      235                      240
Ser His Ile Thr Val Ile Ser Ile Ala Tyr Ile Ser Asn Ile Phe Arg

```

```

                245                250                255
Tyr Val Arg Pro Ser Gln Ser His Ser Met Gly Phe Asp Lys Val Thr
                260                265                270
Ala Val Pro Thr Met Val Thr Pro Leu Leu Asn Pro Phe Thr Tyr Ser
                275                280                285
Leu Arg Asn Glu Lys Val Lys Ala Val Leu Lys Glu Ala Val Ser Lys
                290                295                300
Ile Met Ser Ser Trp His Arg Arg Thr Xaa Asn Phe
305                310                315

```

&lt;210&gt; 1129

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g45 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1129

```

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly
 1                5                10                15
Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu
                20                25                30
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
                35                40                45
Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50                55                60
Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys
65                70                75                80
Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly
                85                90                95
Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val
                100                105                110
Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
                115                120                125
Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu
130                135                140
Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
145                150                155                160
Ala Leu Ile Leu Pro Leu Pro Phe Cys Asp Pro Asn Ile Ile Asp Asn
                165                170                175
Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
180                185                190
Ser Leu Leu Glu Phe Leu Met Ile Phe Asn Ser Gly Leu Leu Val Ile
195                200                205
Ile Trp Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met
210                215                220
Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys
225                230                235                240
Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr
                245                250                255
Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser
260                265                270
Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
275                280                285
Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys
290                295                300
Leu Val Ile Cys Arg Glu
305                310

```

&lt;210&gt; 1130

<211> 311  
 <212> PRT  
 <213> Unknown (H38g46 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(311)  
 <223> Xaa = Any Amino Acid

<400> 1130  
 Asp Gln Glu Asn Gln Thr Ser Glu Val Thr Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Ser Glu Tyr Pro Asp Leu Gln Thr Pro Leu Phe Leu Val Phe Leu Thr  
 20 25 30  
 Ile Tyr Thr Val Thr Val Leu Gly Asn Leu Gly Met Ile Ile Val Ile  
 35 40 45  
 Arg Ile Ser Pro Lys Leu His Thr Pro Met Cys Phe Phe Leu Ser His  
 50 55 60  
 Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu  
 65 70 75 80  
 Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys  
 85 90 95  
 Thr Met Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe  
 100 105 110  
 Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro  
 115 120 125  
 Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val  
 130 135 140  
 Ala Thr Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa  
 145 150 155 160  
 Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe  
 165 170 175  
 Val Cys Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys  
 180 185 190  
 Val Ser Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser  
 195 200 205  
 Ser Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro  
 210 215 220  
 Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu  
 225 230 235 240  
 Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val  
 245 250 255  
 Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe  
 260 265 270  
 Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg  
 275 280 285  
 Asn Lys Asp Val Lys Glu Thr Val Arg Arg Leu Leu Ile Thr Lys Leu  
 290 295 300  
 Leu Cys Leu Ile Leu Xaa Asn  
 305 310

<210> 1131  
 <211> 334  
 <212> PRT  
 <213> Unknown (H38g47 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(334)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1131

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1           5           10           15
Glu Val Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
          20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
          35           40           45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65           70           75           80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85           90           95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
          130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
          165          170          175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Ser His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Ile Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Phe Ser Lys Ile
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225          230          235          240
Leu Ser Thr Cys Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Leu Val Thr Pro Met Leu
          275          280          285
Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Val Leu
          290          295          300
Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Ile Cys Ser
305          310          315          320
Ile Pro Phe Val Val Trp Val Gln Lys Gly Ser Lys Val Lys
          325          330

```

&lt;210&gt; 1132

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g48 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1132

```

Met Glu Thr Gly Asn Leu Thr Trp Val Ser Asp Phe Val Phe Leu Gly
 1           5           10           15
Leu Ser Gln Thr Arg Glu Leu Gln Arg Phe Leu Phe Leu Met Phe Leu
          20           25           30

```

Phe Val Tyr Ile Thr Thr Val Met Gly Asn Ile Leu Ile Ile Ile Thr  
           35                  40                  45  
 Val Thr Ser Asp Ser Gln Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
           50                  55                  60  
 Asn Leu Ala Val Leu Asp Leu Cys Phe Ser Ser Val Thr Ala Pro Lys  
           65                  70                  75                  80  
 Met Leu Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Tyr Gln Gly  
                   85                  90                  95  
 Cys Met Gly Gln Ile Phe Phe Phe His Phe Leu Gly Gly Ala Met Val  
                   100                  105                  110  
 Phe Phe Leu Ser Val Met Ala Phe Asp Arg Leu Ile Ala Ile Ser Arg  
                   115                  120                  125  
 Pro Leu Arg Tyr Val Thr Val Met Asn Thr Gln Leu Trp Val Gly Leu  
                   130                  135                  140  
 Val Val Ala Thr Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu  
                   145                  150                  155                  160  
 Ala Leu Met Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn  
                   165                  170                  175  
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr  
                   180                  185                  190  
 Ser Leu Leu Glu Phe Leu Lys Ile Ser Asn Ser Gly Leu Leu Asp Val  
                   195                  200                  205  
 Val Trp Phe Phe Leu Leu Leu Met Ser Tyr Leu Phe Ile Leu Val Met  
                   210                  215                  220  
 Leu Arg Ser His Pro Gly Glu Ala Arg Arg Lys Ala Ala Ser Thr Cys  
                   225                  230                  235                  240  
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Val Pro Ser Ile Tyr  
                   245                  250                  255  
 Leu Tyr Ala Arg Pro Phe Thr Pro Phe Pro Met Asp Lys Leu Val Ser  
                   260                  265                  270  
 Ile Gly His Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr  
                   275                  280                  285  
 Leu Arg Asn Gln Asp Met Gln Ala Ala Val Arg Arg Leu Gly Arg His  
                   290                  295                  300  
 Arg Leu Val  
 305

&lt;210&gt; 1133

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g49 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1133

His Thr Glu Pro Gln Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu  
           1                  5                  10                  15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
                   20                  25                  30  
 Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser  
                   35                  40                  45  
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Asn Leu Cys  
                   50                  55                  60  
 Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val  
                   65                  70                  75                  80  
 Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr

```
<210> 1135
<211> 356
<212> PRT
<213> Unknown (H38g51 protein)
```

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(356)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1135

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe
 20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
 35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
 50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
 65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
 85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
 100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
 115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
 130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
 145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
 165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
 180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
 195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
 210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
 225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
 245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
 260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
 275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
 290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
 305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
 325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
 340          345          350
Arg Xaa Tyr Pro
 355

```

&lt;210&gt; 1136

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g52 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1136

```

Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met Leu Leu Gly Phe Pro
1           5           10           15
Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly Val Val Phe Phe Phe
           20           25           30
Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu Ile Leu Leu Pro Leu
           35           40           45
Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe Phe Leu Arg Asn Leu
           50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
           65           70           75           80
Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr Phe Gly Gly Cys Ala
           85           90           95
Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr Val Glu Cys Met Leu
           100          105          110
Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala Val Cys Lys Pro Leu
           115          120          125
Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys Gln Gly Leu Val Ala
           130          135          140
Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met Ile Leu Ser Pro Cys
           145          150          155          160
Pro Val Ser Leu Pro Arg Cys Gly Asp His His Leu Asp His Tyr Phe
           165          170          175
Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys Gly Ala Thr Thr Val
           180          185          190
Met Glu Glu Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile
           195          200          205
Phe Leu Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
           210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
           225          230          235          240
Gly Thr Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr
           245          250          255
Val Arg Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu
           260          265          270
Gly Lys Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn
           275          280          285
Pro Tyr Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu
           290          295          300
Ile Gly Lys Glu Lys Gly Ser Gly Asp Thr Ile Gly His
           305          310          315

```

&lt;210&gt; 1137

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g53 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1137

```

Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
1           5           10           15
Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
           20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
           35           40           45
Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
           50           55           60

```



```

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
65      70      75      80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
      85      90      95
Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
      100      105      110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115      120      125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
      130      135      140
Val Ala Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser
145      150      155      160
Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
      165      170      175
Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
      180      185      190
Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
      195      200      205
Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
      210      215      220
Arg Ile Asn Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly Thr Cys Ser
225      230      235      240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245      250      255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe
      260      265      270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr
      275      280      285
Thr Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Gly
      290      295      300
Lys Glu Met Gly Leu Thr Gln Ser
305      310

```

&lt;210&gt; 1138

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g54 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(343)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1138

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
1      5      10      15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
      20      25      30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
      35      40      45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
      50      55      60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
65      70      75      80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
      85      90      95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
      100      105      110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His

```

```

      115      120      125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
  130      135      140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
  145      150      155      160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165      170      175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180      185      190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195      200      205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210      215      220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
  225      230      235      240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245      250      255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260      265      270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
      290      295      300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
  305      310      315      320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325      330      335
Tyr Leu Ser Tyr Thr His His
      340

```

&lt;210&gt; 1139

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g55 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1139

```

Met Phe Ala Ala Leu Val Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly
  1      5      10      15
Asn Ser Ala Leu Val Leu Leu Ala Val Arg Asp Pro Arg Leu His Thr
      20      25      30
Pro Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe
      35      40      45
Thr Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala
      50      55      60
Leu Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu
  65      70      75      80
Ala Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp
      85      90      95
Arg Ala Ala Lys Lys Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser
      100      105      110
Leu Gly Arg Gly Gln Ala Gly Gln Ser Ala Ser Trp Leu Ser Gly Leu
      115      120      125
Thr Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys
      130      135      140
Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu
  145      150      155      160
Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe
      165      170      175

```

Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala  
 180 185 190  
 Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly  
 195 200 205  
 Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val  
 210 215 220  
 Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln  
 225 230 235 240  
 Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val  
 245 250 255  
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys  
 260 265 270  
 Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln  
 275 280 285  
 Ala Gly Gln  
 290

&lt;210&gt; 1140

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g56 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1140

Glu Leu Ile Thr Asn Ser Ser Ser Val Pro Ser Cys Glu Arg Thr Ile  
 1 5 10 15  
 Gln Ile Phe Leu Phe Ser Leu Ile Thr Thr Ile Tyr Ala Leu Thr Ile  
 20 25 30  
 Thr Gly Asn Gly Ala Ile Ala Phe Ala Leu Trp Cys Asp Arg Arg Leu  
 35 40 45  
 His Thr Pro Met Tyr Met Phe Leu Gly Asp Phe Ser Phe Leu Glu Ile  
 50 55 60  
 Trp Tyr Val Phe Ser Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser  
 65 70 75 80  
 Glu Lys Thr Asn Ile Ser Phe Ala Gly Cys Phe Leu Gln Ile Tyr Phe  
 85 90 95  
 Phe Phe Ser Leu Asn Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala  
 100 105 110  
 Phe Asp Gln Asn Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Asn Ile  
 115 120 125  
 Met Thr Gly His Leu Cys Ala Lys Leu Ala Ile Leu Cys Trp Val Cys  
 130 135 140  
 Gly Phe Leu Trp Phe Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro  
 145 150 155 160  
 Phe Cys Gly Pro Asn Ile Ile Asp His Val Val Cys Asp Pro Gly Pro  
 165 170 175  
 Leu Phe Ala Leu Asp Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys  
 180 185 190  
 Tyr Thr Leu Ser Ser Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile  
 195 200 205  
 Gly Ser Tyr Thr Ile Val Leu Lys Val Val Leu Gly Thr Pro Ser Ser  
 210 215 220  
 Thr Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val  
 225 230 235 240  
 Val Ser Leu Cys Tyr Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly

245 250 255  
 Leu Gly His Ser Thr Glu Met Gln Lys Ile Val Thr Leu Phe Tyr Ala  
 260 265 270  
 Met Val Thr Ser Leu Phe Asn Pro Leu Ile Tyr Ser Leu Gln Asn Lys  
 275 280 285  
 Glu Ile Lys Ala Ala Leu Arg Lys Val Leu Val Ser Ser Asn Ile Ile  
 290 295 300  
 Xaa Gly Ile  
 305

<210> 1141  
 <211> 221  
 <212> PRT  
 <213> Unknown (H38g57 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(221)  
 <223> Xaa = Any Amino Acid

<400> 1141  
 Ala Cys Lys His Asp Met Ile Leu Thr Val Met Ala Tyr Asp Cys Leu  
 1 5 10 15  
 Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His  
 20 25 30  
 Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Ile Ser Met Xaa Asp  
 35 40 45  
 Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Ile Ile Lys Asn  
 50 55 60  
 Val Glu Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu  
 65 70 75 80  
 Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser  
 85 90 95  
 Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Phe  
 100 105 110  
 Lys Ile Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr  
 115 120 125  
 Lys Ala Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe  
 130 135 140  
 Tyr Gly Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Leu Ser Pro Pro  
 145 150 155 160  
 Pro Arg Asn Gly Val Met Ala Ser Val Met Tyr Ala Val Val Thr Pro  
 165 170 175  
 Met Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser  
 180 185 190  
 Ala Leu Trp Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe  
 195 200 205  
 His Pro Phe Ser Cys Val Gly Lys Gly Asn His Ile Lys  
 210 215 220

<210> 1142  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g58 protein)

<220>  
 <223> Synthetic construct

<400> 1142

```

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1          5          10          15
Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
 20          25          30
Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
 35          40          45
Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
 65          70          75          80
Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
 85          90          95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
 100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
 115          120          125
Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
 130          135          140
Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
 145          150          155          160
Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
 165          170          175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180          185          190
Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
 195          200          205
Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
 210          215          220
Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
 225          230          235          240
Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
 245          250          255
Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
 260          265          270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
 290          295          300
Ala Arg Arg Leu Gln Val Ser Leu Ser Met
305          310

```

&lt;210&gt; 1143

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g59 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1143

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
 20          25          30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35          40          45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```

```

      50      55      60
Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser
65      70      75      80
Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile
      85      90      95
Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly
      100      105      110
Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val
      115      120      125
Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val
      130      135      140
Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala
145      150      155      160
Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val
      165      170      175
Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys
      180      185      190
Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe
      195      200      205
Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile
      210      215      220
Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly
225      230      235      240
Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met
      245      250      255
Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val
      260      265      270
Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr
      275      280      285
Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys
      290      295      300
Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn
305      310      315

```

&lt;210&gt; 1144

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g61 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(351)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1144

```

Met Asp Ile Leu Val Ile Asp Asn Gly Ser Glu Val Thr Glu Phe Ile
1      5      10      15
Leu Val Gly Leu Tyr Asn His Pro Lys Phe Gln Ile Ala Phe Tyr Arg
      20      25      30
Thr Met Val Val Val Tyr Leu Ile Thr Phe Val Gly Ser Ser Leu Ile
      35      40      45
Ile Val Val Val Lys Val Asp Gly Trp Leu His Thr Pro Met Cys Phe
      50      55      60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Asn Ser
65      70      75      80
Val Pro Phe Leu Leu Phe Asn Gly Leu Arg Asp Tyr Pro Thr Ile Ser
      85      90      95
Tyr Asn Ser Cys Tyr Ala Gln Met Thr Ser Ala Phe Phe Leu Gly Met
      100      105      110

```

```

Thr Gly Cys Leu Leu Leu Ala Val Met Ala Tyr Glu Arg Phe Val Val
      115      120      125
Ile Ser Asn Pro Leu Arg Tyr Ile Ile Ile Met Asn Asn Lys Val Cys
      130      135      140
Ile Gln Leu Ala Met Val Thr Trp Ala Ser Ala Ser Pro Tyr Val Ile
145      150      155      160
Asn Thr Ile Ile Ala Ile Ile His Cys Asn Asn Thr Leu Ile Ala Met
      165      170      175
Ile Ala Leu Ser Ile Pro Ala His Phe Cys Gly His Asn Val Ile Asn
      180      185      190
His Phe Thr Cys Glu Val Gln Glu Leu Leu Lys Leu Val Cys Ser Asp
      195      200      205
Ile Pro Gly Ser Leu Ile Leu Gly Leu Val Ile Gly Ile Phe Thr Leu
      210      215      220
Ser Leu Pro Phe Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Phe Ala
225      230      235      240
Tyr Ala His Ile Val Val Ala Val Leu Arg Ile Asn Ser Ala Glu Ala
      245      250      255
Arg Leu Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Ile Ile
      260      265      270
Ile Phe Tyr Gly Thr Ala Thr Tyr Met Tyr Leu Lys Pro Gln Ser Arg
      275      280      285
Glu Ser Gln Asp Glu Gly Lys Val Ile Ser Val Phe Phe Leu Lys Val
      290      295      300
Glu Lys Gln His Gln Asn Asp Ser Ile Ser Val Phe Tyr Gly Val Val
305      310      315      320
Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asp Lys Asp Ala
      325      330      335
Lys His Ala Leu Arg Lys Ile Ile Arg Lys Lys Glu Ser Xaa Lys
      340      345      350

```

&lt;210&gt; 1145

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g62 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1145

```

Met Asp Lys Ile Asn Gln Thr Phe Val Arg Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Ser Gly Tyr Pro Lys Leu Glu Ile Ile Phe Phe Ala Leu Ile Leu
      20      25      30
Val Met Tyr Val Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
      35      40      45
Ser Ile Leu Asp Ser Arg Leu His Met Pro Met Tyr Phe Phe Leu Gly
      50      55      60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Ser
      65      70      75      80
Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
      85      90      95
Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
      100      105      110
Phe Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Pro Ile Ile Met Asn Lys Val Val Tyr Val Leu Leu
      130      135      140
Thr Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Thr Val Gln Thr
145      150      155      160
Ser Leu Ala Met Arg Trp Pro Phe Cys Gly Asn Asn Ile Ile Asn His

```

```

          165          170          175
Phe Leu Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ser Asp Ile
          180          185          190
Ser Val Asn Ile Val Thr Leu Ala Val Ser Asn Ile Ala Phe Leu Val
          195          200          205
Leu Pro Leu Leu Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
          210          215          220
Ile Leu Arg Thr Asn Ser Ala Thr Gly Arg His Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
          245          250          255
Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Leu Gly Lys Asp Asn
          260          265          270
Leu Gln Ala Thr Glu Gly Leu Val Ser Met Phe Tyr Gly Val Val Thr
          275          280          285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
290          295          300
Ala Ala Ile Lys Tyr Leu Leu Ser Arg Lys Ala Ile Asn Gln
305          310          315

```

&lt;210&gt; 1146

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g63 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1146

```

Met Phe Pro Ala Asn Trp Thr Ser Val Lys Val Phe Phe Phe Leu Gly
 1          5          10          15
Phe Phe His Tyr Pro Lys Val Gln Val Ile Ile Phe Ala Val Cys Leu
          20          25          30
Leu Met Tyr Leu Ile Thr Leu Leu Gly Asn Ile Phe Leu Ile Ser Ile
          35          40          45
Thr Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Leu Asp Ile Trp Tyr Ser Ser Ala Leu Ser Pro
65          70          75          80
Met Leu Ala Asn Phe Val Ser Gly Arg Asn Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Ala Thr Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
          100          105          110
Val Leu Leu Pro Met Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Pro Val Ile Met Asn Arg Arg Thr Cys Val Gln Ile
          130          135          140
Ala Ala Gly Ser Trp Met Thr Gly Cys Leu Thr Ala Met Val Glu Met
145          150          155          160
Met Ser Val Leu Pro Leu Ser Leu Cys Gly Asn Ser Ile Ile Asn His
          165          170          175
Phe Thr Cys Glu Ile Leu Ala Ile Leu Lys Leu Val Cys Val Asp Thr
          180          185          190
Ser Leu Val Gln Leu Ile Met Leu Val Ile Ser Val Leu Leu Leu Pro
          195          200          205
Met Pro Met Leu Leu Ile Cys Ile Ser Tyr Ala Phe Ile Leu Ala Ser
          210          215          220
Ile Leu Arg Ile Ser Ser Val Glu Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240
Cys Thr Ala His Leu Met Val Val Val Leu Phe Tyr Gly Thr Ala Leu
          245          250          255

```



Ser Met His Leu Lys Pro Ser Ala Val Asp Ser Gln Glu Ile Asp Lys  
                   260                  265                  270  
 Phe Met Ala Leu Val Tyr Ala Gly Gln Thr Pro Met Leu Asn Pro Ile  
                   275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Val Ala Leu Lys Lys Leu  
                   290                  295                  300  
 Leu Ile Arg Asn His Phe Asn Thr Ala Phe Ile Ser Ile Leu Lys  
 305                  310                  315

&lt;210&gt; 1147

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g64 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1147

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala  
 1                  5                  10                  15  
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu  
                   20                  25                  30  
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu  
                   35                  40                  45  
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser  
                   50                  55                  60  
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln  
 65                  70                  75                  80  
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg  
                   85                  90                  95  
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys  
                   100                  105                  110  
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln  
                   115                  120                  125  
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu  
                   130                  135                  140  
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr  
 145                  150                  155                  160  
 Val Ser Ala Phe Thr Leu Ser Phe Cys Gly Thr Ser Glu Ile Asp Phe  
                   165                  170                  175  
 Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Thr Cys Gly Glu Ser  
                   180                  185                  190  
 Tyr Thr Gln Glu Val Leu Ile Ile Met Phe Ala Ile Phe Val Ile Pro  
                   195                  200                  205  
 Ala Ser Met Val Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala  
                   210                  215                  220  
 Ile Met Gly Ile Pro Ala Gly Ser Gln Ala Lys Thr Phe Ser Thr Cys  
 225                  230                  235                  240  
 Thr Ser His Leu Thr Ala Val Ser Leu Phe Phe Gly Thr Leu Ile Phe  
                   245                  250                  255  
 Met Tyr Leu Arg Gly Asn Ser Asp Gln Ser Ser Glu Lys Asn Arg Val  
                   260                  265                  270  
 Val Ser Val Leu Tyr Thr Glu Val Ile Pro Met Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile Leu  
                   290                  295                  300  
 Asn Arg Ala Lys Leu Ser  
 305                  310

&lt;210&gt; 1148

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g65 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1148

```

Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Phe Val Leu Thr
 1           5           10           15
Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile Val
          20           25           30
Phe Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu
          35           40           45
Leu Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
          50           55           60
Ser Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro
65          70          75          80
Lys Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu
          85          90          95
Gly Cys Ala Val Gln Ile Phe Leu Tyr Leu Thr Leu Ile Gly Gly Glu
          100         105         110
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
          115         120         125
Asn Pro Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe
130         135         140
Met Val Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu
145         150         155         160
Thr Pro Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn
          165         170         175
His Phe Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp
          180         185         190
Thr Ser Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu
          195         200         205
Leu Ile Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu
210         215         220
Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
225         230         235         240
Thr Cys Ser Ser His Ile Met Ala Val Ser Val Phe Tyr Gly Ala Ala
          245         250         255
Phe Tyr Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp
          260         265         270
Lys Val Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
          275         280         285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Leu Arg Lys
          290         295         300
Val Leu Gly Arg Cys Gly Ser Ser Gln Ser Ile Arg Val Ala Thr Val
305         310         315         320
Ile

```

&lt;210&gt; 1149

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g66 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1149

```

Met Ala His Thr Asn Glu Ser Met Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15

```

Leu Ser Asn Ser Trp Gly Leu Gln Leu Phe Phe Phe Ala Ile Phe Ser  
                   20                  25                  30  
 Ile Val Tyr Val Thr Ser Val Leu Gly Asn Val Leu Ile Ile Val Ile  
                   35                  40                  45  
 Ile Ser Phe Asp Ser His Leu Asn Ser Pro Met Tyr Phe Leu Leu Ser  
                   50                  55                  60  
 Asn Leu Ser Phe Ile Asp Ile Cys Gln Ser Asn Phe Ala Thr Pro Lys  
                   65                  70                  75                  80  
 Met Leu Val Asp Phe Phe Ile Glu Arg Lys Thr Ile Ser Phe Glu Gly  
                   85                  90                  95  
 Cys Met Ala Gln Ile Phe Val Leu His Ser Phe Val Gly Ser Glu Met  
                   100                  105                  110  
 Met Leu Leu Val Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys  
                   115                  120                  125  
 Pro Leu His Tyr Ser Thr Ile Met Asn Arg Arg Leu Cys Val Ile Phe  
                   130                  135                  140  
 Val Ser Ile Ser Trp Ala Val Gly Val Leu His Ser Val Ser His Leu  
                   145                  150                  155                  160  
 Ala Phe Thr Val Asp Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser  
                   165                  170                  175  
 Phe Phe Cys Asp Leu Pro Leu Val Ile Glu Leu Ala Cys Met Asp Thr  
                   180                  185                  190  
 Tyr Glu Met Glu Ile Met Thr Leu Thr Asn Ser Gly Leu Ile Ser Leu  
                   195                  200                  205  
 Ser Cys Phe Leu Ala Leu Ile Ile Ser Tyr Thr Ile Ile Leu Ile Gly  
                   210                  215                  220  
 Val Arg Cys Arg Ser Ser Ser Gly Ser Ser Lys Ala Leu Ser Thr Leu  
                   225                  230                  235                  240  
 Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Cys Ile Tyr  
                   245                  250                  255  
 Phe Tyr Ile Trp Pro Phe Ser Arg Leu Pro Val Asp Lys Phe Leu Ser  
                   260                  265                  270  
 Val Phe Tyr Thr Val Cys Thr Pro Leu Leu Asn Pro Ile Ile Tyr Ser  
                   275                  280                  285  
 Leu Arg Asn Glu Asp Val Lys Ala Ala Met Trp Lys Leu Arg Asn Arg  
                   290                  295                  300  
 His Val Asn Ser Trp Lys Asn  
                   305                  310

&lt;210&gt; 1150

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g67 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1150

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly  
   1                  5                  10                  15  
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu  
                   20                  25                  30  
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu  
                   35                  40                  45  
 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser  
                   50                  55                  60  
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln  
                   65                  70                  75                  80  
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly  
                   85                  90                  95  
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys

100	105	110
Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg		
115	120	125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met		
130	135	140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr		
145	150	155
Val Leu Ile Leu Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His		
165	170	175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr		
180	185	190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu		
195	200	205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala		
210	215	220
Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr		
225	230	235
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile		
245	250	255
Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys		
260	265	270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu		
275	280	285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val		
290	295	300
Leu Trp Lys Asn Tyr Asp Ser Arg		
305	310	

&lt;210&gt; 1151

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g68 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1151

Met Cys Ser Gly Asn Gln Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp		
1	5	10
Phe Thr Leu Thr Gly Leu Phe Ala Glu Ser Lys His Ala Ala Leu Leu		
20	25	30
Tyr Thr Val Thr Phe Leu Leu Phe Leu Met Ala Leu Thr Gly Asn Ala		
35	40	45
Leu Leu Ile Leu Leu Ile His Ser Glu Pro Arg Leu His Thr Pro Met		
50	55	60
Tyr Phe Phe Ile Ser Gln Leu Ala Leu Met Asp Leu Met Tyr Leu Cys		
65	70	75
Val Thr Val Pro Lys Met Leu Val Gly Gln Val Thr Gly Asp Asp Thr		
85	90	95
Ile Ser Pro Ser Gly Cys Gly Ile Gln Met Phe Phe His Leu Thr Leu		
100	105	110
Ala Gly Ala Glu Val Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr		
115	120	125
Ala Ala Val Cys Arg Pro Leu His Tyr Pro Leu Leu Met Asn Gln Arg		
130	135	140
Val Cys Gln Leu Leu Val Ser Ala Cys Trp Val Leu Gly Met Val Asp		
145	150	155
Gly Leu Leu Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Gln Ser		
165	170	175
Arg Lys Ile Leu Ser Phe Phe Cys Glu Thr Pro Ala Leu Leu Lys Leu		
180	185	190

Ser Cys Ser Asp Val Ser Leu Tyr Lys Met Leu Thr Tyr Leu Cys Cys  
 195 200 205  
 Ile Leu Met Leu Leu Thr Pro Ile Met Val Ile Ser Ser Ser Tyr Thr  
 210 215 220  
 Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala Ala Gly Arg Arg  
 225 230 235 240  
 Lys Ala Leu Ala Thr Cys Ser Ser His Met Ile Ile Val Leu Leu Leu  
 245 250 255  
 Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr  
 260 265 270  
 Ala Glu Gln Asp Met Met Val Ser Ala Phe Tyr Thr Ile Phe Thr Pro  
 275 280 285  
 Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Arg  
 290 295 300  
 Ala Met Arg Ser Met Met Gln Ser Arg  
 305 310

&lt;210&gt; 1152

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g69 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1152

Met Asp Val Gly Asn Lys Ser Thr Met Ser Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Ser Asn Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser  
 20 25 30  
 Leu Leu Tyr Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr  
 35 40 45  
 Val Ile Val Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr  
 50 55 60  
 Asn Leu Ser Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys  
 65 70 75 80  
 Met Ile Thr Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile  
 100 105 110  
 Ile Leu Leu Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu  
 130 135 140  
 Val Val Ala Ser Trp Ile Met Gly Val Met His Ser Met Ser Gln Val  
 145 150 155 160  
 Ile Phe Ala Leu Thr Leu Pro Phe Cys Gly Pro Tyr Glu Val Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Val Val Phe Gln Leu Ala Cys Val Asp Thr  
 180 185 190  
 Tyr Val Leu Gly Leu Phe Met Ile Ser Thr Ser Gly Ile Ile Ala Leu  
 195 200 205  
 Ser Cys Phe Ile Val Leu Phe Asn Ser Tyr Val Ile Val Leu Val Thr  
 210 215 220  
 Val Lys His His Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Thr Ala His Phe Ile Val Val Phe Leu Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Met Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Pro Thr Leu Asn Pro Ile Ile Tyr Thr

275                      280                      285  
 Leu Arg Asn Gln Glu Val Lys Ile Ala Met Arg Lys Leu Lys Asn Arg  
 290                      295                      300  
 Phe Leu Asn Phe Asn Lys Ala Met Pro Ser  
 305                      310

<210> 1153  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g70 protein)

<220>  
 <223> Synthetic construct

<400> 1153  
 Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe  
 1                      5                      10                      15  
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu  
 20                      25                      30  
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile  
 35                      40                      45  
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His  
 50                      55                      60  
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met  
 65                      70                      75                      80  
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg  
 85                      90                      95  
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu  
 100                      105                      110  
 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro  
 115                      120                      125  
 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala  
 130                      135                      140  
 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val  
 145                      150                      155                      160  
 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe  
 165                      170                      175  
 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His  
 180                      185                      190  
 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly  
 195                      200                      205  
 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile  
 210                      215                      220  
 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys  
 225                      230                      235                      240  
 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile  
 245                      250                      255  
 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr  
 260                      265                      270  
 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile  
 275                      280                      285  
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu  
 290                      295                      300  
 Gly Val Glu Arg Ala Leu  
 305                      310

<210> 1154  
 <211> 323  
 <212> PRT  
 <213> Unknown (H38g71 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1154

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Leu Pro Val Leu Ala Leu Leu Ser
 20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
 35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro His Thr Pro Val Tyr Phe Phe
 50      55      60
Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Pro Thr Val
 65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His
 85      90      95
Ala Gly Cys Leu Ala Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile
 100     105     110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Ser Phe Val Ala Ile
 115     120     125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
 130     135     140
Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
 145     150     155     160
His Gly Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile
 165     170     175
Ser Asn Phe Leu Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
 180     185     190
Asp Ser Val Thr Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
 195     200     205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val
 210     215     220
Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
 225     230     235     240
Thr Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr
 245     250     255
Gly Ile Gly Met Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg Asn
 260     265     270
Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
 275     280     285
Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg
 290     295     300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe
 305     310     315     320
Phe Leu Cys

```

&lt;210&gt; 1155

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g72 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1155

Met Ala Trp Ser Asn Gln Ser Ala Val Thr Glu Phe Ile Leu Arg Gly

```

1           5           10           15
Leu Ser Ser Ser Leu Glu Leu Gln Ile Phe Tyr Phe Leu Phe Phe Ser
20
Ile Val Tyr Ala Ala Thr Val Leu Gly Asn Leu Leu Ile Val Val Thr
35
Ile Ala Ser Glu Pro His Leu His Ser Pro Thr Tyr Phe Leu Leu Gly
50
Asn Leu Ser Phe Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
65
Met Ile Ala Asp Phe Leu Arg Glu His Lys Ala Ile Ser Phe Glu Gly
85
Cys Met Thr Gln Met Phe Phe Leu His Leu Leu Gly Gly Ala Glu Ile
100
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Lys
115
Pro Leu His Tyr Leu Thr Ile Met Ser Arg Arg Met Cys Val Gly Leu
130
Val Ile Leu Ser Trp Ile Val Gly Ile Phe His Ala Leu Ser Gln Leu
145
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
165
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Val Asp Thr
180
Tyr Ile Leu Gly Val Phe Met Ile Ser Thr Ser Gly Met Ile Ala Leu
195
Val Cys Phe Ile Leu Leu Val Ile Ser Tyr Thr Ile Ile Leu Val Thr
210
Val Arg Gln Arg Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Cys
225
Ser Ala His Phe Thr Val Val Thr Leu Phe Phe Gly Pro Cys Thr Phe
245
Ile Tyr Val Trp Pro Phe Thr Asn Phe Pro Ile Asp Lys Val Leu Ser
260
Val Phe Tyr Thr Ile Tyr Thr Pro Leu Leu Asn Pro Val Ile Tyr Thr
275
Val Arg Asn Lys Asp Val Lys Tyr Ser Met Arg Lys Leu Ser Ser His
290
Ile Phe Lys Ser Arg Lys Thr Asp His Thr Pro
305
310
315

```

&lt;210&gt; 1156

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g73 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1156

```

Met Lys Lys Tyr Met Glu Arg Thr Asn Xaa Thr Thr Glu Phe Glu Leu
1           5           10           15
Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu Phe
20
Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg Ile
35
Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His Gly
50
55
60

```



```

Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro Ser
65      70      75      80
Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr Asp
      85      90      95
Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu Cys
      100      105      110
Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser Lys
      115      120      125
Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys Lys
      130      135      140
Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe Leu
145      150      155      160
Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys Gly
      165      170      175
Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Ala Leu
      180      185      190
Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly Lys
      195      200      205
Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile Phe
      210      215      220
Ser Phe Leu Tyr Phe His His Leu Cys Cys Ile Glu Ile Asn Ser Ala
225      230      235      240
Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr Val
      245      250      255
Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser Thr
      260      265      270
Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly Val
      275      280      285
Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met Glu
      290      295      300
Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp Cys
305      310      315      320
Trp

```

<210> 1157  
 <211> 325  
 <212> PRT  
 <213> Unknown (H38g74 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(325)  
 <223> Xaa = Any Amino Acid

```

<400> 1157
His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu
      35      40      45
Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Gln Leu His Thr Pro Met
      50      55      60
Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser
65      70      75      80
Pro Met Val Pro Lys Met Ile Met Asp Met Gln Ser His Ser Arg Val
      85      90      95
Ile Ser His Ala Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe

```

100	105	110
Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe		
115	120	125
Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His		
130	135	140
Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp		
145	150	155
Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Asn Asn		
165	170	175
Val Glu Ile Ala Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu		
180	185	190
Asp Cys Ser Asp Thr Val Ile Asn Ser Val Phe Ile Tyr Phe Asp Ser		
195	200	205
Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys		
210	215	220
Ile Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys		
225	230	235
Ala Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp		
245	250	255
Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro		
260	265	270
Arg Asn Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met		
275	280	285
Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala		
290	295	300
Leu Gln Arg Leu Ser Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro		
305	310	315
Ser Phe Phe Leu Cys		
325		

&lt;210&gt; 1158

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g75 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1158

Met Gly Asn Trp Thr Ala Ala Val Thr Glu Phe Val Leu Leu Gly Phe		
1	5	10
Ser Leu Ser Arg Glu Val Glu Leu Leu Leu Val Leu Leu Pro		
20	25	30
Thr Phe Leu Leu Thr Leu Leu Gly Asn Leu Leu Ile Ile Ser Thr Val		
35	40	45
Leu Ser Cys Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn		
50	55	60
Leu Ser Ile Leu Asp Ile Leu Phe Thr Ser Val Ile Ser Pro Lys Val		
65	70	75
Leu Ala Asn Leu Gly Ser Arg Asp Lys Thr Ile Ser Phe Ala Gly Cys		
85	90	95
Ile Thr Gln Cys Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Leu		
100	105	110
Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Thr Ile Cys Cys Pro		
115	120	125
Leu Arg Tyr Thr Thr Ile Met Arg Pro Ser Val Cys Ile Gly Thr Val		
130	135	140
Val Phe Ser Trp Val Gly Gly Phe Leu Ser Val Leu Phe Pro Thr Ile		
145	150	155
Leu Ile Ser Gln Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe		
165	170	175

Phe Cys Asp Ser Gly Pro L u Leu Ala Leu Ala Cys Ala Asp Thr Thr  
 180 185 190  
 Ala Ile Glu Leu Met Asp Phe Met Leu Ser Ser Met Val Ile Leu Cys  
 195 200 205  
 Cys Ile Val Leu Val Ala Tyr Ser Tyr Thr Tyr Ile Ile Leu Thr Ile  
 210 215 220  
 Val Arg Ile Pro Ser Ala Ser Gly Arg Lys Lys Ala Phe Asn Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Thr Ile Val Ile Ile Pro Ser Gly Ile Thr Val Phe  
 245 250 255  
 Ile Tyr Val Thr Pro Ser Gln Lys Glu Tyr Leu Glu Ile Asn Lys Ile  
 260 265 270  
 Pro Leu Val Leu Ser Ser Val Val Thr Pro Phe Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Asp Thr Val Gln Gly Val Leu Arg Asp Val Trp  
 290 295 300  
 Val Arg Val Arg Gly Val Phe Glu Lys Arg Met Arg Ala Val Leu  
 305 310 315

&lt;210&gt; 1159

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g76 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1159

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly  
 1 5 10 15  
 Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu  
 20 25 30  
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr  
 35 40 45  
 Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ala Leu Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Lys  
 65 70 75 80  
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Val Gly Ala Ser Glu Met  
 100 105 110  
 Phe Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Ala Thr Ile Met Asn Arg Arg Leu Cys Cys Ile Leu  
 130 135 140  
 Val Ala Leu Ser Trp Met Gly Gly Phe Ile His Ser Ile Ile Gln Val  
 145 150 155 160  
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser  
 165 170 175  
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr  
 180 185 190  
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val  
 195 200 205  
 Val Trp Phe Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu  
 210 215 220  
 Leu Lys Lys His Ser Gly Ser Asp Glu Asn Thr Asn Arg Ala Met Ser  
 225 230 235 240  
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser  
 245 250 255  
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val

<210> 1160  
<211> 313  
<212> PRT  
<213> Unknown (H38g77 protein)

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid
```

<400>	1160
Met Glu Ser Gln Arg Asn Ile Xaa Lys Phe Ile Leu Met Ser Leu Ser 1               5               10               15	
Ser Ile Gln Asn Ile Gln Ile Phe Val Phe Val Phe Leu Phe Cys Asn 20               25               30	
Val Ala Ile Leu Val Gly Asn Phe Leu Ile Leu Ile Ser Ile Xaa Cys 35               40               45	
Ser Pro Leu Phe Asn Gln Pro Met His Tyr Phe Leu Gly Tyr Met Asn 50               55               60	
Ile Tyr Tyr Thr Ser Cys Val Thr Pro Lys Ile Ile Gly Asp Leu Val 65               70               75               80	
<Val Gly Arg Ile Asn Ile Ser Tyr Asp Arg Ile Phe Pro Met His Phe 85               90               95	
Phe Gly Ile Ile Glu Ile Phe Ile Leu Thr Val Met Ala Phe Asp His 100               105               110	
Tyr Val Ala Ile Cys Lys Pro Pro Arg Tyr Leu Ile Ile Met Asn Arg 115               120               125	
Thr Lys Tyr Asn Thr Leu Ile Ser Val Ala Trp Leu Gly Leu Ile 130               135               140	
His Ser Leu Phe Gln Phe Ser Met Lys Ile Trp Leu Pro Phe Cys Gly 145               150               155               160	
Ser Asn Lys Val Asp Asp Xaa Tyr Xaa Asp Ile Phe Pro Leu Leu Lys 165               170               175	
Val Ala Cys Thr Asp Thr Cys Ile Thr Gly Val Leu Val Val Ala Asn 180               185               190	
Ser Gly Met Phe Ala Leu Val Thr Phe Val Leu Ser Phe Gly Ser Tyr 195               200               205	
Val Ile Ile Leu Phe Pro Leu Lys Asn His Ser Val Glu Gly Arg Cys 210               215               220	
Lys Ala Leu Ser Thr Cys Gly Ser His Ile Thr Met Val Ile Phe Phe 225               230               235               240	
Phe Glu Pro Ser Ile Phe Ala Tyr Leu Arg Pro Ser Thr Phe Pro Glu 245               250               255	
Asp Lys Ile Ser Ala Leu Phe Tyr Thr Ile Ile Ala Pro Met Phe Asn 260               265               270	
His Leu Ile Tyr Asn Leu Arg Asn Thr Glu Met Lys Lys Ala Met Arg 275               280               285	
Lys Val Trp Tyr Gln Ile Ser Phe Ser Glu Glu Lys Gln Leu Ile Cys 290               295               300	
Pro Thr Xaa Cys Thr Lys Glu Leu Tyr 305               310	

<210> 1161  
 <211> 304  
 <212> PRT  
 <213> Unknown (H38g78 protein)

<220>  
 <223> Synthetic construct

<400> 1161  
 Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro  
 1 5 10 15  
 Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr  
 20 25 30  
 Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp  
 35 40 45  
 Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu  
 50 55 60  
 Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu  
 65 70 75 80  
 Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu  
 85 90 95  
 Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile  
 100 105 110  
 Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu  
 115 120 125  
 His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu  
 130 135 140  
 Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu  
 145 150 155 160  
 Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr  
 165 170 175  
 Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile  
 180 185 190  
 Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser  
 195 200 205  
 Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu  
 210 215 220  
 Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met  
 245 250 255  
 Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val  
 260 265 270  
 Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr  
 290 295 300

<210> 1162  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g79 protein)

<220>  
 <223> Synthetic construct

<400> 1162  
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu  
 1 5 10 15  
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro

```
<210> 1163
<211> 323
<212> PRT
<213> Unknown (H38g80 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(323)
<223> Xaa = Any Amino Acid
```

<400> 1163																
Met	Gly	Asn	His	Thr	Thr	Val	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Ser	
1				5					10					15		
Glu	Thr	Cys	Glu	Leu	Gln	Met	Leu	Ile	Phe	Leu	Gly	Leu	Leu	Leu	Thr	
			20					25					30			
Tyr	Leu	Leu	Thr	Leu	Leu	Gly	Asn	Leu	Val	Ile	Val	Val	Ile	Thr	Leu	
		35					40					45				
Met	Asp	Arg	Arg	Leu	His	Thr	Thr	Met	Tyr	Tyr	Phe	Leu	Arg	Asn	Phe	
	50					55					60					

```

Ala Val Pro Glu Ile Trp Phe Thr Ser Val Ile Phe Pro Lys Val Leu
65          70          75          80
Ala Asn Ile Leu Thr Gly Tyr Lys Thr Ile Ser Leu Pro Gly Cys Phe
          85          90          95
Leu Gln Ser Leu Leu Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu
          100         105         110
Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Asn Pro Leu
          115         120         125
His Tyr Ala Thr Ile Met Ser Lys Arg Val Cys Val Gln Leu Val Leu
          130         135         140
Cys Xaa Trp Met Thr Gly Phe Leu Leu Ile Ile Ile Pro Ser Phe Leu
145          150         155         160
Val Leu Gln Gln Pro Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe
          165         170         175
Cys Asp Asn Phe Pro Leu Leu Lys Leu Ile Cys Ala Asp Met Thr Leu
          180         185         190
Ile Glu Leu Leu Gly Phe Val Ile Ala Asn Val Ser Leu Leu Gly Thr
          195         200         205
Leu Ser Met Thr Ala Thr Cys Tyr Gly His Ile Leu His Ala Ile Leu
210         215         220
His Ile Pro Ser Ala Lys Glu Lys Gln Lys Ala Phe Ser Ala Cys Ser
225         230         235         240
Ser His Ile Ile Val Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met
          245         250         255
Tyr Ile Gln Ser Gly Lys Ser Asp Gln Lys Glu Asp Arg Asn Lys Val
260         265         270
Ala Ala Leu Leu Asn Thr Val Val Thr Leu Met Leu Asn Pro Phe Ile
275         280         285
Tyr Thr Leu Arg Asn Lys Gln Val Lys Gln Val Phe Arg Gln Gln Val
290         295         300
Ser Lys Leu Leu Ile Xaa Ser Cys Val Lys Lys Lys Leu Lys Leu Ser
305         310         315         320
Ile Pro Arg

```

&lt;210&gt; 1164

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g81 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1164

```

Glu Ile Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu
1          5          10          15
Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile
          20          25          30
Leu Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe
          35          40          45
Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu
50         55         60
Gly Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro
65         70         75         80
Arg Met Leu Val Asp Phe Leu Ser Ala Lys Asn Val Ile Ser Tyr Arg
          85         90         95
Gly Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu
          100         105         110
Gly Leu Leu Leu Val Ile Val Ala Phe Asp Arg Tyr Ile Ala Ile Cys
          115         120         125
Arg Pro Leu His Tyr Ser Thr Leu Met Asn Pro Arg Ala Cys Tyr Ala

```

130	135	140
Met Met Leu Ala Leu Trp	Leu Gly Gly Phe Val His	Ser Ile Ile Gln
145	150	155
Val Val Leu Ile Leu Arg	Leu Pro Phe Cys Gly	Pro Asn Gln Leu Asp
165	170	175
Asn Phe Phe Cys Asp Val	Pro Gln Val Ile Lys	Leu Ala Cys Thr Asp
180	185	190
Thr Phe Val Val Glu Leu	Leu Met Val Phe Asn	Ser Gly Leu Met Thr
195	200	205
Leu Leu Cys Phe Leu Gly	Leu Leu Ala Ser Tyr	Ala Val Ile Leu Cys
210	215	220
His Val Arg Lys Ala Ala	Ser Glu Leu Lys Asn	Lys Ala Met Ser Thr
225	230	235
Cys Thr Thr His Val Ile	Ile Ile Leu Leu Met	Phe Gly Pro Ala Ile
245	250	255
Phe Ile Tyr Met His Pro	Phe Arg Ala Leu Pro	Ala Asp Lys Val Val
260	265	270
Ser Phe Phe His Thr Val	Ile Phe Pro Leu Met	Asn Pro Met Ile Tyr
275	280	285
Thr Leu Arg Asn Gln Glu	Val Lys Thr Ser Met	Lys Arg Leu Leu Ser
290	295	300
Arg His Val Val Cys Gln	Val Asp Phe Ile Ile	Arg Asn
305	310	315

&lt;210&gt; 1165

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g82 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(287)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1165

Val Ile Arg Asn Gln Thr	Met Val Thr Glu Phe Thr	Leu Val Ser Leu
1	5	10
Pro Ala Val Gln Glu Leu	Gln Ile Trp Leu Cys Val	Leu Leu Trp Leu
20	25	30
Val His Met Leu Thr Ile	Thr Gly Asn Leu Phe Val	Ile Phe Leu Thr
35	40	45
Trp Thr Asp Asn Cys Leu	Gln Thr Pro Met Asp	Leu Phe Leu Glu Lys
50	55	60
Lys Val Ile Ser Phe Ser	Gly Cys Ile Thr Gln Ile	Tyr Phe Tyr Phe
65	70	75
Phe Leu Gly Thr Val Ala	Phe Ile Pro Leu Ala Val	Thr Ser Phe Lys
85	90	95
His Cys Met Ala Thr Cys	Asp Pro Leu Cys Ser Thr	Ile Ile Ala Lys
100	105	110
Ser Arg Ala Cys Leu Leu	Leu Ala Leu Gly Cys Trp	Met Gly Thr Phe
115	120	125
Leu Ala Val Leu Arg Leu	Thr Ile Val Val Ser Arg	Leu Pro Asp Cys
130	135	140
Thr Glu Lys Ile Ser Pro	Phe Phe Cys Asp Ile Ala	Ser Leu Leu Gln
145	150	155
Val Ala Cys Ile Asp Ile	His Phe Ile Glu Met Ile	Ser Phe Leu Xaa
165	170	175
Ser Ser Leu Met Val Leu	Thr Ser Leu Val Leu	Asn Ala Thr Ser Tyr
180	185	190



Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys  
 195 200 205  
 Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile  
 210 215 220  
 Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr  
 225 230 235 240  
 Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr  
 245 250 255  
 Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu  
 260 265 270  
 Gly Ser Thr Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr  
 275 280 285

&lt;210&gt; 1166

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g83 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1166

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Val Leu  
 20 25 30  
 Ile Phe Tyr Phe Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr  
 35 40 45  
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Thr Val Ala Pro Arg  
 65 70 75 80  
 Met Leu Val Asp Phe Leu Ser Ala Lys Lys Ile Ile Ser Tyr Arg Gly  
 85 90 95  
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly  
 100 105 110  
 Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys Tyr Ala Met  
 130 135 140  
 Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val  
 145 150 155 160  
 Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn  
 165 170 175  
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu  
 195 200 205  
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg  
 210 215 220  
 Ile Arg Gly Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys  
 225 230 235 240  
 Ile Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe  
 245 250 255  
 Ile Tyr Thr Arg Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser  
 260 265 270  
 Leu Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys  
 290 295 300  
 His Ile Ala

305

&lt;210&gt; 1167

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g84 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1167

```

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1              5              10              15
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met
      20              25              30
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile
      35              40              45
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu
      50              55              60
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile
      65              70              75              80
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu
      85              90              95
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu
      100             105             110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115             120             125
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly
      130             135             140
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe
      145             150             155             160
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
      165             170             175
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile
      180             185             190
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile
      195             200             205
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys
      210             215             220
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
      225             230             235             240
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
      245             250             255
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser
      260             265             270
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275             280             285
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu
      290             295             300
Ala Leu Ala Gly Lys
305

```

&lt;210&gt; 1168

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g85 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1168

```

Val Glu Asp Met Val Pro Phe Ser Met Arg Ile Ser Gly Ile Phe Gln
 1          5          10          15
Ile Phe Phe Tyr Gly Tyr His His Leu Ile Tyr Xaa Tyr Ser Val Leu
          20          25          30
Thr Cys Val Pro Phe Gln Phe Thr Tyr Ser His Ile Val Lys Cys Xaa
          35          40          45
Leu Gln Gly Asn Leu Pro Gln Thr Gln Thr Ile Asn Val Thr Ser Glu
          50          55          60
Thr Ile Trp Ile Lys Ile Ile His Asp Phe Leu His Glu Pro Lys Thr
65          70          75          80
Ile Ser Phe Glu Gly Cys Met Ala Gln Ile Phe Leu Phe His Val Phe
          85          90          95
Ala Gly Gly Glu Met Val Leu Leu Val Ala Met Ala Tyr Asp Ile Tyr
          100          105          110
Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Asn Leu Cys
          115          120          125
Thr Cys Thr Gly Leu Val Val Gly Ser Trp Val Thr Gly Val Met His
          130          135          140
Ser Leu Ser Gln Leu Ala Phe Thr Val Ser Leu Pro Phe Cys Gly Pro
145          150          155          160
Asn Ile Val Asp Ser Tyr Tyr Cys Asp Leu Thr Leu Val Ile Lys Leu
          165          170          175
Ala Cys Thr Asp Thr Tyr Ile Pro Glu Ala Leu Met Leu Leu Asp Ser
          180          185          190
Gly Leu Met Gly Val Thr Ser Phe Leu Leu Leu Leu Ile Ser Tyr Thr
          195          200          205
Val Ile Leu Ile Thr Val Gln Arg Pro Ser Ser Ala Gly Met Ala Lys
          210          215          220
Ala Arg Ser Thr Leu Thr Ala His Val Thr Val Val Thr Leu Phe Phe
225          230          235          240
Gly Pro Cys Ile Phe Ile Tyr Ala Trp Pro Phe Ser Asn Leu Pro Val
          245          250          255
Asp Asn Ile Leu Ser Val Phe Ser Thr Val Phe Thr Pro Ile Leu Asn
          260          265          270
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala Ile His
          275          280          285
Asn Leu Lys Thr Gln Tyr Val Thr Ser Arg Leu Ser Ser Gln Leu Ser
          290          295          300
Leu Ile Gly Leu Asp Leu Leu
305          310

```

&lt;210&gt; 1169

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g86 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1169

```

Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1          5          10          15
Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu

```

```

      20      25      30
Gly His Ser Val Leu Gly Leu Ser Ser Leu Leu Asn Ile His Gly Glu
      35      40      45
Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
      50      55      60
Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg
65      70      75      80
Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
      85      90      95
Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
      100      105      110
Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
      115      120      125
Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
      130      135      140
Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
145      150      155      160
Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
      165      170      175
Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu
      180      185      190
Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
      195      200      205
Ala Phe
      210

```

&lt;210&gt; 1170

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g87 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1170

```

Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile Asn Pro Lys Leu
1      5      10      15
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Val Asp Phe
      20      25      30
Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu Asn Leu Val Val
      35      40      45
Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met Gln Phe Phe Phe
      50      55      60
Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu Ala Ala Met Ala
65      70      75      80
Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala
      85      90      95
Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala Ser Tyr Ser Trp
      100      105      110
Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu Leu Thr Leu Ser
      115      120      125
Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys Glu His Ala Ala
      130      135      140
Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser Gln Lys Val Ile
145      150      155      160
Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Ile Leu
      165      170      175
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr
      180      185      190
Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala
      195      200      205

```

```

Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 210                215                220
Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
225                230                235                240
Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
                245                250                255
Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr Lys Leu Leu Cys
                260                265                270
His Lys

```

```

<210> 1171
<211> 348
<212> PRT
<213> Unknown (H38g88 protein)

```

```

<220>
<223> Synthetic construct

```

```

<221> VARIANT
<222> (1)...(348)
<223> Xaa = Any Amino Acid

```

```

<400> 1171
Met Thr Asn Ser Ser Val Lys Gly Asp Phe Ile Leu Val Gly Phe Ser
 1                5                10                15
His Gln Pro His Leu Glu Lys Ile Leu Phe Val Ala Val Leu Ile Ser
                20                25                30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Val Ile Ile Leu Ile Cys Ser
                35                40                45
Val Asp Pro Lys Leu Lys Thr Pro Met Tyr Phe Phe Leu Ser His Leu
 50                55                60
Ser Leu Val Asp Ile Cys Phe Thr Thr Ser Ile Val Pro Gln Leu Leu
65                70                75                80
Trp Asn Leu Lys Gly Pro Asp Lys Thr Ile Thr Phe Leu Gly Cys Val
                85                90                95
Ile Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys Val Leu
                100                105                110
Leu Ala Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
                115                120                125
His Tyr Thr Ala Val Met Asn Pro Gln Leu Cys Gln Val Leu Ala Gly
130                135                140
Val Ala Trp Leu Ser Gly Val Gly Asn Thr Leu Ile Gln Gly Thr Val
145                150                155                160
Thr Leu Trp Leu Pro Arg Cys Gly His Arg Leu Leu Gln His Phe Phe
                165                170                175
Cys Glu Val Pro Ser Met Ile Lys Leu Ala Cys Val Asp Ile His Asp
                180                185                190
Asn Glu Val Gln Leu Phe Val Ala Ser Leu Val Leu Leu Leu Pro
                195                200                205
Leu Val Leu Ile Leu Leu Ser Tyr Gly His Ile Ala Lys Val Val Ile
210                215                220
Arg Ile Lys Ser Val Gln Ala Trp Cys Lys Gly Leu Gly Thr Cys Gly
225                230                235                240
Ser His Leu Ile Val Val Ser Leu Phe Cys Gly Thr Ile Thr Ala Val
                245                250                255
Tyr Ile Gln Ser Asn Ser Ser Tyr Ala His Ala His Gly Lys Phe Ile
                260                265                270
Ser Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu Ile Tyr
                275                280                285
Thr Leu Arg Asn Asn Asp Val Lys Gly Ala Leu Arg Leu Phe Asn Arg

```

```

      290              295              300
Asp Leu Gly Thr Xaa Lys Met Lys Gln Ser Thr Gln Arg Ser Thr Phe
305              310              315              320
Phe Thr Lys Gln Leu Xaa Arg Ser Tyr Leu Tyr Asn Phe Ser Leu Lys
              325              330              335
Asn Phe Ala Ser Leu Xaa Arg Lys Arg Cys Asn Leu
              340              345

```

&lt;210&gt; 1172

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g89 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1172

```

Met Asp Lys Ser Asn Ser Ser Val Val Ser Glu Phe Val Leu Leu Gly
1              5              10              15
Leu Cys Ser Ser Gln Lys Leu Gln Leu Phe Tyr Phe Cys Phe Phe Ser
              20              25              30
Val Leu Tyr Thr Val Ile Val Leu Gly Asn Leu Leu Ile Ile Leu Thr
              35              40              45
Val Thr Ser Asp Thr Ser Leu His Ser Pro Met Tyr Phe Leu Leu Gly
50              55              60
Asn Leu Ser Phe Val Asp Ile Cys Gln Ala Ser Phe Ala Thr Pro Lys
65              70              75              80
Met Ile Ala Asp Phe Leu Ser Ala His Glu Thr Ile Ser Phe Ser Gly
              85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Leu Phe Thr Gly Gly Glu Met
              100              105              110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
              115              120              125
Pro Leu Tyr Tyr Val Val Ile Met Ser Arg Arg Thr Cys Thr Val Leu
130              135              140
Val Met Ile Ser Trp Ala Val Ser Leu Val His Thr Leu Ser Gln Leu
145              150              155              160
Ser Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Val Val Asp Ser
              165              170              175
Phe Phe Cys Asp Leu Pro Arg Val Thr Lys Leu Ala Cys Leu Asp Ser
              180              185              190
Tyr Ile Ile Glu Ile Leu Ile Val Val Asn Ser Gly Ile Leu Ser Leu
195              200              205
Ser Thr Phe Ser Leu Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Thr
210              215              220
Val Trp Leu Lys Ser Ser Ala Ala Met Ala Lys Ala Phe Ser Thr Leu
225              230              235              240
Ala Ser His Ile Ala Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe
              245              250              255
Ile Tyr Val Trp Pro Phe Thr Ile Ser Pro Leu Asp Lys Phe Leu Ala
260              265              270
Ile Phe Tyr Thr Val Phe Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
275              280              285
Leu Arg Asn Arg Asp Met Lys Ala Ala Val Arg Lys Ile Val Asn His
290              295              300
Tyr Leu Arg Pro Arg Arg Ile Ser Glu Met Ser Leu Val Val Arg
305              310              315

```

&lt;210&gt; 1173

&lt;211&gt; 312

&lt;212&gt; PRT

<213> Unknown (H38g90 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1173

```

Met Pro Ala Lys Asn Ser Ser Ser Val Thr Ala Phe Ile Leu Ser Gly
 1          5          10          15
Leu Thr Asp Gln Pro Gly Leu Gln Ile Pro Ala Phe Phe Leu Phe Leu
      20          25          30
Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
      35          40          45
Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
 50          55          60
Asn Leu Ser Phe Ile Asp Phe Ser Tyr Ser Thr Thr Leu Ala Pro Lys
65          70          75          80
Met Leu Met Ser Phe Val Ser Glu Asn Ile Ile Ser Tyr Ala Gly Cys
      85          90          95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser Tyr
      100          105          110
Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Gly Ile Cys Asn Pro
      115          120          125
Leu Leu Tyr Thr Val Thr Met Ser Pro Gln Met Cys Leu Leu Leu Leu
      130          135          140
Leu Gly Val Tyr Gly Met Gly Tyr Phe Gly Ala Val Ala His Met Gly
145          150          155          160
Asn Ile Met Phe Met Ser Phe Cys Gly Asp Asn Leu Val Asn His Tyr
      165          170          175
Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
      180          185          190
Ile Asn Leu Leu Val Val Phe Ile Ile Val Thr Val Gly Ile Gly Val
      195          200          205
Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly Phe Ile Leu Ser Ser Ile
      210          215          220
Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
225          230          235          240
Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
      245          250          255
Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys Val
      260          265          270
Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met Phe Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Phe
      290          295          300
Cys Arg Lys Leu Val Ser Xaa Lys
305          310

```

<210> 1174

<211> 357

<212> PRT

<213> Unknown (H38g91 protein)

<220>

<223> Synthetic construct

<400> 1174

```

Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu Val

```

```

      1             5             10             15
Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe Leu
      20             25             30
Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
      35             40             45
Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50             55             60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
      65             70             75             80
Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly Gly
      85             90             95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
      100             105             110
Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys Arg
      115             120             125
Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln Leu
      130             135             140
Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
      145             150             155             160
Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp His
      165             170             175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
      180             185             190
Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu Leu
      195             200             205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
      210             215             220
Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly Thr
      225             230             235             240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245             250             255
Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
      260             265             270
Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
      275             280             285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg Leu
      290             295             300
Val Ala Lys Ser Leu Leu Asn Gln Glu Ile Arg Asn Met Gln Met Ile
      305             310             315             320
Ser Phe Ala Lys Asp Thr Val Leu Thr Tyr Leu Thr Asn Phe Ser Ala
      325             330             335
Ser Cys Pro Ile Phe Val Ile Thr Ile Glu Asn Tyr Cys Asn Leu Pro
      340             345             350
Gln Arg Lys Phe Pro
      355

```

&lt;210&gt; 1175

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g92 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1175

```

His Thr Glu Pro Arg Asn Leu Thr Gly Ala Xaa Glu Leu Leu Leu Leu
  1             5             10             15

```



Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser  
                   20                  25                  30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ser Leu  
                   35                  40                  45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
   65                  70                  75                  80  
 Lys Met Ile Val Asp Met Arg Ser His Ser Gly Val Ile Ser Tyr Ala  
                   85                  90                  95  
 Asp Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Val Glu  
                  100                 105                 110  
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
                  115                 120                 125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe  
   130                 135                 140  
 Leu Val Ser Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu Arg  
   145                 150                 155                 160  
 Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
                  165                 170                 175  
 Asn Phe Val Cys Asp Pro Ser Gln Pro Leu Lys Leu Ala Cys Ser Asp  
                  180                 185                 190  
 Ser Ile Ile Asp Ser Met Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly  
                  195                 200                 205  
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
   210                 215                 220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Xaa Tyr Lys Ala Phe Ser  
   225                 230                 235                 240  
 Ala Cys Gly Ser His Leu Pro Val Val Cys Leu Phe Tyr Gly Thr Gly  
                  245                 250                 255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly  
                  260                 265                 270  
 Val Val Ala Ser Val Thr Tyr Ala Val Val Thr Pro Met Leu Asn Pro  
                  275                 280                 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg  
   290                 295                 300  
 Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His Pro Phe Ser  
   305                 310                 315                 320

&lt;210&gt; 1176

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g93 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1176

Met Glu Gly Phe Asn Cys Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
   1                  5                  10                  15  
 Leu Thr Asp Ser Pro Glu Leu Gln Arg Phe Phe Phe Val Val Phe Ser  
                   20                  25                  30  
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
                   35                  40                  45  
 Val Leu Ser Thr Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ser  
   50                  55                  60  
 Asn Leu Ser Leu Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys

```

65          70          75          80
Met Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly
      85          90
Cys Ile Ser Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100          105          110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115          120          125
Pro Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu
      130          135          140
Val Ala Val Ser Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145          150          155          160
Ala Phe Thr Leu Tyr Leu Pro Phe Cys Gly Pro Asn Val Glu Ser Phe
      165          170          175
Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Met Asp Ile Tyr
      180          185          190
Val Leu Gly Ile Phe Met Ile Ser Thr Ser Gly Val Ile Ala Leu Ile
      195          200          205
Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Ile Thr Val
      210          215          220
Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr
225          230          235          240
Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe Ile
      245          250          255
Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser Val
      260          265          270
Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275          280          285
Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Xaa Leu Asn Ile Gln
      290          295          300
Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305          310

```

&lt;210&gt; 1177

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g94 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(338)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1177

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
  1          5          10          15
Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
      20          25          30
Gln Leu Glu His Ile Ile Ser Val Val Phe Ile Ile Tyr Ile Val
      35          40          45
Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
      50          55          60
Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
65          70          75          80
Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
      85          90          95
Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
      100          105          110
Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val
      115          120          125

```

Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr  
 130 135 140  
 Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala  
 145 150 155 160  
 Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly  
 165 170 175  
 His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys  
 180 185 190  
 Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe  
 195 200 205  
 Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr  
 210 215 220  
 Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu  
 225 230 235 240  
 Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu  
 245 250 255  
 Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile  
 260 265 270  
 Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro  
 275 280 285  
 Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser  
 290 295 300  
 Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met  
 305 310 315 320  
 Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala  
 325 330 335  
 Phe Ile

&lt;210&gt; 1178

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g95 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1178

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly  
 1 5 10 15  
 Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu  
 20 25 30  
 Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Val Pro Lys  
 65 70 75 80  
 Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly  
 85 90 95  
 Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn  
 100 105 110  
 Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Val Val Val Leu Ser Pro Lys Asn Cys Ala Leu  
 130 135 140  
 Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His

```

145          150          155          160
Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr
165          170          175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
180          185          190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
195          200          205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
210          215          220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
245          250          255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
260          265          270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
275          280          285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
290          295          300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
305          310

```

&lt;210&gt; 1179

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g96 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1179

```

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
1      5      10      15
Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
20     25     30
Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
35     40     45
Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
50     55     60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65     70     75     80
Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
85     90     95
Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
100    105    110
Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
115    120    125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
130    135    140
Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
145    150    155    160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
165    170    175
Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
180    185    190
Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
195    200    205
Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
210    215    220
Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
225    230    235    240

```

<400> 1180															
Met	Ala	Ala	Glu	Asn	Ser	Ser	Ser	Val	Thr	Glu	Phe	Ile	Leu	Ala	Gly
1				5					10					15	
Leu	Ile	His	Gln	Pro	Gly	Leu	Gln	Val	Pro	Val	Phe	Phe	Leu	Phe	Leu
			20					25					30		
Gly	Phe	Tyr	Ala	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Leu	Ile	Ile	Leu
		35					40					45			
Ile	Gly	Leu	Asn	Ser	Arg	Leu	His	Ile	Pro	Met	Tyr	Phe	Phe	Pro	Phe
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Phe	Ser	Phe	Ser	Thr	Thr	Ile	Ile	Pro	Lys
65					70					75					80
Met	Leu	Met	Ser	Phe	Val	Ser	Arg	Lys	Asn	Ile	Ile	Ser	Phe	Thr	Gly
				85					90					95	
Cys	Met	Ser	Gln	Phe	Phe	Phe	Phe	Cys	Phe	Phe	Val	Phe	Ser	Glu	Ser
			100					105					110		
Phe	Ile	Leu	Ser	Ala	Met	Val	Xaa	Asp	Arg	Tyr	Val	Gly	Ile	Cys	Asn
		115					120					125			
Pro	Leu	Leu	Tyr	Thr	Ile	Thr	Met	Ser	Pro	Gln	Val	Cys	Leu	Leu	Leu
	130					135					140				
Leu	Leu	Gly	Val	Tyr	Gly	Met	Gly	Val	Phe	Gly	Ala	Val	Ala	His	Thr
145					150					155					160
Gly	Asn	Ile	Val	Phe	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Leu	Val	Asn	His
				165					170					175	
Tyr	Met	Cys	Asp	Ile	Leu	Pro	Leu	Leu	Glu	Leu	Ser	Cys	Asn	Gly	Ser
			180					185					190		
Tyr	Ile	Asn	Val	Leu	Val	Ile	Phe	Ile	Val	Val	Thr	Val	Gly	Ile	Gly
		195					200					205			
Val	Pro	Ile	Val	Ala	Val	Phe	Ile	Ser	Tyr	Gly	Phe	Ile	Leu	Ser	Ser
	210					215					220				
Ile	Leu	Arg	Val	Ser	Ser	Ala	Glu	Gly	Arg	Ser	Lys	Ala	Phe	Ser	Ser
225					230						235				240
Cys	Ser	Ser	Tyr	Ile	Ile	Ala	Val	Ser	Leu	Phe	Phe	Gly	Ser	Gly	Ala
				245					250					255	
Phe	Thr	Tyr	Leu	Lys	Pro	Pro	Ser	Ile	Leu	Pro	Leu	Asp	Gln	Gly	Lys
			260					265					270		
Val	Ser	Ser	Leu	Phe	Tyr	Thr	Thr	Val	Val	Pro	Met	Phe	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala	Leu	Lys	Arg	Thr

290		295		300
Phe Ser Arg Ile Ser	Phe Ser Glu Lys Asn	Phe Arg Asn Arg Lys Glu		
305	310	315		320
Ile Leu Gly Phe Phe	Xaa Asn Gln Ile Ala Phe			
	325	330		

<210> 1181  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g98 protein)

<220>  
 <223> Synthetic construct

<400> 1181

Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu																			
1		5		10		15													
Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu																			
	20			25		30													
Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu																			
	35			40		45													
Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met																			
	50			55		60													
Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser																			
	65			70		75													
Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met																			
		85		90		95													
Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly																			
	100			105		110													
Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr																			
	115			120		125													
Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser																			
	130			135		140													
Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His																			
	145			150		155													
Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser																			
		165		170		175													
Asn Ile Ile His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile																			
	180			185		190													
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser																			
	195			200		205													
Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr																			
	210			215		220													
Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg																			
	225			230		235													
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr																			
		245		250		255													
Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala																			
	260			265		270													
Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro																			
	275			280		285													
Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp																			
	290			295		300													
Ser Phe Thr Lys Met Val Lys Arg Asn Val																			
305		310																	

<210> 1182  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g99 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1182

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
           20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
           35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
           50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
           85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
           100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
           115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
           130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
           165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
           180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
           195          200          205
Ile Cys Val Leu Cys Leu Ile Ser Tyr Thr Asn Val Phe Ser Thr
           210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
           245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
           260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
           275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
           290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
305          310

```

&lt;210&gt; 1183

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g100 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1183

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu

```

```

                20                25                30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
   35                40                45
Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
   50                55                60
Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
   65                70                75                80
Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Val Ser Leu Pro Glu
                85                90                95
Ser Lys Ile Gln Phe Phe Ser Phe Ala Ile Ser Val Thr Thr Glu Cys
                100                105                110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
                115                120                125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys Ile Arg Leu
                130                135                140
Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Gly Phe Leu Phe Arg
   145                150                155                160
Leu Thr Phe Cys Asn Ser Asn Val Val His His Ile Tyr Cys Asp Ile
                165                170                175
Ile Pro Leu Ser Lys Ile Ser Cys Thr Asp Ser Ser Ile Asn Phe Leu
                180                185                190
Met Val Phe Ile Phe Ser Gly Ser Ile Gln Val Phe Thr Ile Gly Thr
                195                200                205
Gly Leu Ile Ser Tyr Thr Phe Val Leu Phe Thr Ile Leu Lys Lys Lys
                210                215                220
Ser Val Lys Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ala His Leu
   225                230                235                240
Leu Ser Val Ser Leu Tyr His Gly Pro Leu Asp Phe Met Tyr Met Gly
                245                250                255
Ser Ala Ser Pro Gln Ala Asp Asp Glu Asp Met Met Glu Ser Leu Phe
                260                265                270
Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Thr Tyr Ser Leu Arg
                275                280                285
Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met Phe Lys Arg Asn Asn
                290                295                300
Ile Xaa Ile Ser Tyr Ser
   305                310

```

&lt;210&gt; 1184

&lt;211&gt; 231

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g101 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(231)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1184

```

Phe Cys Leu Phe Pro Ala Thr Val Ser Lys Ala Val Val Lys Phe Leu
   1                5                10                15
Ala Glu Thr Ile Ser Phe Ser Tyr Tyr Val Ile Gln Met Leu Val Phe
                20                25                30
Leu Phe Phe Val Thr Thr Glu Cys Asn Leu Leu Ala Ser Leu Gly Lys
                35                40                45
Asp Ile Tyr Met Pro Ile Arg Gln Pro Met Leu Tyr Pro Val Thr Met
                50                55                60
Ser Gln Val Cys Cys Ile Gln Leu Val Ala Ser Cys Tyr Gly His Gly
   65                70                75                80

```



Val Ile His Thr Met Phe Leu Gly Gly Ser Ile Ser Ile Phe Ala Phe  
                                     85                                    90                                    95  
 Cys Lys Ser Gln Thr Ile Ile Ser Phe Phe Gly Asp Ser Phe Pro Leu  
                                     100                                    105                                    110  
 Leu Val Leu Ser Cys Ser Asp Thr Tyr Ile Met Asn Ser Leu Phe Phe  
                                     115                                    120                                    125  
 Phe Thr Gly Cys Phe Ile Trp Met Ser Ser Xaa Pro Val Ile Leu Val  
                                     130                                    135                                    140  
 Ser His Met Phe Ile Ile Val Thr Phe Leu Arg Ile Phe Ser Val Val  
                                     145                                    150                                    155                                    160  
 Val Glu Ser Lys Gly Phe Leu Ala Phe Ser Ser His Leu Thr Ala Ile  
                                     165                                    170                                    175  
 Ile Leu Phe Tyr Gly Asp Ile Met Ser Leu Tyr Met Xaa His Ser Ser  
                                     180                                    185                                    190  
 Asn Tyr Phe Leu Asn Gln Asp Gln Thr Val Ser Ile Phe Tyr Met Val  
                                     195                                    200                                    205  
 Arg Ile Leu Leu Leu Ser Pro Ile Ile Tyr Cys Leu Ile Lys Met Gln  
                                     210                                    215                                    220  
 Val Ile Cys Phe Leu Glu Asn  
                                     225                                    230

&lt;210&gt; 1185

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g102 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(216)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1185

Leu Phe Phe Phe Val Xaa His Ser Ile Leu Thr Xaa Xaa Glu Gly Val  
   1                                    5                                    10                                    15  
 Lys Glu Ile Trp Tyr Phe Gln Glu Phe Leu Thr Tyr Pro Arg His Arg  
                                     20                                    25                                    30  
 Xaa Leu Leu Phe Val Ser Ser Cys Met Tyr Tyr Ser Ser Arg Ile Phe  
                                     35                                    40                                    45  
 Leu Arg Arg Thr Val Asn Ile Leu Phe Leu Leu Lys Val Ile Ser Leu  
                                     50                                    55                                    60  
 Leu Cys Tyr Gly Ser Lys Leu Ser Leu Phe Ile Phe Val Val Thr Ala  
                                     65                                    70                                    75                                    80  
 Glu Phe Xaa Leu Leu Ala Ser Arg Ile Cys His Cys Tyr Ile Ile Ile  
                                     85                                    90                                    95  
 Cys Asn Pro Phe Ser Thr Gln Phe Ser His Xaa Lys Leu Leu Ile Ser  
                                     100                                    105                                    110  
 Ile Leu Thr Ala His Tyr Asn Lys Arg Val Cys Ile Ser Ile Thr Thr  
                                     115                                    120                                    125  
 Ser Asn Thr Met Ser Xaa Leu Phe Phe Gly Arg Ser Asn Val Val Asn  
                                     130                                    135                                    140  
 Asn Phe Ser Asp Leu Leu Leu Leu Leu Asp Leu Ser Cys Thr Phe Val  
                                     145                                    150                                    155                                    160  
 Ser Phe Xaa Ser Pro Ser Gln Leu Pro Asp His Ser Pro Gly Pro His  
                                     165                                    170                                    175  
 Asn Phe Ile Ile Val Val Asn Ile Lys Ile Xaa Leu Ala Glu Gly Lys  
                                     180                                    185                                    190  
 His Lys Asp Phe Ser Ile Cys Pro Leu Xaa Phe Ala Thr Val Ser Asn  
                                     195                                    200                                    205  
 Phe Leu Met Ala His Ile His Ile

210

215

<210> 1186  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g103 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(312)  
 <223> Xaa = Any Amino Acid

<400> 1186  
 Phe Met Glu Asn Arg Asn Ile Val Thr Val Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ser Gln Asn Lys Asn Ile Glu Val Phe Trp Phe Val Leu Phe Val Phe  
 20 25 30  
 Cys Tyr Ile Ala Ile Trp Met Glu Asn Phe Ile Ile Met Ile Ser Ile  
 35 40 45  
 Met Tyr Ile Xaa Leu Ile Asp Gln Pro Met Tyr Phe Phe Leu Asn Tyr  
 50 55 60  
 Leu Ala Leu Ser Asp Leu Cys Tyr Ile Ser Thr Val Ala Pro Lys Leu  
 65 70 75 80  
 Met Ile Asp Leu Leu Thr Glu Arg Lys Ile Val Ser Tyr Asn Asn Cys  
 85 90 95  
 Met Ile Gln Leu Phe Ile Thr His Phe Leu Gly Asp Ile Glu Ile Phe  
 100 105 110  
 Ile Leu Lys Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Lys His  
 115 120 125  
 Leu His Tyr Thr Ile Ile Thr Thr Lys Gln Ser Cys Asn Thr Ile Ile  
 130 135 140  
 Ile Ala Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu  
 145 150 155 160  
 Leu Thr Ile Phe Leu Pro Phe Cys Gly Leu Asn Glu Ile Asp Gln Tyr  
 165 170 175  
 Phe Cys Tyr Val Tyr Pro Leu Leu Lys Leu Ala Arg Ile Asp Ile Tyr  
 180 185 190  
 Arg Ile Gly Phe Leu Val Ile Val Asn Ser Gly Leu Ile Ser Leu Leu  
 195 200 205  
 Ala Phe Val Ile Leu Met Val Ser Tyr Tyr Leu Ile Leu Ser Thr Ile  
 210 215 220  
 Arg Val Tyr Ser Ala Glu Ser His Thr Lys Ala Leu Ser Thr Cys Ser  
 225 230 235 240  
 Ser His Ile Ile Val Val Val Leu Phe Phe Val Pro Ala Leu Phe Ile  
 245 250 255  
 Tyr Ile Arg Pro Ala Ile Thr Phe Pro Glu Asp Lys Val Phe Val Leu  
 260 265 270  
 Phe Cys Ala Ile Ile Ala Pro Met Phe Ser Leu Leu Ile Tyr Met Leu  
 275 280 285  
 Arg Lys Val Glu Met Lys Asn Ala Val Arg Lys Met Trp Cys His Gln  
 290 295 300  
 Leu Leu Leu Ala Arg Lys Xaa Leu  
 305 310

<210> 1187  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g104 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1187

```

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1           5           10           15
Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
          20           25           30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
          35           40           45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
65           70           75           80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
          85           90           95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
          100          105          110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
          115          120          125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
          130          135          140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
145          150          155          160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
          165          170          175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
          180          185          190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
          195          200          205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
210          215          220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
          245          250          255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
          260          265          270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
290          295          300
Leu Lys Arg Thr
305

```

&lt;210&gt; 1188

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g105 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1188

```

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu

```

```

                20                25                30
Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
                35                40                45
Val Ser Ser Asp Ser His Leu His Ser Pro Met Xaa Phe Phe Leu Ser
                50                55                60
Asn Leu Ser Phe Val Asp Thr Cys Phe Ile Cys Thr Thr Val Pro Lys
65                70                75                80
Met Leu Val Asn Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
                85                90                95
Cys Leu Thr Gln Val Tyr Phe Xaa Met Met Phe Ala Gly Met Asp Thr
                100                105                110
Phe Leu Leu Ala Val Ile Ala Tyr Asp Arg Phe Val Ala Ile Cys His
                115                120                125
Pro Leu Gln Tyr Met Val Ile Ile Asn Pro His Leu Cys Gly Leu Leu
                130                135                140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145                150                155                160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
                165                170                175
Phe Phe Cys Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Ala
                180                185                190
Leu Leu Ile Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
                195                200                205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
                210                215                220
Leu Met Arg Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr
225                230                235                240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
                245                250                255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
                260                265                270
Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
                275                280                285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg Leu
                290                295                300
Leu Ser Arg Ala Ala Ser Cys Pro Leu Thr Val His Asn Leu Arg Thr
305                310                315                320
Lys Arg Met Leu

```

&lt;210&gt; 1189

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g106 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1189

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
1                5                10                15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
                20                25                30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
                35                40                45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
                50                55                60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
65                70                75                80
Ile Met Asp Phe Phe Ala Leu Arg Asn Thr Ile Ser Phe Glu Gly Cys
                85                90                95

```

```

Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
      100      105      110
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
      115      120      125
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
      130      135      140
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
      145      150      155      160
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
      165      170      175
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
      180      185      190
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
      195      200      205
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
      210      215      220
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
      245      250      255
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
      260      265      270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
      275      280      285
Leu Arg Asn
      290

```

&lt;210&gt; 1190

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g107 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1190

```

Tyr Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
      20      25      30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65      70      75      80
Lys Met Ile Val Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Glu
      85      90      95
Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp
      100      105      110
Asp Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Arg Ile Ile Met Asn Pro Arg Leu Cys Gly Phe
      130      135      140
Leu Ile Leu Leu Ser Phe Phe Ile Ser Leu Leu Asp Ser Gln Leu His
      145      150      155      160
Asn Leu Ile Met Leu Gln Leu Thr Cys Phe Lys Asp Val Asp Ile Ser
      165      170      175
Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu His Leu Arg Cys Ser Asp
      180      185      190
Thr Phe Ile Asn Glu Met Val Ile Tyr Phe Met Gly Ala Ile Phe Gly

```

```

      195              200              205
Cys Leu Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
 210              215              220
Pro Ile Leu Arg Val Pro Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser
 225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255
Leu Val Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser
      260              265              270
Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Gln Ser Ala Leu Cys Arg
      290              295              300
Leu His Gly Arg Ile Ile Lys Ser His His Leu His Pro Phe Val Ile
 305              310              315              320
Trp Asp Arg Asn Gly Ser Lys Ile
      325

```

&lt;210&gt; 1191

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g108 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1191

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
 1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
      20              25              30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met
      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
      50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
 65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
 145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
 225              230              235              240

```

Ala Phe Asp Thr Cys Gly Ser His Ile Gly Ala Val Ala Val Phe Tyr  
 245 250 255  
 Ile Pro Trp Val Val Leu Ser Val Val His Arg Phe Phe His Lys Ala  
 260 265 270  
 Ser Pro Tyr Val His Pro Leu Leu Ser Asn Ile Tyr Phe Leu Gly Pro  
 275 280 285  
 Ser Arg Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg  
 290 295 300  
 Arg Ala Ile Leu Lys Leu Phe Gln Thr Lys Ser Lys Glu Met Xaa Trp  
 305 310 315 320  
 Gly Leu Phe Phe Leu  
 325

&lt;210&gt; 1192

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g109 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(295)

&lt;223&gt; Xaa = Any Amino Acid.

&lt;400&gt; 1192

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr  
 1 5 10 15  
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu  
 20 25 30  
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile  
 35 40 45  
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu  
 50 55 60  
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu  
 65 70 75 80  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu  
 85 90 95  
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 100 105 110  
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile  
 115 120 125  
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe  
 130 135 140  
 Cys Asp Pro Ser Gln His Pro Thr Leu Ala Cys Cys Asp Thr Phe Thr  
 145 150 155 160  
 Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro  
 165 170 175  
 Ile Ser Gly Thr Phe Ser Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu  
 180 185 190  
 Arg Val Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly  
 195 200 205  
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly  
 210 215 220  
 Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala  
 225 230 235 240  
 Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
 245 250 255  
 Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg  
 260 265 270  
 Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val

275 280 285  
 Xaa Val Arg Lys Gly Ser Lys  
 290 295

<210> 1193  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g110 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1193  
 Tyr Thr Asp Ser Gln Asn Leu Thr Gly Val Leu Glu Phe Leu Phe Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Val Gly Leu Phe  
 20 25 30  
 Leu Ser Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Cys Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Leu Thr Ser Ala Thr Ile Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ile Ile Ser Tyr Glu  
 85 90 95  
 Gly Cys Leu Met Gln Met Tyr Phe Ile Tyr Phe Val Cys Met Asn Asp  
 100 105 110  
 Met Val Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu  
 130 135 140  
 Val Leu Val Ser Phe Ile Leu Ser Leu Leu Asn Ser Gln Leu His Asn  
 145 150 155 160  
 Gln Ile Val Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Phe Asn  
 165 170 175  
 Phe Phe Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Asn Ile Phe Met Tyr Leu Asp Ser Val Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu  
 245 250 255  
 Gly Ala Tyr Leu Ser Ser Ala Ala Ser Ser Phe Pro Arg Lys Gly Ala  
 260 265 270  
 Val Thr Ser Val Met Tyr Thr Val Val Ile Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Ala Leu Trp Arg Leu  
 290 295 300  
 His Ser Arg Thr Val Xaa Ser His Tyr Leu Phe His Pro Phe Cys Ser  
 305 310 315 320

<210> 1194  
 <211> 318  
 <212> PRT



<213> Unknown (H38g111 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1194

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Met Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
          85          90          95
Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp
          100          105          110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys
          115          120          125
His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
130          135          140
Leu Val Leu Met Ser Phe Ile Leu Ser Leu Leu Asp Ser Xaa Leu His
145          150          155          160
Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn
          165          170          175
Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Val
          180          185          190
Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe Leu
          195          200          205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
210          215          220
Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
          245          250          255
Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val
          260          265          270
Ala Ser Val Leu Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe Ile
          275          280          285
Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu Cys
          290          295          300
Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser
305          310          315

```

<210> 1195

<211> 350

<212> PRT

<213> Unknown (H38g112 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400> 1195

```

Met Ser Gln Leu Gly Arg Asp Asn Ile Thr Trp Val Ser Glu Phe Ile
 1          5          10          15
Leu Met Gly Leu Ser Ser Asp Arg Gln Thr Gln Ala Gly Leu Phe Ile
          20          25          30
Leu Phe Gly Ala Ala Tyr Leu Leu Thr Leu Leu Gly Asn Gly Leu Ile
          35          40          45
Leu Leu Leu Ile Trp Leu Asp Val Arg Leu His Leu Pro Met Tyr Phe
          50          55          60
Phe Leu Cys Asn Leu Ser Leu Val Asn Ile Cys Tyr Thr Ser Ser Arg
65          70          75          80
Val Pro Gln Met Leu Val His Leu His Gln Gln Arg Lys Thr Ile Ser
          85          90          95
Phe Ala Arg Cys Gly Thr Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly
          100          105          110
Thr Glu Phe Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
          115          120          125
Val Cys Asp Pro Leu Cys Tyr Ile Ala Val Met Ser Pro Arg Leu Cys
130          135          140
Met Ala Leu Ala Ala Val Ser Trp Leu Val Gly Leu Ala Asn Ser Ala
145          150          155          160
Met Glu Thr Ala Leu Thr Met His Leu Pro Thr Cys Gly His Asn Val
          165          170          175
Leu Asn His Val Ala Cys Glu Thr Leu Ala Leu Val Arg Ser Ala Cys
          180          185          190
Val Asp Ile Thr Phe Asn Gln Val Val Ile Val Ala Ser Ser Val Val
          195          200          205
Val Leu Leu Val Pro Cys Cys Leu Val Ser Leu Ser Tyr Thr Leu Ile
          210          215          220
Val Val Ala Val Leu Gln Ile His Ser Thr Gln Gly His Arg Lys Ala
225          230          235          240
Phe Gly Thr Cys Ala Ser His Leu Thr Val Val Ser Ile Ser Tyr Gly
          245          250          255
Met Ala Leu Phe Thr Tyr Met Gln Pro Arg Ser Met Ala Ser Ala Glu
          260          265          270
Gln Glu Lys Val Met Val Leu Ser Tyr Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu
          290          295          300
Ser Arg Ala Leu Met Arg Ser Ser Glu Leu Lys His Xaa Arg Val Val
305          310          315          320
Xaa Val Thr Arg Arg Pro His Ser Glu Asn Ser Gly His Trp Thr Val
          325          330          335
Leu Ser Ser Ile Thr Cys Val Arg Met Cys Val Tyr Val Cys
          340          345          350

```

<210> 1196

<211> 320

<212> PRT

<213> Unknown (H38g113 protein)

<220>

<223> Synthetic construct

<400> 1196

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1          5          10          15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu Leu
          20          25          30

```

```

Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
   35           40           45
Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
   50           55           60
Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
   65           70           75           80
Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
   85           90           95
Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
  100           105           110
Gly Ala Glu Cys Phe Leu Leu Ala Met Ala Asn Asp Arg Tyr Val
  115           120           125
Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
  130           135           140
Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
  145           150           155           160
Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
  165           170           175
Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
  180           185           190
Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
  195           200           205
Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
  210           215           220
Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
  225           230           235           240
Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
  245           250           255
Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
  260           265           270
Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
  275           280           285
Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
  290           295           300
Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
  305           310           315           320

```

&lt;210&gt; 1197

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g114 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1197

```

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
   1           5           10           15
Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
  20           25           30
Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
  35           40           45
Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
  50           55           60
Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
  65           70           75           80
Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
  85           90           95
Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
  100           105           110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile

```

```

      115      120      125
Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly
 130      135      140
Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro
145      150      155      160
Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu
      165      170      175
Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr
      180      185      190
Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr
      195      200      205
Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
 210      215      220
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
225      230      235      240
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
      245      250      255
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
      260      265      270
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
      275      280      285
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly
 290      295      300
Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe
305      310      315

```

&lt;210&gt; 1198

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g115 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(289)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1198

```

Phe His Gly Trp Ile Ser Met Pro Phe Cys Cys Ile Tyr Leu Met Pro
 1      5      10      15
Leu Leu Ser Asn Ala Thr Ile Leu Leu Thr Ile Trp Ser Asp Arg Thr
      20      25      30
Leu Arg Asp Pro Met Phe Tyr Phe Leu Ala Ile Leu Ser Ala Ile Asp
      35      40      45
Leu Ala Leu Ser Thr Ser Ser Val Pro Arg Met Leu Gly Ile Phe Trp
 50      55      60
Phe Asp Ala His Lys Ile Gly Phe Gly Ala Trp Val Ala Gln Met Phe
65      70      75      80
Leu Ile His Thr Phe Thr Gly Met Glu Ser Thr Val Leu Leu Ala Met
      85      90      95
Ala Phe Asp Arg Tyr Val Ala Ile Cys Thr Ser Leu His Tyr Thr Ser
      100      105      110
Thr Leu Thr Pro Arg Val Leu Ala Gly Ile Gly Val Ser Ile Ile Met
      115      120      125
Arg Pro Val Leu Leu Met Leu Pro Ile Leu Tyr Leu Thr His Arg Leu
      130      135      140
Pro Phe Cys Glu Ala Arg Ile Ile Ala His Ser Tyr Cys Glu His Met
145      150      155      160
Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile His Ile Asn Ala Ile Tyr
      165      170      175

```

Gly Leu Phe Val Ala Ser Phe Leu Asp Val Ala Leu Val Gly Ile Ser  
 180 185 190  
 Tyr Thr Tyr Ile Leu Arg Ala Val Phe His Leu Pro Ser Gln Asp Ala  
 195 200 205  
 Arg His Lys Ala Leu Arg Thr Cys Gly Ser His Val Gly Val Met Cys  
 210 215 220  
 Val Phe Tyr Thr Pro Ser Leu Phe Ser Phe Leu Thr Tyr Arg Phe Ala  
 225 230 235 240  
 Lys Lys Ile Pro Arg Tyr Val His Ile Leu Val Ala Asn Leu Tyr Val  
 245 250 255  
 Val Ile Pro Pro Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys  
 260 265 270  
 Gln Ile His Glu His Val Val His Thr Phe Thr Ser Lys Xaa Gly Leu  
 275 280 285  
 Leu

&lt;210&gt; 1199

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g116 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(174)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1199

Thr Cys Trp Val Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly  
 1 5 10 15  
 Leu Ser Gly Ala Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe  
 20 25 30  
 Cys Asp Asp Asn Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys  
 35 40 45  
 Leu Ile Xaa Asn Thr Ser Gly Asn Ser Lys Ile Ile Val Ile Phe  
 50 55 60  
 Asp Ser Phe Leu Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr  
 65 70 75 80  
 Leu Leu Ile Ile Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Lys Ala  
 85 90 95  
 Lys Xaa Phe Tyr Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr  
 100 105 110  
 Phe Leu Trp Asp Pro His Leu Gln Tyr Met Xaa Ser Thr Ser Asp Lys  
 115 120 125  
 Ser Leu Thr Glu Asp Lys Leu Ala Ser Val Thr Cys Thr Ile Phe Ile  
 130 135 140  
 Pro Met Leu Glu Leu Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val  
 145 150 155 160  
 Ala Phe Lys Lys Ala Ile Gly Asn Phe Trp Val Phe Glu Arg  
 165 170

&lt;210&gt; 1200

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g117 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1200

```

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1           5           10           15
Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
           20           25           30
Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
           35           40           45
Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
           50           55           60
Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
65           70           75           80
Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
           85           90           95
Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
           100          105          110
Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
           115          120          125
Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
130          135          140
Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
145          150          155          160
Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
           165          170          175
Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
           180          185          190
Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
           195          200          205
Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
210          215          220
Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
225          230          235          240
Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
           245          250          255
Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala
           260          265          270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
           275          280          285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
290          295          300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
305          310          315

```

&lt;210&gt; 1201

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g118 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1201

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15

```

Phe Leu Cys Gln Gln Gly Phe Leu Trp Glu Ile Pro Leu Phe Leu Ala  
                   20                  25                  30  
 Phe Leu Val Ile Asp Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile  
                   35                  40                  45  
 Phe Leu Ile Trp Lys Asp Pro His Leu His Ile Ser Met Tyr Leu Phe  
                   50                  55                  60  
 Leu Gly Ser Leu Ala Phe Val Asp Thr Trp Leu Ser Ser Thr Val Thr  
                   65                  70                  75                  80  
 Pro Lys Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu  
                   85                  90                  95  
 Ser Glu Cys Met Val Gln Phe Phe Ser Leu Ala Ile Ser Val Thr Thr  
                   100                  105                  110  
 Glu Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Ala Asp Ile  
                   115                  120                  125  
 Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile  
                   130                  135                  140  
 Trp Leu Phe Val Leu Ser Phe Leu Gly Gly Leu Phe His Ala Leu Ile  
                   145                  150                  155                  160  
 His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Met Ile  
                   165                  170                  175  
 Gln His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr  
                   180                  185                  190  
 Asp Ser Cys Ile Asn Phe Leu Met Phe Phe Ile Phe Ser Gly Ser Ile  
                   195                  200                  205  
 Gln Val Leu Thr Ile Gly Ile Val Phe Val Ser Tyr Met Phe Val Leu  
                   210                  215                  220  
 Phe Thr Ile Leu Lys Lys Lys Ser Asn Lys Gly Ile Arg Glu Ala Phe  
                   225                  230                  235                  240  
 Ser Thr Cys Gly Ala His Tyr Ile Pro Leu Ser Leu Cys Tyr Gly Leu  
                   245                  250                  255  
 Leu Leu Phe Met Tyr Val Gly Pro Ala Ala Pro Gln Ala Asp Asn Gln  
                   260                  265                  270  
 Asp Met Met Glu Tyr Leu Phe Tyr Pro Ile Ile Val Arg Leu Leu Asn  
                   275                  280                  285  
 Pro Tyr Tyr Tyr Ser Leu Arg Asn Lys Gln Val Ile Gly Ser Leu Thr  
                   290                  295                  300  
 Lys Met Leu Lys Xaa Asn Ile Cys Ile Ala Tyr  
                   305                  310                  315

&lt;210&gt; 1202

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g119 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1202

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu  
                   1                  5                  10                  15  
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro  
                   20                  25                  30  
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu  
                   35                  40                  45  
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Gly Pro Met Tyr Tyr Phe  
                   50                  55                  60  
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu  
                   65                  70                  75                  80  
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Thr Ser Ser  
                   85                  90                  95  
 Ser Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu

```

      100      105      110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
      115      120      125
His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
      130      135      140
Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
145      150      155      160
Phe Pro Phe Thr Leu Arg Ser Leu Arg Tyr Cys Lys Lys Asn Gln Leu
      165      170      175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
      180      185      190
Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
      195      200      205
Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
210      215      220
Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Glu Leu Lys Ala Leu Asn
225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
      245      250      255
Ile Asn Leu Ala Val Val His Arg Phe Ala Gly His Val Ser Pro Leu
      260      265      270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Met
      275      280      285
Lys Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
290      295      300
Val Ala Lys Leu Cys Gln Trp Lys Ile
305      310

```

&lt;210&gt; 1203

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g120 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1203

```

Met Glu Glu Lys Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Leu
 1      5      10      15
Phe Leu Tyr Gln Pro His Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
      20      25      30
Val Ile Tyr Leu Ile Thr Ile Phe Gly Asn Leu Gly Leu Ile Ala Val
      35      40      45
Val Trp Lys Asp Pro His Leu His Ile Pro Ile Tyr Leu Phe Leu Glu
50      55      60
Asn Leu Ala Phe Val Asp Asp Leu Leu Ser Ser Thr Val Thr Leu Lys
65      70      75      80
Met Leu Ile Asn Phe Thr Lys Ser Lys Leu Ile Ser Leu Glu Cys
      85      90      95
Trp Ile His Phe Phe Ser Phe Ala Ile Gly Val Thr Thr Glu Cys Phe
      100      105      110
Ile Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
      115      120      125
Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu Leu
130      135      140
Ile Leu Ser Phe Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Ala
145      150      155      160

```



[illegible]

<210> 1204  
<211> 171  
<212> PRT  
<213> Unknown (H38q121 protein)

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(171)
<223> Xaa = Any Amino Acid
```

<400> 1204															
Cys	Xaa	Val	Gln	Val	Ser	Xaa	Val	Ala	Glu	Lys	Tyr	Xaa	Xaa	Ile	Leu
1				5					10					15	
Phe	Val	Ala	Leu	Phe	Asn	Lys	Thr	Lys	Ser	Ile	Cys	Gln	Pro	Gln	Asn
			20					25					30		
Ile	Ala	Thr	Pro	Arg	Pro	Trp	Ala	Phe	Pro	Gln	His	Ser	Phe	Thr	Ser
		35					40					45			
Thr	Ser	Cys	Phe	Gly	Gly	Thr	Ser	Thr	Gly	Leu	Ser	Xaa	Ala	Val	Lys
	50				55					60					
Ser	Pro	Ile	Ser	Ser	Val	Cys	Pro	Leu	Leu	Gln	Leu	Leu	Leu	Gln	Tyr
65					70				75					80	
Pro	Cys	Asn	Asn	Ile	Thr	Cys	Leu	Xaa	Asn	Ala	Ala	Asp	Arg	Glu	Phe
				85				90						95	
Leu	Ser	Phe	Xaa	Asp	Pro	Leu	Leu	Ala	Val	Gly	Ser	Phe	Thr	Ile	Ser
		100						105					110		
Ser	Cys	Leu	Leu	Met	Leu	Lys	Leu	Ile	Ser	Phe	Ser	Ser	Ser	Arg	Ile
		115				120					125				
Ile	Ala	Ser	Leu	Leu	Ser	Arg	Cys	Pro	Thr	Glu	Ser	His	Arg	Ser	Pro
	130				135						140				
Phe	Xaa	Tyr	Ser	Phe	Cys	His	Leu	Phe	Cys	Leu	Phe	Phe	Phe	Met	Thr
145					150				155					160	
Glu	Asn	Pro	Trp	Xaa	Tyr	Leu	Xaa	Phe	Pro	Ser					
				165					170						

```
<210> 1205
<211> 308
<212> PRT
<213> Unknown (H38g122 protein)
```

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1205

```

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1           5           10           15
Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
           20           25           30
Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
 35           40           45
Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
 50           55           60
Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
 65           70           75           80
Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
           85           90           95
Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
           100          105          110
Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
           115          120          125
Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
 130          135          140
Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
 145          150          155          160
Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
           165          170          175
Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
           180          185          190
Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
 195          200          205
Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
 210          215          220
Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
 225          230          235          240
Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
           245          250          255
Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile
           260          265          270
Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val
           275          280          285
Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met
 290          295          300
Phe Phe Asn Lys
305

```

&lt;210&gt; 1206

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g123 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1206

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Phe Leu His Gln Pro Asp Cys Lys Ile Pro Leu Phe Leu Ala Phe Leu
           20           25           30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
 35           40           45

```

Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Leu Gly  
 50 55 60  
 Ser Leu Ala Phe Val Asp Ala Ser Leu Ser Ser Thr Val Thr Pro Lys  
 65 70 75 80  
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu  
 85 90 95  
 Cys Met Val Gln Phe Phe Ser Leu Val Thr Thr Val Thr Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile Gln Leu  
 130 135 140  
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu  
 145 150 155 160  
 Ala Phe Ser Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His  
 165 170 175  
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser  
 180 185 190  
 Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ala Gly Ser Val Gln Val  
 195 200 205  
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Ile Ile Leu Phe Thr  
 210 215 220  
 Ile Leu Glu Lys Lys Ser Ile Lys Gly Ile Arg Lys Ala Val Ser Thr  
 225 230 235 240  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Thr  
 245 250 255  
 Phe Lys Tyr Leu Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
 260 265 270  
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met  
 290 295 300  
 Phe Lys Ser Asn Val  
 305

&lt;210&gt; 1207

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g124 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(308)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1207

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr  
 20 25 30  
 Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr Ala  
 35 40 45  
 Ser Pro Ser Leu Arg Ser Pro Met Xaa Phe Phe Leu Ala Tyr Leu Ser  
 50 55 60  
 Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Val Ser Lys Leu Ile Thr  
 65 70 75 80  
 Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr  
 85 90 95  
 Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu Leu

```

      100      105      110
Thr Val Met Ala Tyr Asp Cys Tyr Val Val Ile Cys Lys Pro Leu Arg
      115      120      125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
      130      135      140
Ser Arg Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe Ile
145      150      155      160
Phe Gln Leu Pro Phe Cys Ser Ser Asn Val Ile Asp His Phe Ile Cys
      165      170      175
Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asn Thr His Thr Leu
      180      185      190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
      195      200      205
Leu Leu Leu Leu Val Ser Tyr Val Val Ile Leu Tyr Ser Leu Arg Thr
      210      215      220
His Ser Leu Glu Ala Arg His Lys Gly Leu Ser Thr Cys Val Ser His
225      230      235      240
Asn Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
      245      250      255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
      260      265      270
Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
      290      295      300
Ser Ser Val Lys
305

```

&lt;210&gt; 1208

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g125 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1208

```

Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20      25      30
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu
      35      40      45
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe
      50      55      60
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile
      65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe
      85      90      95
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met
      100      105      110
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro
145      150      155      160
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile
      165      170      175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala
      180      185      190

```

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu  
 195 200 205  
 Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys  
 210 215 220  
 Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala  
 245 250 255  
 Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu  
 275 280 285  
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val  
 290 295 300  
 Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu  
 305 310 315 320  
 Ile

&lt;210&gt; 1209

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g126 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1209

Met Arg Asn His Thr Met Val Thr Glu Phe Ile Leu Leu Gly Ile Pro  
 1 5 10 15  
 Glu Thr Glu Gly Leu Glu Thr Ala Leu Phe Leu Phe Ser Ser Phe  
 20 25 30  
 Tyr Leu Cys Thr Leu Leu Gly Asn Val Leu Ile Leu Thr Ala Ile Ile  
 35 40 45  
 Ser Ser Thr Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu  
 50 55 60  
 Ser Ile Phe Asp Leu Gly Phe Ser Ser Thr Thr Val Pro Lys Met Leu  
 65 70 75 80  
 Phe Tyr Leu Ser Gly Asn Ser His Ala Ile Ser Tyr Ala Gly Cys Val  
 85 90 95  
 Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu  
 100 105 110  
 Tyr Thr Val Met Ala Cys Asp Arg Phe Val Ala Ile Cys Phe Pro Leu  
 115 120 125  
 Arg Tyr Thr Val Ile Met Asn His Arg Val Cys Phe Met Leu Ala Thr  
 130 135 140  
 Gly Thr Trp Met Ile Gly Cys Val His Ala Met Ile Leu Thr Pro Leu  
 145 150 155 160  
 Thr Phe Gln Leu Pro Tyr Cys Gly Pro Asn Lys Val Gly Tyr Tyr Phe  
 165 170 175  
 Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu  
 180 185 190  
 Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys  
 195 200 205  
 Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser  
 210 215 220  
 Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser  
 225 230 235 240  
 Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile  
 245 250 255  
 Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile

260                      265                      270  
 Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
           275                      280                      285  
 Arg Asn Lys Asp Val Lys Ser Asp Gln Pro  
           290                      295

<210> 1210  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g127 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 1210  
 Met Glu Glu Glu Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly  
   1                      5                      10                      15  
 Phe Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu  
           20                      25                      30  
 Val Ile Xaa Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu  
           35                      40                      45  
 Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Arg Gly  
           50                      55                      60  
 Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Thr Val Thr Pro Lys  
           65                      70                      75                      80  
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu  
           85                      90                      95  
 Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu Cys  
           100                      105                      110  
 Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
           115                      120                      125  
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln Leu  
           130                      135                      140  
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu  
           145                      150                      155                      160  
 Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His  
           165                      170                      175  
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser  
           180                      185                      190  
 Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln Val  
           195                      200                      205  
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu Ile  
           210                      215                      220  
 Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser Thr  
           225                      230                      235                      240  
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Val  
           245                      250                      255  
 Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met  
           260                      265                      270  
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser Met  
           275                      280                      285  
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met  
           290                      295                      300  
 Phe Lys Arg Asn Val Xaa Ile Ser Tyr Asn Leu Cys Ser Leu Phe Thr  
           305                      310                      315                      320  
 Lys Ile Phe Pro

<210> 1211  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g128 protein)

<220>  
 <223> Synthetic construct

<400> 1211  
 Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe  
 1 5 10 15  
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe  
 20 25 30  
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile  
 35 40 45  
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn  
 50 55 60  
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala  
 65 70 75 80  
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys  
 85 90 95  
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu  
 100 105 110  
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro  
 115 120 125  
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala  
 130 135 140  
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly  
 145 150 155 160  
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe  
 165 170 175  
 Phe Cys Glu Val Pro Pro Leu Leu Leu Ser Cys Ser Ser Thr Tyr  
 180 185 190  
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val  
 195 200 205  
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile  
 210 215 220  
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr  
 245 250 255  
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu  
 260 265 270  
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe  
 290 295 300  
 Pro Phe Phe Arg  
 305

<210> 1212  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g129 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1212

```

Met Asp Asp Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
1          5          10          15
Leu Thr Tyr Gln Ser Glu Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
20          25          30
Val Ile Tyr Leu Ile Thr Ile Met Ala Asn Leu Gly Leu Ile Ala Val
35          40          45
Ile Trp Lys Asp Ser His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
50          55          60
Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Ser Val Thr Pro Lys
65          70          75          80
Met Leu Ile Ser Phe Leu Ala Lys Ser Met Ile Ile Ser Val Ser Glu
85          90          95
Cys Lys Ile Gln Phe Phe Ser Phe Gly Ile Ser Gly Thr Thr Glu Cys
100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu
130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Phe Leu His Ala Leu Ile His Glu
145          150          155          160
Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Pro
180          185          190
Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser Gly Ser Ile Gln Val
195          200          205
Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Thr Phe Val Leu Phe Thr
210          215          220
Ile Leu Lys Lys Lys Ser Ala Lys Asp Ile Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Leu
245          250          255
Phe Met Tyr Val His Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
260          265          270
Val Glu Ser Leu Phe Tyr Thr Val Ile Ile Pro Phe Leu Asn Pro Ile
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Leu Thr Lys Thr
290          295          300
Leu Lys Gly Asn Val Xaa Ile Ser Tyr Trp Asn Val Phe Ser Ile
305          310          315

```

&lt;210&gt; 1213

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g130 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1213

```

Met Val Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
1          5          10          15
Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
20          25          30
Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
35          40          45
Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
50          55          60

```



```

Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
65          70          75          80
Met Leu Glu Asn Phe Phe Ser Glu Gly Lys Arg Ile Ser Leu Tyr Glu
      85          90          95
Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
      100        105        110
Phe Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115        120        125
Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
      130        135        140
Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
      145        150        155        160
Gly Leu Val Phe Arg Leu Val Phe Cys Gly Leu Asn His Ile Asn His
      165        170        175
Phe Tyr Cys Asp Thr Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
      180        185        190
Phe Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
      195        200        205
Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
      210        215        220
Ile Phe Arg Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
      225        230        235        240
Cys Ala Ser His Phe Ser Ser Val Ser Leu Phe Tyr Gly Ser Ile Phe
      245        250        255
Phe Leu Tyr Ile Arg Pro Asn Leu Leu Glu Glu Gly Gly Asn Asp Ile
      260        265        270
Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
      275        280        285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Ser Val Leu Arg Lys Ile
      290        295        300
Leu Leu Lys Ile Lys Ser Gln
      305        310

```

&lt;210&gt; 1214

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38gl31 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1214

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
1          5          10          15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
      20          25          30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
      35          40          45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
      50          55          60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
      65          70          75          80
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
      85          90          95
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
      100        105        110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys

```

```

      115              120              125
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130              135              140
Leu Val Leu Leu Ser Phe Phe Ser Val Phe Xaa His Ser Gln Leu
 145              150              155              160
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile
      165              170              175
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
      180              185              190
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe
 195              200              205
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val
 210              215              220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe
 225              230              235              240
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr
      245              250              255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
      260              265              270
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
      275              280              285
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp
 290              295              300
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His
 305              310              315              320
Leu Phe His Ser Phe Cys Arg Met
      325

```

&lt;210&gt; 1215

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g132 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1215

```

Met Glu Pro Gln Phe Thr Thr Gln Gly Ser Met Phe Val Leu Leu Gly
 1              5              10              15
Xaa Ser Gln Thr Gln Glu Leu Gln Arg Val Met Phe Ile Leu Phe Leu
      20              25              30
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
      35              40              45
Val Thr Phe Asp Cys Arg Leu His Pro Met Tyr Phe Leu Leu Arg Asn
      50              55              60
Leu Ala Leu Ile Asp Val Cys Tyr Ser Thr Val Thr Ser Pro Lys Met
 65              70              75              80
Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly Cys
      85              90              95
Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val Phe
      100              105              110
Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln Pro
      115              120              125
Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu Val
 130              135              140
Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu Ala
 145              150              155              160

```

```
<221> VARIANT
<222> (1) ... (335)
```

<223> Xaa = Any Amino Acid

<400> 1217

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
      20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
      35           40           45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65           70           75           80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Phe Tyr Ala
      85           90           95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100          105          110
Glu Asn Thr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115          120          125
Cys His Pro Leu Cys His Ser Ala Ser Met Asn Pro Cys Phe Cys Gly
      130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Thr Gln
      145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Asp
      165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
      180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
      195          200          205
Phe Gly Phe Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
      210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala
      225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
      245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
      260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
      275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
      290          295          300
Arg Arg Pro Gln Gly Ser Lys Val Xaa Tyr Gln Tyr Leu Leu Ile Cys
      305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
      325          330          335

```

<210> 1218

<211> 319

<212> PRT

<213> Unknown (H38gl35 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1218

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1           5           10           15

```

Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu  
                   20                  25                  30  
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Leu Val Val Thr Ile Thr  
                   35                  40                  45  
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
                   50                  55                  60  
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile  
                   65                  70                  75                  80  
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met  
                   85                  90                  95  
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu  
                   100                  105                  110  
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu  
                   115                  120                  125  
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val  
                   130                  135                  140  
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe  
                   145                  150                  155                  160  
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
                   165                  170                  175  
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr  
                   180                  185                  190  
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn  
                   195                  200                  205  
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys  
                   210                  215                  220  
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser  
                   225                  230                  235                  240  
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr  
                   245                  250                  255  
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Val Phe  
                   260                  265                  270  
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
                   275                  280                  285  
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val  
                   290                  295                  300  
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg  
                   305                  310                  315

&lt;210&gt; 1219

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g136 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1219

Met Glu Ile Gly Asn His Thr Thr Val Thr Glu Phe Ile Ile Leu Gly  
   1                  5                  10                  15  
 Leu Thr Glu Asp Pro Thr Leu Cys Asp Ile Phe Phe Val Ile Phe Leu  
                   20                  25                  30  
 Gly Ile Tyr Ile Val Thr Leu Ile Gly Asn Ile Ser Ile Ile Lys Lys  
                   35                  40                  45  
 Arg Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser His Leu Ala  
                   50                  55                  60  
 Phe Val Asp Ile Gly Leu Ala Thr Val Val Thr Pro Ile Met Leu Met

```

65      70      75      80
Gly Phe Leu Arg Arg Gly Thr Ala Leu Pro Val Thr Ser Cys Glu Ala
      85      90
Gln Leu Cys Ser Val Val Met Phe Gly Thr Ser Glu Cys Phe Leu Leu
      100      105      110
Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu Val
      115      120      125
Asn Ser Thr His Leu Ser Pro Ile Ile Cys Ile Leu Leu Val Gly Val
      130      135      140
Cys Tyr Leu Gly Gly Trp Val Asn Ala Ser Thr Phe Thr Ser Cys Leu
145      150      155      160
Leu Ser Leu Ser Phe Cys Gly Pro Asn Gln Ile Asp His Phe Phe Cys
      165      170      175
Asp Phe Ser Pro Leu Leu Lys Leu Ser Cys Ser Asn Ile Ser Ile Pro
      180      185      190
Glu Ile Ile Pro Ser Ile Ser Ser Gly Ser Ile Ile Val Val Thr Val
      195      200      205
Phe Ala Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys
      210      215      220
Met Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys Thr Ser
225      230      235      240
His Leu Ala Ala Val Thr Leu Tyr Tyr Gly Thr Ile Thr Phe Ile Tyr
      245      250      255
Val Met Pro Lys Ser Ser Tyr Ser Thr Ser Gln Asn Arg Leu Ile Ser
      260      265      270
Leu Ser Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Phe Ile Tyr Ser
      275      280      285
Leu Arg Asn Arg Asp Val Lys Glu Ala Leu Arg Lys Ala Thr Val Arg
290      295      300
Ile Tyr Ser Xaa Asp Gln Phe Val
305      310

```

&lt;210&gt; 1220

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g137 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1220

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Pro Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
50      55      60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65      70      75      80
Val Ser Lys Thr Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
115      120      125

```

```

Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg
260          265          270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290          295          300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310          315          320
Phe Phe Trp Cys

```

&lt;210&gt; 1221

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g138 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1221

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
1          5          10          15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
20          25          30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
35          40          45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
50          55          60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Asp Ile Val Leu
65          70          75          80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
85          90          95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
100          105          110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
115          120          125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
130          135          140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145          150          155          160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
165          170          175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
180          185          190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val

```

```

      195              200              205
Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser
  210              215              220
Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala
  225              230              235              240
Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu
      245              250              255
Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg
      260              265              270
Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His
      275              280              285
Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys
      290              295              300
Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg
  305              310              315

```

&lt;210&gt; 1222

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g139 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(236)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1222

```

Pro Lys Val Pro Asp Phe Phe Val Phe Gly Leu Arg Ala Ile Ser Phe
  1              5              10              15
Pro Ala Gly Phe Leu Gln Lys Tyr Ile Lys Asn Cys Phe Gln Ala Met
      20              25              30
Glu Phe Trp Pro Phe Lys Val Arg Ala Met Asp Arg Xaa Gly Thr Leu
      35              40              45
Cys His Pro Leu Lys Tyr Pro Ser Ile Ile Thr Asp Pro Phe Gly Val
      50              55              60
Lys Ala Ala Arg Phe Ile Leu Pro Arg Asn Val Leu Met Thr Leu Pro
      65              70              75              80
Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn Val Ile
      85              90              95
Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser Cys Asp
      100              105              110
Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp Thr Leu
      115              120              125
Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile Leu
      130              135              140
Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys Ala Leu
      145              150              155              160
Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser Thr Ile
      165              170              175
Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val Ser Pro
      180              185              190
Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro Ala Ala
      195              200              205
Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys Gln Gly
      210              215              220
Met Gln Arg Leu Leu Lys Lys Gly Cys Xaa Gln Gly
  225              230              235

```

&lt;210&gt; 1223



<211> 308  
 <212> PRT  
 <213> Unknown (H38g140 protein)

<220>  
 <223> Synthetic construct

<400> 1223

```

Met Asn Ser Leu Lys Asp Gly Asn His Thr Ala Leu Thr Gly Phe Ile
 1           5           10           15
Leu Leu Gly Leu Thr Asp Asp Pro Ile Leu Arg Val Ile Leu Phe Met
 20           25           30
Ile Ile Leu Ser Gly Asn Leu Ser Ile Ile Ile Leu Ile Arg Ile Ser
 35           40           45
Ser Gln Leu His His Pro Met Tyr Phe Phe Leu Ser His Leu Ala Phe
 50           55           60
Ala Asp Met Ala Tyr Ser Ser Ser Val Thr Pro Asn Met Leu Val Asn
 65           70           75           80
Phe Leu Val Glu Arg Asn Thr Val Ser Tyr Leu Gly Cys Ala Ile Gln
 85           90           95
Leu Gly Ser Ala Ala Phe Phe Ala Thr Val Glu Cys Val Leu Leu Ala
 100          105          110
Ala Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Ser Pro Leu Leu Tyr
 115          120          125
Ser Thr Lys Met Ser Thr Gln Val Ser Val Gln Leu Leu Val Val
 130          135          140
Tyr Ile Ala Gly Phe Leu Ile Ala Val Ser Tyr Thr Thr Ser Phe Tyr
 145          150          155          160
Phe Leu Leu Phe Cys Gly Pro Asn Gln Val Asn His Phe Phe Cys Asp
 165          170          175
Phe Ala Pro Leu Leu Glu Leu Ser Cys Ser Asp Ile Ser Val Ser Thr
 180          185          190
Val Val Leu Ser Phe Ser Ser Gly Ser Ile Ile Val Val Thr Val Cys
 195          200          205
Val Ile Ala Val Cys Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys Met
 210          215          220
Arg Ser Thr Glu Gly His His Lys Ala Phe Ser Thr Cys Thr Ser His
 225          230          235          240
Leu Thr Val Val Thr Leu Phe Tyr Gly Thr Ile Thr Phe Ile Tyr Val
 245          250          255
Met Pro Asn Phe Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val
 260          265          270
Leu Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 275          280          285
Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu Leu Val Arg Lys
 290          295          300
Ile Leu Ser His
305

```

<210> 1224  
 <211> 335  
 <212> PRT  
 <213> Unknown (H38g141 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(335)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1224

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
          35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
          65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
          85          90          95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
          100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
          115          120          125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
          130          135          140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Pro Arg Leu Leu Asp Ser Gln
          145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
          165          170          175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
          195          200          205
Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Lys Tyr Lys Ala
          225          230          235          240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
          290          295          300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
          305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
          325          330          335

```

&lt;210&gt; 1225

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g142 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1225

```

Met Gly Thr Gly Asn Asp Thr Thr Val Val Glu Phe Thr Leu Leu Gly
 1          5          10          15
Leu Ser Glu Asp Thr Thr Val Cys Ala Ile Leu Phe Leu Val Phe Leu
          20          25          30
Gly Ile Tyr Val Val Thr Leu Met Gly Asn Ile Ser Ile Ile Val Leu
          35          40          45
Ile Arg Arg Ser His His Leu His Thr Pro Met Tyr Ile Phe Leu Cys
          50          55          60

```

His Leu Ala Phe Val Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro Val  
 65 70 75 80  
 Met Leu Met Ser Phe Leu Arg Lys Glu Thr Ser Leu Pro Val Ala Gly  
 85 90 95  
 Cys Val Ala Gln Leu Cys Ser Val Val Thr Phe Gly Thr Ala Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu Leu Tyr Ser Thr Cys Met Ser Pro Gly Val Cys Ile Ile Leu  
 130 135 140  
 Val Gly Met Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Thr Phe Ile  
 145 150 155 160  
 Gly Cys Leu Leu Arg Leu Ser Phe Cys Gly Pro Asn Lys Val Asn His  
 165 170 175  
 Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ala Cys Ser His Asp  
 180 185 190  
 Phe Thr Phe Glu Ile Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile Val  
 195 200 205  
 Ala Thr Val Cys Val Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr  
 210 215 220  
 Ile Leu Lys Met His Ser Thr Lys Gly Arg His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Thr  
 245 250 255  
 Phe Ile Tyr Val Met Pro Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys  
 260 265 270  
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu  
 290 295 300  
 Leu Arg Ile Lys Ile Phe Ser  
 305 310

&lt;210&gt; 1226

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38gl43 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1226

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu  
 1 5 10 15  
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu  
 20 25 30  
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile  
 35 40 45  
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu  
 50 55 60  
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr  
 65 70 75 80  
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly  
 85 90 95  
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser  
 100 105 110  
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile  
 130 135 140  
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile

```

145          150          155          160
Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
          180          185          190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
          195          200          205
Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
          210          215          220
Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
          245          250          255
Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
          260          265          270
His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
          275          280          285
Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
          290          295          300
Arg Val Leu Arg Val Phe Thr Gln Lys Asp
305          310

```

&lt;210&gt; 1227

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g144 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1227

```

Met Thr Lys Gly Asn Arg Thr Thr Val Thr Glu Phe Val Leu Met Gly
 1          5          10          15
Phe Thr Asp Arg Pro Glu Leu Gln Leu Pro Leu Phe Val Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Leu Leu
          35          40          45
Ile Arg Ala Asp Ser Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
          50          55          60
His Leu Ala Phe Ile Asp Leu Cys Tyr Ser Ser Ile Gly Pro Lys
65          70          75          80
Met Leu Gln Asn Val Leu Val Lys Lys Lys Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Phe Ala Gln Leu Tyr Phe Ser Gly Ala Phe Ala Thr Thr Glu Xaa
          100          105          110
Phe Leu Leu Ala Thr Met Pro Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Ile Tyr Thr Ala Ile Met Thr Gln Arg Val Cys Arg Glu Leu
          130          135          140
Val Ile Gly Val Tyr Thr Tyr Gly Phe Arg Asn Ser Val Ile Gln Thr
145          150          155          160
Ala Leu Thr Phe Gln Leu Ser Phe Cys Asn Ser Asp Val Ile His His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
          180          185          190
His Asn Lys Glu Lys Gln Leu Met Ile Phe Ser Ala Val Asn Leu Thr
          195          200          205

```

Gly Ser Leu Leu Thr Ile Phe Ile Ser Tyr Ile Cys Ile Leu Phe Ser  
 210 215 220  
 Ile Ile Lys Ile Gln Ser Ser Glu Gly Lys Cys Arg Ala Phe Ser Thr  
 225 230 235 240  
 Arg Ala Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Thr Leu Phe  
 245 250 255  
 Phe Met Tyr Leu Gln Gln Pro Lys Ala Gly Asn Ser Trp Lys Pro Asn  
 260 265 270  
 Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Arg Leu Arg Asn Thr Glu Val Lys Asp Ala Leu Lys Lys  
 290 295 300  
 Met Leu Glu Gly Lys Glu Leu Xaa Xaa Val Ser  
 305 310 315

&lt;210&gt; 1228

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g145 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1228

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe  
 1 5 10 15  
 Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser  
 20 25 30  
 Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr  
 35 40 45  
 Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr  
 50 55 60  
 Tyr Leu Leu Ser Leu Leu Ser Lys Leu Asp Ile Val Leu Cys Leu Thr  
 65 70 75 80  
 Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile  
 85 90 95  
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu  
 100 105 110  
 Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe  
 130 135 140  
 Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr  
 145 150 155 160  
 Leu Ala Ile Pro Ile Leu Ser Ala Gln Leu Leu Gly Thr Met Phe  
 165 170 175  
 Leu Lys Pro Phe Cys Gly Lys Cys Phe Val His Asn Phe Cys Gly Asp  
 180 185 190  
 Ala Pro Xaa Xaa Pro Tyr Thr Phe Leu Lys  
 195 200

&lt;210&gt; 1229

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g146 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1229

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
          20           25           30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
          35           40           45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65           70           75           80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
          85           90           95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
          100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Ser Lys Leu Ala Cys Ile Asp Thr
          180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser
          195          200

```

## &lt;210&gt; 1230

## &lt;211&gt; 304

## &lt;212&gt; PRT

## &lt;213&gt; Unknown (H38g147 protein)

## &lt;220&gt;

## &lt;223&gt; Synthetic construct

## &lt;400&gt; 1230

```

Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
          20           25           30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
          35           40           45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
          50           55           60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
65           70           75           80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
          85           90           95
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
          100          105          110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
          115          120          125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
130          135          140
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
145          150          155          160
Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175

```

```

Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
      180      185      190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
      195      200      205
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
      210      215      220
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
      245      250      255
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
      260      265      270
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
      275      280      285
Ala Leu Asn Pro Leu Val Tyr Arg Val Lys Thr Gln Lys Ile His Gln
      290      295      300

```

<210> 1231  
 <211> 110  
 <212> PRT  
 <213> Unknown (H38g148 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(110)  
 <223> Xaa = Any Amino Acid

```

<400> 1231
Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
  1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
      20      25      30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
      35      40      45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
      50      55      60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
      65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
      85      90      95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
      100      105      110

```

<210> 1232  
 <211> 327  
 <212> PRT  
 <213> Unknown (H38g149 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(327)  
 <223> Xaa = Any Amino Acid

```

<400> 1232
Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
  1      5      10      15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe

```

```

      20      25      30
Cys Phe Met Phe Phe Leu Ser Leu Thr Gly Asn Gly Val Leu Leu Phe
      35      40      45
Leu Ile Arg Thr Glu Cys Ser Leu Arg Gln Pro Met Phe Leu Phe Leu
      50      55      60
Ala Met Leu Ser Phe Val Asp Leu Val Leu Ser Leu Ser Thr Leu Pro
      65      70      75      80
Lys Met Leu Ala Ile Phe Trp Phe Gly Ala Thr Ala Ile Ser Ser His
      85      90      95
Ser Cys Leu Ser Gln Met Phe Phe Ile His Ala Phe Ser Ala Met Glu
      100      105      110
Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Ser Val Ala Ile Cys
      115      120      125
Asn Pro Leu Arg Tyr Ala Thr Ile Leu Pro Pro Val Val Val Ala Lys
      130      135      140
Ile Gly Gly Leu Val Val Leu Xaa Gly Val Gly Leu Thr Ile Ser Phe
      145      150      155      160
Pro Ser Leu Ala His Arg Leu His Tyr His Gly Ser His Met Ile Ala
      165      170      175
Tyr Thr Phe Cys Glu His Met Ala Val Val Lys Leu Ala Cys Glu Ala
      180      185      190
Thr Thr Val Asp Asn Leu Tyr Ala Phe Val Val Ala Ile Phe Leu Gly
      195      200      205
Gly Gly Asp Val Val Cys Ile Ala Tyr Ser Tyr Gly Leu Ile Val Arg
      210      215      220
Thr Val Met His Phe Pro Ser Pro Glu Glu Arg Ala Lys Ala Gly Ser
      225      230      235      240
Thr Cys Thr Ala His Val Cys Val Ile Leu Phe Phe Tyr Gly Leu Gly
      245      250      255
Phe Leu Ser Val Val Met Gln Arg Phe Gly Ala Pro Thr Ala Ser Thr
      260      265      270
Ala Lys Val Ile Leu Ala Asn Leu Tyr Leu Leu Phe Pro Pro Ala Leu
      275      280      285
Asp Pro Ile Val Tyr Gly Met Glu Thr Lys Gln Ile Xaa Glu Arg Leu
      290      295      300
Leu Met Ile Leu Ser Pro Lys Gln Ile Glu Leu Thr Xaa Val Xaa Leu
      305      310      315      320
Ser Pro Ala Gly Leu Gln Gly
      325

```

&lt;210&gt; 1233

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g150 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(241)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1233

```

Leu Arg Gln Leu His Asn Leu Phe Leu Pro Val Gly Phe Phe Leu Ser
  1      5      10      15
Ser Tyr Ser Phe Xaa Val Ile Trp His Asn Leu Asn Ser Val Thr Lys
      20      25      30
Phe Ser Ser Lys Thr Asp Glu Ser Lys Leu Lys Ser Xaa Cys Lys Val
      35      40      45
Lys Ser Leu Phe Phe Thr Tyr Ala Gly Cys Cys Glu Lys Leu Leu Leu
      50      55      60

```



Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu  
65 70 75 80  
His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val  
85 90 95  
Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys  
100 105 110  
Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu  
115 120 125  
Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro  
130 135 140  
Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro  
145 150 155 160  
His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser  
165 170 175  
Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly  
180 185 190  
Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val  
195 200 205  
Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val  
210 215 220  
Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly  
225 230 235 240  
Pro

&lt;210&gt; 1234

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g151 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1234

Met Ala Ser Pro Asn Asn Asp Ser Thr Ala Pro Val Ser Glu Phe Leu  
1 5 10 15  
Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Trp Leu Ser Leu  
20 25 30  
Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala Asn Thr Thr Leu  
35 40 45  
Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln Pro Leu Tyr Tyr  
50 55 60  
Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val  
65 70 75 80  
Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Ser  
85 90 95  
Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Thr  
100 105 110  
Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val Ala  
115 120 125  
Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp Gln Phe Val  
130 135 140  
Ala Arg Ala Val Val Phe Val Ile Ala Arg Asn Ala Phe Val Ser Leu  
145 150 155 160  
Pro Val Pro Met Leu Ser Ala Arg Leu Arg Tyr Cys Ala Gly Asn Ile  
165 170 175  
Ile Lys Asn Cys Ile Cys Ser Asn Leu Ser Val Ser Lys Leu Ser Cys  
180 185 190  
Asp Asp Ile Thr Phe Asn Gln Leu Tyr Gln Phe Val Ala Gly Trp Thr  
195 200 205  
Leu Leu Gly Ser Asp Leu Ile Leu Ile Val Ile Ser Tyr Ser Phe Ile

```

      210              215              220
Leu Lys Val Val Leu Arg Ile Lys Ala Glu Gly Ala Val Ala Lys Ala
225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Thr
      245              250              255
Val Leu Leu Val Leu Val Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro
      260              265              270
Pro Asp Val Pro Ile Leu Leu Asn Ile Leu His His Leu Ile Pro Pro
      275              280              285
Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln
      290              295              300
Gly Ile Gln Asn Leu Leu Lys Arg Leu
305              310

```

<210> 1235  
 <211> 135  
 <212> PRT  
 <213> Unknown (H38g152 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(135)  
 <223> Xaa = Any Amino Acid

```

<400> 1235
Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1              5              10              15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
      20              25              30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
      35              40              45
Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
      50              55              60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
      65              70              75              80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
      85              90              95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
      100             105             110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
      115             120             125
Arg Arg Leu Xaa Lys Ile Lys
      130             135

```

<210> 1236  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g153 protein)

<220>  
 <223> Synthetic construct

```

<400> 1236
Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1              5              10              15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
      20              25              30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
      35              40              45

```

```

Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
 50          55          60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
 65          70          75          80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
      85          90          95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
      100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
      115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
      130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
      145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
      165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
      180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
      195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
      210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
      225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
      245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
      260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
      275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
      290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
      305          310          315

```

&lt;210&gt; 1237

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g154 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1237

```

Met Phe Leu Pro Asn Asn Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20          25          30
Phe Cys Ala Val Tyr Ile Ile Ala Leu Ile Gly Arg Phe Thr Ile Leu
      35          40          45
Leu Val Ile Lys Thr Asp Ser Ser Leu Tyr Gln Pro Met Phe Tyr Phe
      50          55          60
Leu Ala Met Leu Ala Thr Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
      65          70          75          80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Arg Glu Ile Ile Cys
      85          90          95
Asp Ala Cys Leu Ile Gln Met Phe Phe Ile His Asn Phe Thr Gly Met

```

```

      100      105      110
Glu Ser Ala Ala Leu Val Gly Met Ala Tyr Asp His Phe Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Ser Ile Ile Leu Thr Lys Lys Ala Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Leu Val Arg Ser Phe Met Ser Val Ile Pro
      145      150      155      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly Asp His Val Ile
      165      170      175
Pro His Thr Asn Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ser
      180      185      190
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Gly Ala Ile Ser Ile Leu
      195      200      205
Val Phe Asp Ile Ile Ala Ile Ala Leu Ser Tyr Val Gln Ile Leu His
      210      215      220
Ala Val Phe His Leu Pro Ser Cys Lys Ala Xaa Leu Lys Ser Leu Ser
      225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Val Thr His Arg Phe Gly Gln Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Val
      290      295      300
Lys Asn Ile Phe Leu Gln Lys Xaa Glu Ile Glu Lys Lys Ser His Leu
      305      310      315      320
Ile His Ile Arg Arg
      325

```

&lt;210&gt; 1238

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g155 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1238

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1      5      10      15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
      65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95
Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
      100      105      110
Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
      115      120      125
His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
      130      135      140

```

Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser  
 180 185 190  
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr  
 195 200 205  
 Met Leu Asp Leu Val Leu Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg  
 210 215 220  
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Thr  
 245 250 255  
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met  
 260 265 270  
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu  
 275 280 285  
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val  
 290 295 300  
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu  
 305 310 315

&lt;210&gt; 1239

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g156 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1239

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu  
 1 5 10 15  
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu  
 65 70 75 80  
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Ile Ser Ser  
 85 90 95  
 Asn Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile  
 115 120 125  
 His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala  
 130 135 140  
 Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro  
 145 150 155 160  
 Phe Pro Phe Thr Leu Arg Asn Leu Arg Tyr Cys Lys Lys Asn Gln Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser  
 180 185 190  
 Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu  
 195 200 205  
 Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys  
 210 215 220  
 Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Gln Leu Lys Ala Leu Asn

```

225          230          235          240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
          245          250          255
Ile Asn Leu Ala Val Val His Arg Phe Ala Arg His Val Ser Pro Leu
          260          265          270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Thr
          275          280          285
Asn Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
          290          295          300
Val Ala Lys Leu Cys Gln Arg Lys Ile
305          310

```

&lt;210&gt; 1240

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g157 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1240

```

Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu Ser
50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile Thr
65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu Leu
          100          105          110
Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu His
          115          120          125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
130          135          140
Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe Ile
145          150          155          160
Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met Trp
          165          170          175
Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr Leu
          180          185          190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
          195          200          205
Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg Thr
210          215          220
His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser His
225          230          235          240
Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
          245          250          255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
          260          265          270
Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
          275          280          285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
          290          295          300
Ser Ser Val Lys
305

```

<210> 1241  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g158 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(321)  
 <223> Xaa = Any Amino Acid

<400> 1241  
 Met Ala Tyr His Gly Asn Arg Gly Thr Phe His Pro Ala Thr Phe Phe  
 1 5 10 15  
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Val His Met Xaa Ile Ser Leu  
 20 25 30  
 His Phe Cys Ser Val Tyr Leu Leu Ala Leu Leu Gly Asn Ala Thr Ile  
 35 40 45  
 Leu Leu Val Ile Lys Ala Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr  
 50 55 60  
 Phe Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser  
 65 70 75 80  
 Val Pro Arg Thr Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn  
 85 90 95  
 Phe Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly  
 100 105 110  
 Met Glu Ala Glu Val Leu Val Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys Asn Pro Leu His Tyr Thr Asn Ile Leu Thr Ser Arg Val Leu  
 130 135 140  
 Val Gly Ile Thr Met Cys Ile Val Ile Arg Pro Val Leu Phe Thr Leu  
 145 150 155 160  
 Pro Ile Ile Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Gly His Ile  
 165 170 175  
 Ile Ala His Ser Tyr Tyr Glu His Met Gly Ile Ala Lys Leu Ser Cys  
 180 185 190  
 Gly Asn Ile Arg Val Asn Ala Ile Tyr Gly Leu Phe Val Val Ser Phe  
 195 200 205  
 Tyr Leu Leu Asn Leu Val Leu Ile Val Ile Ser Tyr Val Tyr Ile Leu  
 210 215 220  
 Cys Ala Val Phe Cys Leu Ala Ser His Asp Ala Arg Leu Lys Ala Leu  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Val Gly Val Ile Cys Val Phe Tyr Ile Pro  
 245 250 255  
 Ser Asp Phe Ser Phe Leu Thr His Xaa Phe Gly His Asn Ile Pro His  
 260 265 270  
 Tyr Met His Ile Leu Val Ala Thr Leu Tyr Leu Val Ile Pro Pro Ser  
 275 280 285  
 Leu Asn Pro Ile Ile Cys Gly Val Arg Thr Lys Trp Lys Arg Glu Arg  
 290 295 300  
 Val Leu Tyr Val Leu Thr Lys Lys Xaa Asp Ser Asp His Val Leu Leu  
 305 310 315 320  
 Leu

<210> 1242  
 <211> 162  
 <212> PRT  
 <213> Unknown (H38g159 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(162)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1242

```

Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr Asp Pro
 1           5           10           15
Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Leu Leu Lys Leu
      20           25           30
Leu Cys Met Gly Thr Thr Asn Thr Leu Gly Phe Phe Val Ala Ala Asn
      35           40           45
Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val Ser Xaa
 50           55           60
Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu Arg Cys
65           70           75           80
Lys Ala Leu Ser Thr Cys Ile Ser His Thr Thr Val Val Ile Leu Phe
      85           90           95
Phe Gly Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu Leu Pro
      100          105          110
Ile Asn Lys Ala Val Ala Val Phe Tyr Thr Met Ile Asn Pro Met Leu
      115          120          125
Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Ala Leu
      130          135          140
Arg Lys Leu Trp Val Lys Arg Xaa Thr Glu Glu Arg Asn Asn Pro Asn
145          150          155          160
Ile Arg

```

&lt;210&gt; 1243

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g160 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1243

```

Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro
      20           25           30
Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu
      35           40           45
Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe
 50           55           60
Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Ala Thr Ser Val
65           70           75           80
Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr
      85           90           95
Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met
      100          105          110
Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Leu Val Leu Val
      130          135          140
Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro
145          150          155          160

```



```

Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile
      165      170      175
Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly
      180      185      190
Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe
      195      200      205
Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg
      210      215      220
Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser
      225      230      235
Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser
      245      250      255
Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr
      260      265      270
Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu
      275      280      285
Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val
      290      295      300
Leu Tyr Val Phe Thr Lys Lys
      305      310

```

&lt;210&gt; 1244

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g161 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1244

```

Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
  1      5      10      15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
      20      25      30
Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile Thr
      35      40      45
Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr Leu
      50      55      60
Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
      65      70      75      80
Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys Met
      85      90      95
Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile Leu
      100      105      110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met Gly
      130      135      140
Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
      145      150      155      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
      165      170      175
Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His Met
      180      185      190
Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
      195      200      205
Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu Arg

```

210	215	220
Thr His Ser Leu Glu	Ala Arg His Lys Ala Leu Ser Thr Cys Val Ser	
225	230	235
His Ile Thr Val Val	Ile Leu Phe Phe Val Pro Cys Ile Phe Val Tyr	240
	245	250
Met Arg Pro Ala Ala	Thr Leu Pro Ile Asp Lys Ala Val Ala Ile Phe	255
	260	265
Tyr Thr Met Ile Thr	Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg	270
	275	280
Asn Ala Gln Met Lys	Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Asp	285
	290	295
Ile Ser Gly Asn Lys	Xaa Met Xaa Leu Glu Leu	300
305	310	315

&lt;210&gt; 1245

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g162 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1245

Ser Asn Thr Gly Met	Ser Ile Leu Asn Thr	Ser Glu Met Glu Ile Ser
1	5	10
Ile Phe Tyr Leu Val	Gly Ile Pro Gly Leu Glu His Ala Asn Ile Trp	15
	20	25
Ile Ser Ile Pro Ile	Cys Leu Met Tyr Thr Val Ala Ile Leu Gly Asn	30
	35	40
Cys Thr Ile Leu Phe	Phe Ile Lys Thr Glu Pro Ser Leu His Glu Pro	45
	50	55
Met Tyr Tyr Phe Leu	Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser	60
	65	70
Leu Ser Ser Leu Pro	Thr Met Leu Arg Ile Phe Leu Phe Asn Ala Pro	75
	85	90
Gly Ile Ser Pro Asp	Ala Cys Ile Ala Gln Glu Phe Phe Ile His Gly	95
	100	105
Phe Ser Ala Met Glu	Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg	110
	115	120
Phe Ile Ala Ile Cys	Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser	125
	130	135
Ala Arg Val Ile Gln	Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu	140
	145	150
Leu Ile Leu Pro Phe	Pro Phe Thr Leu Lys His Leu Lys Tyr Cys Lys	155
	165	170
Lys Asn Leu Leu Ser	Gln Ser Tyr Cys Leu His Gln Asp Val Met Lys	175
	180	185
Leu Ala Cys Thr Asp	Asn Lys Val Asn Ile Ile Tyr Gly Leu Phe Val	190
	195	200
Ala Leu Thr Gly Ile	Leu Asp Leu Thr Phe Ile Phe Met Ser Tyr Met	205
	210	215
Leu Ile Leu Lys Ala	Val Leu Ser Ile Ala Ser Xaa Lys Lys Arg Leu	220
	225	230
Lys Val Leu Asn Thr	Cys Val Ser His Ile Cys Ala Val Leu Ile Phe	235
	245	250
Tyr Val Pro Ile Ile	Ser Leu Ala Val Ile Tyr Arg Phe Ala Lys His	255
	260	265
		270

Ser Phe Pro Ile Thr Arg Ile Leu Ile Ala Asp Ala Phe Leu Leu Val  
 275 280 285  
 Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val Lys Ser Gln Gln Ile  
 290 295 300  
 Arg Asn Leu Val Leu Glu Lys Leu Cys Gln Lys Gln Ser Xaa Ser Gly  
 305 310 315 320  
 Cys Leu

<210> 1246

<211> 319

<212> PRT

<213> Unknown (H38g163 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1246

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu  
 1 5 10 15  
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu  
 20 25 30  
 Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile  
 35 40 45  
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys  
 100 105 110  
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu  
 145 150 155 160  
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

&lt;210&gt; 1247

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g164 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1247

Met	Arg	Leu	Ile	Xaa	Asp	Glu	Glu	Met	Ser	Arg	Arg	Asn	Tyr	Thr	Glu
1				5					10					15	
Leu	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Thr	Ser	Arg	Pro	Glu	Leu	Arg
			20					25					30		
Val	Ala	Phe	Leu	Ala	Leu	Phe	Leu	Phe	Val	Tyr	Ile	Ala	Thr	Val	Val
			35					40					45		
Gly	Asn	Leu	Gly	Met	Ile	Ile	Leu	Ile	Lys	Val	Asp	Ser	Arg	Leu	His
			50			55					60				
Thr	Pro	Met	Xaa	Phe	Phe	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Asp	Leu	Cys
65					70					75				80	
Phe	Ser	Thr	Asn	Phe	Thr	Pro	Lys	Met	Leu	Glu	Asn	Phe	Leu	Ser	Glu
			85						90					95	
Lys	Lys	Thr	Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Met	Gln	Cys	Tyr	Val	Val
			100					105					110		
Ile	Ala	Val	Val	Leu	Ala	Glu	His	Cys	Met	Leu	Ala	Val	Met	Ala	Tyr
			115				120					125			
Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Ser	Ser	Lys	Met
			130			135					140				
Ser	Gln	Gly	Val	Cys	Val	His	Leu	Val	Ile	Val	Pro	Tyr	Val	Tyr	Gly
145					150					155					160
Phe	Leu	Leu	Ser	Val	Met	Glu	Thr	Leu	Arg	Thr	Tyr	Asn	Leu	Ser	Phe
				165					170					175	
Cys	Gly	Thr	Asn	Glu	Ile	Asn	His	Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu
			180				185					190			
Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr	Ser	Lys	Glu	Leu	Ser	Met	Tyr
			195				200					205			
Ile	Val	Ala	Gly	Tyr	Ser	Asn	Val	Gln	Ser	Leu	Leu	Ile	Ile	Leu	Thr
			210			215					220				
Ser	Tyr	Met	Phe	Ile	Leu	Val	Ala	Ile	Leu	Arg	Ser	His	Ser	Ala	Glu
225					230					235					240
Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val
				245					250					255	
Thr	Ile	Phe	Tyr	Gly	Thr	Leu	Phe	Cys	Met	His	Leu	Arg	Arg	Pro	Thr
			260				265					270			
Asp	Glu	Ser	Val	Glu	Gln	Gly	Lys	Met	Val	Ala	Val	Phe	Tyr	Thr	Thr
			275				280					285			
Val	Ile	Leu	Met	Leu	Asn	Ser	Met	Ile	Tyr	Gly	Leu	Arg	Asn	Lys	Asp
			290			295					300				
Val	Lys	Glu	Ala	Leu	Lys	Lys	Ala	Ile	Gly	Lys	Gln	Thr	Leu	Gly	Lys
305					310					315					320

&lt;210&gt; 1248

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g165 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1248

```

Arg Arg Met Gly Asn His Thr Ala Val Ser Leu Phe Leu Leu Trp Gly
 1           5           10           15
Phe Ser Ser Phe Ser Asp Leu Gln Ser Leu Leu Phe Val Val Ile Leu
 20           25           30
Leu Leu His Val Thr Ile Leu Ala Ala Asn Val Ser Ile Met Gly Ala
 35           40           45
Ile Lys Leu Ser His Asn Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50           55           60
Gly Leu Ser Phe Ser Glu Thr Cys Thr Thr Val Val Val Ile Pro Arg
 65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu
 85           90           95
Cys Ala Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys
100           105           110
Phe Ile Met Ala Ala Met Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn
115           120           125
Pro Leu Gln Tyr His Thr Leu Met Thr Arg Lys Ile Cys Leu Gln Met
130           135           140
Met Met Ala Ser Trp Met Val Gly Phe Leu Phe Ser Leu Cys Ile Ile
145           150           155           160
Val Thr Val Phe Asn Leu Ser Leu Cys Asp Leu Asn Thr Ile Gln His
165           170           175
Tyr Phe Cys Asp Ile Ser Pro Val Val Ser Leu Ala Cys Asn Tyr Thr
180           185           190
Phe Tyr His Glu Met Ala Ile Phe Val Leu Ser Ala Phe Val Leu Val
195           200           205
Gly Ser Cys Ile Leu Ile Met Ile Ser Tyr Val Phe Ile Val Phe Ile
210           215           220
Val Ile Lys Met Pro Ser Ala Lys Gly Arg Ser Lys Ala Phe Ser Thr
225           230           235           240
Cys Ser Ser His Leu Thr Val Val Ser Ile His Tyr Gly Phe Ala Cys
245           250           255
Phe Val Tyr Leu Arg Pro Lys Asn Ser Asn Ser Phe Asp Glu Asp Met
260           265           270
Leu Thr Ala Met Ile Tyr Thr Ile Leu Met Pro Leu Leu Asn Pro Ile
275           280           285
Val Tyr Ser Leu Arg Asn Lys Glu Met Gln Ile Ala Leu Arg Lys Thr
290           295           300
Leu Gly Ser Val Phe Gly Val Phe Pro Gln Lys Thr
305           310           315

```

&lt;210&gt; 1249

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g166 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1249

```

Met Ser Ala Tyr Asn Asn Thr Asn Ala Arg Pro Ser Thr Phe Ile Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro
 20           25           30
Phe Cys Val Val Tyr Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu
 35           40           45
Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe

```

50	55	60
Leu Cys Met Leu Ala Val Val Asp Leu Val Val Cys Ser Thr Ala Val		
65	70	75
Pro Lys Leu Leu Ser Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe		
	85	90
Glu Thr Cys Leu Thr Gln Met Phe Leu Ile His Ser Cys Ser Thr Met		
	100	105
Glu Ser Gly Phe Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile		
	115	120
Cys Asn Pro Leu Arg His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly		
	130	135
Arg Val Gly Leu Ala Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro		
145	150	155
His Ser Phe Leu Leu Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile		
	165	170
Ser His Thr Tyr Cys Glu Phe Met Ala Leu Ile Arg Ile Ala Cys Ala		
	180	185
Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile Val Ala Phe Leu Thr		
	195	200
Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser Tyr Val Leu Ile Leu		
	210	215
His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala Arg Leu Lys Ser Leu		
225	230	235
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Val Ser Tyr Thr Pro		
	245	250
Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Ala Pro		
	260	265
His Phe His Ile Phe Val Ala Asn Ile Tyr Leu Leu Val Pro Pro Met		
	275	280
Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Arg Ile Trp Asp Arg		
	290	295
Phe Leu Lys Val Phe Ser Phe Ser Lys Pro Leu Ser Lys Ser Phe		
305	310	315

&lt;210&gt; 1250

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g167 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1250

Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr		
1	5	10
Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val		
	20	25
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys		
	35	40
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu		
	50	55
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu		
65	70	75
Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu		
	85	90
Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile		
	100	105
Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu		
	115	120
Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr		
	130	135
		140

Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp  
 145 150 155 160  
 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr  
 165 170 175  
 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val  
 180 185 190  
 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser  
 195 200 205  
 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu  
 210 215 220  
 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met  
 245 250 255  
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val  
 260 265 270  
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser  
 290 295 300  
 Arg Ser Cys  
 305

&lt;210&gt; 1251

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g168 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1251

Met Thr Met Thr Thr Glu Asn Pro Asn Gln Thr Val Val Ser His Phe  
 1 5 10 15  
 Phe Leu Glu Gly Leu Arg Tyr Thr Ala Lys His Ser Ser Leu Phe Phe  
 20 25 30  
 Leu Leu Phe Leu Leu Ile Tyr Ser Ile Thr Val Ala Gly Asn Leu Leu  
 35 40 45  
 Ile Leu Leu Thr Val Gly Ser Asp Ser His Leu Ser Leu Pro Met Tyr  
 50 55 60  
 His Phe Leu Gly His Leu Ser Phe Leu Asp Ala Trp Leu Ser Thr Val  
 65 70 75 80  
 Thr Val Pro Lys Val Met Ala Gly Leu Leu Thr Leu Asp Gly Lys Val  
 85 90 95  
 Ile Ser Phe Glu Gly Cys Ala Val Gln Leu Tyr Cys Phe His Phe Leu  
 100 105 110  
 Ala Ser Thr Glu Cys Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Ala Met Asn Arg Arg  
 130 135 140  
 Met Cys Ala Glu Met Ala Gly Ile Thr Trp Ala Ile Gly Ala Thr His  
 145 150 155 160  
 Ala Ala Ile His Thr Ser Leu Thr Phe Arg Leu Leu Tyr Cys Gly Pro  
 165 170 175  
 Cys His Ile Ala Tyr Phe Phe Cys Asp Ile Pro Pro Val Leu Lys Leu  
 180 185 190  
 Ala Cys Thr Asp Thr Thr Ile Asn Glu Leu Val Met Leu Ala Ser Ile  
 195 200 205  
 Gly Ile Val Ala Ala Gly Cys Leu Ile Leu Ile Val Ile Ser Tyr Ile  
 210 215 220  
 Phe Ile Val Ala Ala Val Leu Arg Ile Arg Thr Ala Gln Gly Arg Gln

```

225          230          235          240
Arg Ala Phe Ser Pro Cys Thr Ala Gln Leu Thr Gly Val Leu Leu Tyr
          245          250          255
Tyr Val Pro Pro Val Cys Ile Tyr Leu Gln Pro Arg Ser Ser Glu Ala
          260          265          270
Gly Ala Gly Ala Pro Ala Val Phe Tyr Thr Ile Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys His Ala Leu
          290          295          300
Gln Arg Leu Leu Cys Ser Ser Phe Arg Glu Ser Thr Ala Gly Ser Pro
305          310          315          320
Pro Pro

```

&lt;210&gt; 1252

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g169 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1252

```

Lys Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val
          20          25          30
Val Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile
          35          40          45
Lys Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
65          70          75          80
Leu Glu Asn Leu Leu Ser Asp Lys Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile
          100          105          110
Phe Ile Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn
          115          120          125
Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu
          130          135          140
Ile Thr Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr
145          150          155          160
Leu Trp Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr
          180          185          190
Phe Val Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr
          195          200          205
Tyr Ser Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala
          210          215          220
Ile Leu Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile
          245          250          255
Phe Met Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys
          260          265          270

```



Met Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met  
           275                          280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val  
           290                          295                  300  
 Ile Ser Arg Ser Cys Xaa Thr Lys Xaa Asn Gln Val Xaa Ile Asn Phe  
 305                          310                          315                  320  
 Val Phe

&lt;210&gt; 1253

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g170 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1253

Met Ser Asn Ala Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro  
   1                          5                          10                          15  
 His Ala Pro Gly Leu Asp Ala Leu Leu Phe Gly Ile Phe Leu Val Val  
                           20                          25                          30  
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg  
           35                          40                          45  
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu  
           50                          55                          60  
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu  
 65                          70                          75                          80  
 Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys  
                           85                          90                          95  
 Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe  
                           100                          105                          110  
 Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro  
           115                          120                          125  
 Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala  
           130                          135                          140  
 Thr Gly Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile  
 145                          150                          155                          160  
 Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr  
                           165                          170                          175  
 Phe Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser  
                           180                          185                          190  
 Ala Asn Val Met Val Ile Phe Val Asp Ile Gly Ile Val Ala Ser Gly  
           195                          200                          205  
 Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile  
           210                          215                          220  
 Leu Arg Ile Arg Thr Ser Asp Gly Arg Arg Arg Ala Phe Gln Thr Cys  
 225                          230                          235                          240  
 Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Val  
                           245                          250                          255  
 Ile Tyr Leu Arg Pro Gly Ser Met Asp Ala Met Asp Gly Val Val Ala  
           260                          265                          270  
 Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr  
           275                          280                          285  
 Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys  
           290                          295                          300  
 Val Ala His Pro Gln Arg Lys  
 305                          310

&lt;210&gt; 1254

&lt;211&gt; 320

<212> PRT  
 <213> Unknown (H38g171 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1254  
 Gly Val Gly Leu Xaa Lys Leu Xaa Trp Gln Ile Ile Phe Ser Gly Asp  
 1 5 10 15  
 Ser Phe Ser Thr Trp Glu Met Phe Ser Leu Ser Ile Leu Gln Leu Pro  
 20 25 30  
 Xaa Met Tyr Thr Val Ala Leu Ser Gly Thr Ser Ile Leu Ile Phe Leu  
 35 40 45  
 Ile Xaa Thr Asp Phe Xaa Val His Thr Ser Leu Tyr Ser Phe Xaa Val  
 50 55 60  
 Leu Ile Asp Ile Ala Ile Ser Val Val Lys Ile Gly Ile Glu Val Phe  
 65 70 75 80  
 Ser Gly Lys Ile Asn Phe Ser His Thr Gly Cys Gly Thr Gln Ile Phe  
 85 90 95  
 Phe Phe Leu Thr Ala Gly Ile Phe Lys Tyr Val Leu Leu Thr Tyr Met  
 100 105 110  
 Ala Tyr Asp His Asn Val Ala Ile Cys Asp Leu Arg Xaa Pro Thr Phe  
 115 120 125  
 Met Ser Asp Gln Val Phe Xaa Gln Trp Ala Val Glu Ser Trp Ile Gly  
 130 135 140  
 Gly Lys Leu Ser Ser Leu Ala His Thr Ile Tyr Ile Phe His Leu Phe  
 145 150 155 160  
 Ser Tyr Lys Ala Lys Glu Ile Ser His Leu Trp Pro Lys Leu Phe Xaa  
 165 170 175  
 Ser Ser Ser Val Gly Ile Pro Tyr Ile Gln Asn Asp Val Phe Phe Thr  
 180 185 190  
 Ile Ile Thr Phe Leu Phe Thr Leu Leu Pro Leu Thr Leu Thr Leu Ser  
 195 200 205  
 Ser Lys Leu Ile Val Phe Thr Ile Leu His Met Asn Ser Ser Asn Gly  
 210 215 220  
 Gly Ala Lys Ser Trp His Thr Tyr Cys Phe His Leu Ser Val Leu Ile  
 225 230 235 240  
 Pro Cys Cys Gly Gln Ala Ile Phe Val Tyr Met Thr Ser Ser Ser Phe  
 245 250 255  
 Xaa Thr Val Asn Lys Tyr Gln Thr Met Ser Val Leu Thr Ala Xaa Leu  
 260 265 270  
 Tyr Pro Leu Leu Lys Pro Leu Ile Asp Ile Leu Lys Asn Ala Glu Val  
 275 280 285  
 Ala Gly Ala Trp Ser Lys Phe Leu Xaa Lys Lys Ala Leu Lys Ser Gln  
 290 295 300  
 His Leu Ile Thr Arg Ser Cys Glu Asn Lys Xaa Thr Thr Glu Gln Ser  
 305 310 315 320

<210> 1255  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g172 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1255

```

Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
 1              5              10              15
Glu Phe Ile Leu Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
      20              25              30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
      35              40              45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
      50              55              60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
65              70              75              80
Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
      85              90              95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
      100              105              110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
      115              120              125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
      130              135              140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
145              150              155              160
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
      165              170              175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
      180              185              190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
      195              200              205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
      210              215              220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
225              230              235              240
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
      245              250              255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
      260              265              270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
      275              280              285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290              295              300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
305              310              315              320

```

&lt;210&gt; 1256

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g173 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(235)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1256

```

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1              5              10              15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro

```

```

      20      25      30
Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val Tyr Val Leu
  35      40      45
Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg Val Tyr Ser
  50      55      60
His Leu His Thr Pro Lys Tyr Tyr Phe Leu Thr Asn Leu Ser Phe Ile
  65      70      75      80
Asp Leu Trp Phe Phe Thr Val Met Val Pro Lys Met Pro Arg Thr Leu
      85      90      95
Leu Ser Leu Cys Gly Lys Ala Val Ser Phe His Ser Cys Met Thr Gln
      100      105      110
Leu Tyr Phe Phe Tyr Phe Leu Gly Ser Thr Glu Cys Leu Leu Tyr Thr
      115      120      125
Val Met Ser Tyr Asp Arg Tyr Arg Gly Asn Thr Gln His Phe Pro Gly
      130      135      140
Ser Glu Asn Leu Pro Thr Lys Xaa Ala Lys Cys Xaa Trp Pro Gly Gly
      145      150      155      160
His Thr Gly Leu Pro Leu Ile Ile Leu Ala Asp Leu Ser Gly Xaa Leu
      165      170      175
Arg Val Asp Ser Xaa Trp Ala Ile Gln Asn Xaa Xaa Tyr Asn Leu
      180      185      190
Val Ile Gln Val Lys Phe Ile Thr Cys Ile Gly Leu Ser Ile Lys His
      195      200      205
Tyr Ser Lys Gln Leu Ala Gln Leu Xaa Phe Phe His Arg Leu Ser Lys
      210      215      220
Thr Phe Leu Asn Ser Gln Leu Asp Phe Tyr Leu
      225      230      235

```

&lt;210&gt; 1257

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g174 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1257

```

Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
  1      5      10      15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Leu Val Tyr Leu Thr Thr Leu
      20      25      30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35      40      45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
      50      55      60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
      65      70      75      80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85      90      95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100      105      110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115      120      125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130      135      140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
      145      150      155      160

```

[illegible]

```
<210> 1258
<211> 157
<212> PRT
<213> Unknown (H38g175 protein)
```

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(157) .
<223> Xaa = Any Amino Acid
```

<400> 1258																
Ile	Cys	His	Asn	Arg	Lys	Val	Ile	Pro	Ala	Ser	Met	Xaa	Asn	Met	Cys	
1				5					10					15		
Xaa	Phe	Leu	Leu	Lys	Val	Ala	Xaa	Asp	Asn	Phe	Leu	His	Val	Leu	Phe	
		20						25					30			
Ile	Leu	Ala	Lys	Thr	Ala	Pro	Pro	Leu	Leu	Phe	Leu	Xaa	Glu	Ile	Pro	
		35					40					45				
Ser	Tyr	Phe	Ser	Ser	Pro	Ser	Xaa	Ile	Ile	Val	Leu	Xaa	Cys	Leu	Pro	
	50					55					60					
Xaa	Phe	Leu	Lys	Gln	Leu	Val	Ile	Leu	Phe	Val	Phe	Leu	Leu	Leu	Asn	
65				70						75					80	
Xaa	Ser	Tyr	Leu	Thr	Leu	Ile	Phe	Met	Leu	Leu	Thr	Met	Lys	Ile	Thr	
				85					90					95		
Ser	Ser	Phe	Lys	Ala	Ser	Thr	Val	Ile	Ser	Cys	Leu	Gln	Phe	Pro	Ser	
			100					105					110			
Lys	Ala	Thr	Cys	Met	His	Gly	Val	Phe	Ser	Ala	Val	Cys	Ala	Gln	Met	
		115					120					125				
Xaa	Pro	Tyr	Tyr	Asn	Gly	Xaa	Ile	Ile	Xaa	His	Pro	Glu	Ser	Ile	Thr	
	130					135					140					
Glu	Ser	Lys	Xaa	Leu	Thr	Cys	Val	Asn	Pro	Xaa	Phe	Asn				
145					150					155						

<210> 1259  
<211> 321  
<212> PRT  
<213> Unknown (H38g176 protein)

**<220>**

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1259

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Ile Leu Phe Leu Val Cys
      20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr
      35           40           45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
      50           55           60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
65           70           75           80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
      85           90           95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
      100          105          110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
      130          135          140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
145          150          155          160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
      165          170          175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
      180          185          190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
      195          200          205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
      210          215          220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
225          230          235          240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
      245          250          255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
      260          265          270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
      275          280          285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
      290          295          300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
305          310          315          320
Pro

```

<210> 1260

<211> 317

<212> PRT

<213> Unknown (H38g177 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

&lt;400&gt; 1260

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Ala Asn His Arg Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr
          20          25          30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile
          35          40          45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 50          55          60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met
65          70          75          80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg
          85          90          95
Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr
          100          105          110
Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
          130          135          140
Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
145          150          155          160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe
          165          170          175
Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
          180          185          190
Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr
          195          200          205
Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr
          210          215          220
Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe
          245          250          255
Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met
          260          265          270
Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu
          290          295          300
Phe Lys Arg Lys Leu Phe Ser Lys Xaa Thr Leu Leu Leu
305          310          315

```

&lt;210&gt; 1261

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g178 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1261

```

Thr Asp Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
 1          5          10          15
Leu Gln Pro Val Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
          20          25          30
Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp

```

```

      35      40      45
Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp
  50      55      60
Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp
  65      70      75      80
Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln
      85      90      95
Met Ser Phe Leu Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr
      100      105      110
Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr
      115      120      125
Pro Ile Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser
      130      135      140
Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu
  145      150      155      160
Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp
      165      170      175
Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn
      180      185      190
Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser
      195      200      205
Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
      210      215      220
Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His
  225      230      235      240
Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Leu Tyr Leu
      245      250      255
Thr Ser Ala Gly Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val
      260      265      270
Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu
      275      280      285
Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Arg Ser Arg Ala
      290      295      300
Val Glu Tyr Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
  305      310      315

```

&lt;210&gt; 1262

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g179 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1262

```

Met Arg Gly Phe Asn Lys Thr Thr Val Val Thr Gln Phe Ile Leu Val
  1      5      10      15
Gly Phe Ser Ser Leu Gly Glu Leu Gln Leu Leu Leu Phe Val Ile Phe
      20      25      30
Leu Leu Leu Tyr Leu Thr Ile Leu Val Ala Asn Val Thr Ile Met Ala
      35      40      45
Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
      50      55      60
Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
  65      70      75      80
Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
      85      90      95
Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
      100      105      110
Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
      115      120      125

```



His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu  
 130 135 140  
 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala  
 145 150 155 160  
 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn  
 165 170 175  
 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp  
 180 185 190  
 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile  
 195 200 205  
 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn  
 210 215 220  
 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser  
 245 250 255  
 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln  
 260 265 270  
 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu  
 275 280 285  
 Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys Arg Val  
 290 295 300  
 Leu Gly Met Pro Val Ala Thr Lys Met Ser  
 305 310

&lt;210&gt; 1263

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g180 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1263

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu  
 130 135 140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser

```

      210              215              220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
      245              250              255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
      260              265              270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
      290              295              300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu
305              310

```

<210> 1264  
 <211> 275  
 <212> PRT  
 <213> Unknown (H38g181 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(275)  
 <223> Xaa = Any Amino Acid

```

<400> 1264
Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
  1              5              10              15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20              25              30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35              40              45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
      50              55              60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
      65              70              75              80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85              90              95
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100              105              110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115              120              125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130              135              140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
      145              150              155              160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165              170              175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180              185              190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195              200              205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210              215              220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
      225              230              235              240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245              250              255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260              265              270

```

Gln Tyr Ser  
275

<210> 1265  
<211> 312  
<212> PRT  
<213> Unknown (H38g182 protein)

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(312)  
<223> Xaa = Any Amino Acid

<400> 1265  
Met Arg Arg Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu  
1 5 10 15  
Thr Asn His Gln Glu Leu Gln Ile Leu Leu Phe Met Leu Phe Leu Ala  
20 25 30  
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Ser Met Ile Ala Leu Ile  
35 40 45  
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His  
50 55 60  
Leu Ser Phe Leu Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met  
65 70 75 80  
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys  
85 90 95  
Leu Val Gln Cys Tyr Leu Tyr Ile Ile Leu Val His Val Glu Ile Tyr  
100 105 110  
Ile Leu Ala Val Met Ala Phe Asp Xaa Tyr Met Ala Ile Xaa Asn Pro  
115 120 125  
Leu Leu Tyr Gly Ser Lys Met Ser Lys Ser Val Cys Ser Phe Leu Ile  
130 135 140  
Thr Val Pro Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met  
145 150 155 160  
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Asn Glu Ile Asn His Phe  
165 170 175  
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr  
180 185 190  
Asn Lys Glu Leu Ser Met Phe Val Val Ala Gly Trp Asn Leu Ser Phe  
195 200 205  
Ser Leu Phe Ile Ile Phe Ile Ser Tyr Phe Tyr Ile Phe Pro Ala Ile  
210 215 220  
Leu Arg Ile Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys  
225 230 235 240  
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ala Thr Leu Phe Phe  
245 250 255  
Met Cys Leu Arg Pro Pro Ser Glu Glu Ser Met Glu Gln Gly Gln Met  
260 265 270  
Val Ala Val Leu Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile  
275 280 285  
Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ser Lys Glu Leu  
290 295 300  
Phe Lys Arg Lys Leu Phe Pro Lys  
305 310

<210> 1266  
<211> 315  
<212> PRT  
<213> Unknown (H38g183 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1266

```

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1          5          10          15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
          20          25          30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Ile Gly Gly Asn Leu Ser Ile
          35          40          45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
          50          55          60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
65          70          75          80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
          85          90          95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
          100          105          110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
115          120          125
Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
130          135          140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145          150          155          160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
          165          170          175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
          180          185          190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
195          200          205
Met Ala Val Ala Pro Leu Val Phe Ile Ser Val Ser Tyr Ala His Val
210          215          220
Val Ala Ala Val Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
          245          250          255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
          260          265          270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
290          295          300
Trp Gln Leu Leu Val Gly Glu Arg Ser Leu Thr
305          310          315

```

&lt;210&gt; 1267

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g184 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1267

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
          20          25          30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
          35          40          45

```

```

Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
 50          55          60
Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
 65          70          75          80
Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val
          85          90          95
Cys Cys Met Thr Gln Thr Tyr Phe Val Phe Cys Val Gly Val Ala Glu
          100          105          110
Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg
          130          135          140
Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu
          145          150          155          160
Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu
          165          170          175
Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp
          180          185          190
Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile
          195          200          205
Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala
          210          215          220
Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser
          225          230          235          240
Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala
          245          250          255
Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp
          260          265          270
Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro
          275          280          285
Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg
          290          295          300
Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val
          305          310          315

```

&lt;210&gt; 1268

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g185 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1268

```

Met Phe Tyr Phe Phe Pro Pro Leu Gln Ile Leu Ala Glu Asn Leu Thr
 1          5          10          15
Met Val Thr Glu Phe Leu Leu Leu Gly Phe Ser Ser Leu Gly Glu Ile
          20          25          30
Gln Leu Ala Leu Phe Val Val Phe Leu Phe Leu Tyr Leu Val Ile Leu
          35          40          45
Ser Gly Asn Val Thr Ile Ile Ser Val Ile His Leu Asp Lys Ser Leu
          50          55          60
His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu Ser Thr Ser Glu Thr
          65          70          75          80
Phe Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser
          85          90          95
Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe
          100          105          110
Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly
          115          120          125
Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu

```

```

      130              135              140
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Ala Cys Ala Ile Gly
145              150              155              160
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro
      165              170              175
Phe Cys Ser Ala Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala
      180              185              190
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Glu Phe Val Ile
      195              200              205
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys
      210              215              220
Val Ser Tyr Leu Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala
225              230              235              240
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val
      245              250              255
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      260              265              270
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr
      275              280              285
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys
      290              295              300
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu
305              310              315              320
Lys Leu Tyr Asn

```

&lt;210&gt; 1269

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g186 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1269

```

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile
1      5      10      15
Ser Phe Thr Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe
      20      25      30
Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val
      35      40      45
Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
      50      55      60
Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro
65      70      75      80
Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu
      85      90      95
Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu
      100      105      110
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr
      115      120      125
Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro
130      135      140
Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His
145      150      155      160
Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg
      165      170      175

```

```

His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
      180      185      190
Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
      195      200      205
Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
      210      215      220
Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
225      230      235      240
Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
      245      250      255
Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
      260      265      270
Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
      275      280      285
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
      290      295      300
Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
305      310      315      320
Val Lys Leu Gln Ile Ile Leu
      325

```

&lt;210&gt; 1270

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g187 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1270

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
1      5      10      15
Leu Ser Lys Pro Pro Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe
      20      25      30
Ser Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe
      35      40      45
Thr Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu
      50      55      60
Ala Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe
65      70      75      80
Phe Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Ile Ile Gln Ile
      85      90      95
Phe Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr
      100      105      110
Met Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu
      115      120      125
Thr Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp
      130      135      140
Ile Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn
145      150      155      160
Leu Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe
      165      170      175
Pro Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val
      180      185      190
Val Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu
      195      200      205
Leu Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser

```

210	215	220
Ser Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr		
225	230	235
Val Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro		240
	245	250
Leu Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu		255
	260	265
Ser Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val		270
	275	280
Ser Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser		285
	290	300
Xaa Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro		
305	310	315

&lt;210&gt; 1271

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g188 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1271

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg		
1	5	10
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe		15
	20	25
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu		30
	35	40
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met		45
	50	55
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr		60
	65	70
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser		75
	80	85
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe		90
	95	100
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr		105
	110	115
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln		120
	125	130
Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr		135
	140	145
Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met		150
	155	160
Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val		165
	170	175
Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala		180
	185	190
Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala		195
	200	205
Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln		210
	215	220
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe		225
	230	235
Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala		240
	245	250
Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro		255
	260	265
Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala		270
	275	280
	285	290
	295	300



Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn  
 305 310 315 320  
 Gly Ala Phe Ser

<210> 1272

<211> 323

<212> PRT

<213> Unknown (H38g189 protein)

<220>

<223> Synthetic construct

<400> 1272

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile  
 130 135 140  
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu  
 145 150 155 160  
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys  
 165 170 175  
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala  
 180 185 190  
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile  
 195 200 205  
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu  
 210 215 220  
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser  
 225 230 235 240  
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val  
 245 250 255  
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser  
 260 265 270  
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr  
 275 280 285  
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 290 295 300  
 Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro  
 305 310 315 320  
 Phe Leu Leu

<210> 1273

<211> 311

<212> PRT

<213> Unknown (H38g190 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1273

```

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1          5          10          15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
 20          25          30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
 35          40          45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
 65          70          75          80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
 85          90          95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
100          105          110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
115          120          125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
130          135          140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
145          150          155          160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
165          170          175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
180          185          190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
195          200          205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
210          215          220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
245          250          255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
260          265          270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
290          295          300
Gln Arg Arg Gln Asp Ser Arg
305          310

```

&lt;210&gt; 1274

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g191 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1274

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1          5          10          15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
 20          25          30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
 35          40          45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu  
 50 55 60  
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser  
 65 70 75 80  
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu  
 85 90 95  
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly  
 100 105 110  
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile  
 115 120 125  
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Ile  
 130 135 140  
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu  
 145 150 155 160  
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
 165 170 175  
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val  
 180 185 190  
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
 195 200 205  
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp  
 210 215 220  
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
 225 230 235 240  
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
 245 250 255  
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
 260 265 270  
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
 275 280 285  
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
 290 295 300  
 Phe  
 305

&lt;210&gt; 1275

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g192 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1275

Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu  
 20 25 30  
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr  
 35 40 45  
 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser  
 100 105 110  
 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu

130	135	140
Val Ala Ala Ala Cys	Ala Cys Gly Phe Thr	Val Ala Gln Ile Ile Thr
145	150	155
Ser Leu Val Phe His	Leu Pro Phe Tyr Ser	Ser Asn Gln Leu His His
165	170	175
Phe Phe Cys Asp Ile	Ala Pro Val Leu Lys	Leu Ala Ser His His Asn
180	185	190
His Phe Ser Gln Ile	Val Ile Phe Met Leu	Cys Thr Leu Val Leu Ala
195	200	205
Ile Pro Leu Leu Leu	Ile Leu Val Ser Tyr	Val His Ile Leu Ser Ala
210	215	220
Ile Leu Gln Phe Pro	Ser Thr Leu Gly Arg	Cys Lys Ala Phe Ser Thr
225	230	235
Cys Val Ser His Leu	Ile Ile Val Thr Val	His Tyr Gly Cys Ala Ser
245	250	255
Phe Ile Tyr Leu Arg	Pro Gln Ser Asn Tyr	Ser Ser Ser Gln Asp Ala
260	265	270
Leu Ile Ser Val Ser	Tyr Thr Ile Ile Thr	Pro Leu Phe Asn Pro Met
275	280	285
Ile Tyr Ser Leu Arg	Asn Lys Glu Phe Lys	Ser Ala Leu Cys Lys Ile
290	295	300
Val Arg Arg Thr Ile	Ser Leu Leu	
305	310	

&lt;210&gt; 1276

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g193 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(244)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1276

Met Met Ile Ser Ser	Asp Glu Glu Asn Asp	Thr Asn Met Met Glu Phe
1	5	10
Ile Leu Val Gly Leu	Ser Arg Gln Pro Ala	Ser Gln Leu Leu Phe Phe
20	25	30
Xaa Ala Ile Leu Phe	Ile Tyr Ser Val Thr	Leu Val Gly Asn Ile Leu
35	40	45
Ile Ile Val Ile Ile	Gln Ile Asp Ser His	Leu Gln Thr Pro Met Tyr
50	55	60
Phe Phe Leu Ile Gln	Val Ser Phe Leu Asp	Ile Cys Ser Thr Pro Thr
65	70	75
Val Leu Val Asn Cys	Xaa Lys Asp Phe Pro	Ser Val Ser Tyr Ser Gly
85	90	95
Cys Leu Phe Xaa Met	Thr Ile Phe Leu Tyr	Leu Gly Val Thr Glu Cys
100	105	110
Val Phe Phe Leu Phe	Cys Phe Glu Cys Phe	Leu Ile Ala Val Met Ala
115	120	125
Tyr Asp Arg Phe Val	Ala Ile Ser Lys Pro	Leu Cys Tyr Pro Phe Ile
130	135	140
Ile Asn Ser Asn Val	Cys Ile Trp Met Val	Ala Gly Val Trp Ala His
145	150	155
Pro Gly Arg Thr Asn	Pro Ile Leu Trp Pro	Gln Cys Ser Gln His Phe
165	170	175
Thr Cys Glu Leu Gln	Val Ile Phe Lys Leu	Thr Cys Ser Pro Val Leu
180	185	190

Val Lys Glu Ile Gln Xaa Phe Met Ile Pro Gly Cys Thr Leu Xaa Ala  
 195 200 205  
 Leu Tyr Gln His Xaa Val Cys Ser Tyr Ser Xaa Ala Arg Gln Gln Thr  
 210 215 220  
 His Pro Arg Ser Xaa Glu Ala Tyr Asn Xaa Gly Ile Arg Xaa Gly Ile  
 225 230 235 240  
 Ile Gly Val His

<210> 1277

<211> 306

<212> PRT

<213> Unknown (H38g194 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(306)

<223> Xaa = Any Amino Acid

<400> 1277

Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly  
 1 5 10 15  
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu  
 20 25 30  
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu  
 35 40 45  
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys  
 65 70 75 80  
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly  
 85 90 95  
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn  
 115 120 125  
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val  
 130 135 140  
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val  
 145 150 155 160  
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp  
 165 170 175  
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu  
 180 185 190  
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu  
 195 200 205  
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn  
 210 215 220  
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His  
 225 230 235 240  
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu  
 245 250 255  
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val  
 260 265 270  
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu  
 275 280 285  
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys  
 290 295 300  
 Leu Phe

305

&lt;210&gt; 1278

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g195 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1278

```

Met Ala Asn Ser Ser Ser Val Thr Glu Phe Leu Val Leu Gly Phe Ser
 1          5          10          15
Ser Leu Gly Glu Leu Gln Leu Val Leu Phe Ala Val Phe Leu Cys Leu
          20          25          30
Tyr Leu Ile Ile Leu Ser Gly Asn Ile Ile Ile Ser Val Ile His
          35          40          45
Leu Asp His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu
          50          55          60
Ser Ile Ser Glu Ile Phe Tyr Thr Thr Val Ile Leu Pro Lys Met Leu
          65          70          75          80
Ile Asn Leu Phe Ser Val Phe Arg Thr Leu Ser Phe Val Ser Cys Ala
          85          90          95
Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn Cys Leu Leu
          100          105          110
Leu Gly Val Met Gly Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
          115          120          125
Gln Tyr Ala Val Leu Met Ser Trp Arg Val Cys Gly Gln Leu Ile Ala
          130          135          140
Thr Cys Ile Ile Ser Gly Phe Leu Ile Ser Leu Val Gly Thr Thr Phe
          145          150          155          160
Val Phe Ser Leu Pro Phe Cys Gly Ser Asn Lys Val Asn His Tyr Phe
          165          170          175
Cys Asp Ile Ser Pro Val Ile Arg Leu Ala Cys Ala Asp Ser Tyr Ile
          180          185          190
Ser Glu Leu Val Ile Phe Ile Phe Gly Val Leu Val Leu Val Val Pro
          195          200          205
Leu Ile Phe Ile Cys Ile Ser Tyr Gly Phe Ile Val Arg Thr Ile Leu
          210          215          220
Lys Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
          225          230          235          240
Ser His Leu Ile Val Val Ile Val His Tyr Gly
          245          250

```

&lt;210&gt; 1279

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g196 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1279

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
          20          25          30

```

Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile  
 35 40 45  
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe  
 50 55 60  
 Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser  
 65 70 75 80  
 Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile  
 85 90 95  
 Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly  
 100 105 110  
 Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val  
 115 120 125  
 Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val  
 130 135 140  
 Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala  
 145 150 155 160  
 Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val  
 165 170 175  
 Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys  
 180 185 190  
 Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe  
 195 200 205  
 Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile  
 210 215 220  
 Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met  
 245 250 255  
 Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val  
 260 265 270  
 Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr  
 275 280 285  
 Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys  
 290 295 300  
 Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn  
 305 310 315

&lt;210&gt; 1280

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g197 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1280

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr  
 1 5 10 15  
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro  
 20 25 30  
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn  
 35 40 45  
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser  
 65 70 75 80  
 Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn  
 85 90 95  
 Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile  
 100 105 110  
 Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg

```

      115      120      125
Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Val Ile Ile Met Ala Glu
  130      135      140
Lys Val Leu Trp Val Leu Val Ile Val Pro Tyr Leu Tyr Ser Thr Phe
  145      150      155      160
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe Lys Leu Ser Phe Cys Gly
      165      170      175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp Cys Ile Pro Leu Met Ser
      180      185      190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu Leu Ile Ile Leu Ile Phe
      195      200      205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser Ile Val Leu Ile Ser Tyr
      210      215      220
Met Phe Ile Leu Val Ala Ile Leu Arg Met Asn Ser Arg Lys Gly Arg
      225      230      235      240
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met
      245      250      255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His
      260      265      270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile
      275      280      285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
      290      295      300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile
      305      310      315

```

&lt;210&gt; 1281

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g198 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1281

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1      5      10      15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
      20      25      30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
      35      40      45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
      50      55      60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
      65      70      75      80
Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
      85      90      95
Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
      100      105      110
Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
      115      120      125
Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
      130      135      140
Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
      145      150      155

```

&lt;210&gt; 1282



<211> 317  
 <212> PRT  
 <213> Unknown (H38g199 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1282

```

Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu
 1      5      10      15
Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu
 20      25      30
Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Ile Leu
 35      40      45
Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg
 50      55      60
Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys
 65      70      75      80
Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala
 85      90      95
Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu
100      105      110
Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser
115      120      125
Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val
130      135      140
Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
145      150      155      160
Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
165      170      175
Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
180      185      190
Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
195      200      205
Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
210      215      220
Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
225      230      235      240
Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
245      250      255
Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
260      265      270
Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
275      280      285
Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
290      295      300
Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
305      310      315

```

<210> 1283  
 <211> 302  
 <212> PRT  
 <213> Unknown (H38g200 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1283

```

Met Thr Asn Leu Asn Ala Ser Gln Ala Asn His Arg Asn Phe Ile Leu
 1           5           10           15
Thr Gly Ile Pro Gly Thr Pro Asp Lys Asn Pro Trp Leu Ala Phe Pro
          20           25           30
Leu Gly Phe Leu Tyr Thr Leu Thr Leu Leu Gly Asn Gly Thr Ile Leu
 35           40           45
Ala Val Ile Lys Val Glu Pro Ser Leu His Glu Pro Thr Tyr Tyr Phe
 50           55           60
Leu Ser Ile Leu Ala Leu Thr Asp Val Ser Leu Ser Met Ser Thr Leu
65           70           75           80
Pro Ser Met Leu Ser Ile Tyr Trp Phe Asn Ala Pro Gln Ile Val Phe
          85           90           95
Asp Ala Cys Ile Met Gln Met Phe Phe Ile His Val Phe Gly Ile Val
          100          105          110
Glu Ser Gly Val Leu Val Ser Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Arg Asn Pro Leu His Tyr Val Ser Ile Leu Thr His Asp Val Ile Arg
          130          135          140
Lys Thr Gly Ile Ser Val Leu Thr Arg Ala Val Cys Val Val Phe Pro
          145          150          155          160
Val Pro Phe Leu Ile Lys Cys Leu Pro Phe Cys His Ser Asn Val Leu
          165          170          175
Ser His Ser Tyr Cys Leu His Gln Asn Met Met Arg Leu Ala Cys Ala
          180          185          190
Ser Thr Arg Ile Asn Ser Leu Tyr Gly Leu Ile Val Val Ile Phe Thr
          195          200          205
Leu Gly Leu Asp Val Leu Leu Thr Leu Leu Ser Tyr Val Leu Thr Leu
          210          215          220
Lys Thr Val Leu Gly Ile Val Ser Arg Gly Glu Arg Leu Lys Thr Leu
          225          230          235          240
Ser Thr Cys Leu Ser His Met Ser Thr Val Leu Leu Phe Tyr Val Pro
          245          250          255
Phe Met Gly Ala Ala Ser Met Ile His Arg Phe Trp Glu His Leu Ser
          260          265          270
Pro Val Val His Met Val Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
          290          295          300

```

&lt;210&gt; 1284

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g201 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1284

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Pro Ala Val Ser Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe
          50           55           60

```

```

Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65          70          75          80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Arg Val Ile Ser
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100         105         110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
          115         120         125
Ile Tyr Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
130         135         140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145         150         155         160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165         170         175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Ser
          180         185         190
Tyr Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
195         200         205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Ser Ser Tyr Tyr Lys Ile
210         215         220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Thr
225         230         235         240
Phe Ser Thr Tyr Gly Ser His Leu Ala Phe Val Cys Xaa Phe Tyr Gly
          245         250         255
Thr Gly Ile Asp Met Tyr Leu Ala Ser Ala Met Ser Pro Thr Pro Arg
          260         265         270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
275         280         285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290         295         300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305         310         315         320
Phe Phe Trp Cys

```

&lt;210&gt; 1285

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g202 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(144)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1285

```

Phe Ser Val Thr Gly Ile Ser Val Val Asp Cys Cys Phe Xaa Ser Thr
1          5          10          15
Val Ile Pro Glu Met Leu Phe Ser Cys Gln Val Gln His Leu Val His
          20          25          30
Asn Pro Lys Gly Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu
          35          40          45
Leu Leu Thr Phe Phe Xaa Lys Ile Ser Phe His Arg Met His Phe Cys
          50          55          60
Ile Arg Asp Ser Ser Ser Gly Lys Ile Thr Val Tyr Tyr Leu Xaa Phe
65          70          75          80
Tyr Ile Cys Gly Gln Ile Val Leu Glu Gln Val Lys His Ile Xaa Glu
          85          90          95
Xaa Ser Leu Ser Leu Glu Phe Val Ile Phe Xaa Tyr Phe Tyr Lys Gly

```

	100		105		110										
Asp	Leu	Ala	Leu	Lys	Gln	Asn	Phe	Ala	Ile	Leu	Arg	Ser	Ile	Pro	Ser
	115		120		125										
Phe	Ser	Xaa	Asp	Leu	Glu	Ile	His	Asn	Val	Arg	Tyr	Gln	His	Phe	
	130		135		140										

&lt;210&gt; 1286

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g203 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1286

Thr	His	Gly	Tyr	Thr	Phe	Ser	Leu	Arg	Leu	Phe	Leu	His	Cys	Leu	Thr
1				5					10					15	
Tyr	Val	Xaa	Val	Ser	His	Cys	Leu	Leu	Ile	Trp	Leu	Ile	Thr	Phe	Ser
			20					25					30		
Pro	Phe	Asn	Leu	Leu	Phe	Lys	Xaa	Asn	Leu	Xaa	Phe	Thr	Ile	Xaa	Leu
		35					40					45			
Ile	Thr	Xaa	Ile	Glu	Ser	Arg	Tyr	Ser	Lys	His	Trp	Pro	Phe	Phe	Leu
	50				55					60					
Leu	Xaa	Cys	Phe	Cys	Asn	Val	Leu	Phe	His	Leu	Asp	Cys	Asp	Ser	Pro
65				70					75					80	
Val	Cys	Asn	Thr	Lys	Arg	Ile	Arg	Ser	Phe	Phe	Val	Leu	Glu	Arg	Xaa
			85					90					95		
Lys	Ser	Ser	Xaa	Lys	Ser	Glu	Lys	Ile	His	Phe	Xaa	Thr	Arg	Asn	Lys
			100					105					110		
Val	Ser	Cys	Phe	Xaa	Asp	Phe	Gly	Ile	Lys	Tyr	Thr	Val	Tyr	Leu	Leu
		115					120					125			
Leu	Leu	Lys	His	Phe	Leu	Leu	Ile	His	Ser	Ile	Leu	Arg	Tyr	Leu	Xaa
	130					135					140				
Val	Ala	Gly	Tyr	Gly	Thr	Ser	Xaa	Phe	Leu	Ser	Arg	Ile	Ser	Ser	Ile
145					150					155				160	
Thr	Leu	Lys	Thr	Ile	Ile	Cys	Ile	Leu	Lys	Lys	Ser	Tyr	His	Phe	Phe
			165					170						175	
Ser	Val	Gln	Tyr	Thr	Ile	Ser	Tyr	Ile	Asp	Pro	Phe	Ile	Asn	Ser	Leu
		180						185					190		
Val	Met	Phe	Val	Val	Phe	Thr	Ala	Phe	Ile	Gln	Ala	Phe	Ala	Phe	Met
	195						200					205			
Ile	Ile	Ile	Val	Ser	Tyr	Thr	Gln	Val	Leu	Phe	Ala	Leu	Leu	Lys	Lys
	210					215				220					
Asn	Ser	Glu	Lys	Gly	Arg	Ser	Lys	Ser	Phe	Leu	Met	Cys	Ser	Ala	His
225					230					235				240	
Leu	Leu	Ser	Val	Ser	Leu	Phe	Tyr	Ser	Ser	Val	Phe	Phe	Met	Tyr	Gly
			245					250					255		
Cys	Pro	Arg	Ser	Gly	Pro	Asp	Xaa	Gln	Trp	Asn	Glu	Met	Tyr	Phe	Pro
			260					265					270		
Phe	Tyr	Met	Ile	Ile	Ile	Pro	Leu	Gln	Thr	Pro	Phe	Ile	Tyr	Ser	Met
	275					280						285			
Lys	Asn	Lys	Glu	Val	Leu	Gly	Thr	Leu	Arg	Thr	Met	Ile	Lys	Lys	Tyr
	290					295					300				
Phe	Trp	Arg	Thr	Leu	Ser	Xaa	Phe	Phe	Pro						
305					310										

&lt;210&gt; 1287

<211> 253  
 <212> PRT  
 <213> Unknown (H38g204 protein)

<220>  
 <223> Synthetic construct

<400> 1287  
 Met Cys Leu Phe Leu Cys His Leu Ser Phe Leu Asp Met Thr Ile Ser  
 1 5 10 15  
 Cys Ala Ile Val Pro Lys Met Leu Ala Gly Phe Leu Leu Gly Ser Arg  
 20 25 30  
 Ile Ile Ser Phe Gly Gly Cys Val Ile Gln Leu Phe Ser Phe His Phe  
 35 40 45  
 Leu Gly Cys Thr Glu Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg  
 50 55 60  
 Phe Leu Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Thr His  
 65 70 75 80  
 Arg Val Cys Asn Ser Leu Ala Leu Gly Thr Trp Leu Gly Gly Thr Ile  
 85 90 95  
 His Ser Leu Phe Gln Thr Ser Phe Val Phe Arg Leu Pro Phe Cys Gly  
 100 105 110  
 Pro Asn Arg Val Asp Tyr Ile Phe Cys Asp Ile Pro Ala Met Leu Arg  
 115 120 125  
 Leu Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Ala Asp  
 130 135 140  
 Ile Gly Phe Leu Ala Leu Thr Cys Phe Met Leu Ile Leu Thr Ser Tyr  
 145 150 155 160  
 Gly Tyr Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Asp Gly Arg  
 165 170 175  
 Arg Asn Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile Val  
 180 185 190  
 Tyr Tyr Val Pro Cys Thr Phe Ile Tyr Leu Arg Pro Cys Ser Gln Glu  
 195 200 205  
 Pro Leu Asp Gly Val Val Ala Val Phe Tyr Thr Val Ile Thr Pro Leu  
 210 215 220  
 Leu Asn Ser Ile Ile Tyr Thr Leu Cys Asn Lys Glu Met Lys Ala Ala  
 225 230 235 240  
 Leu Gln Arg Leu Gly Gly His Lys Glu Val Gln Pro His  
 245 250

<210> 1288  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g205 protein)

<220>  
 <223> Synthetic construct

<400> 1288  
 Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe  
 20 25 30  
 Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu  
 35 40 45  
 Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln  
 65 70 75 80  
 Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly

								85			90			95		
Cys	Val	Ala	Gln	Leu	Phe	Ile	Tyr	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	
								100			105			110		
Val	Leu	Leu	Val	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Arg	
								115			120			125		
Pro	Leu	His	Tyr	Met	Ala	Ile	Met	His	Pro	His	Leu	Cys	Gln	Thr	Leu	
								130			135			140		
Ala	Ile	Ala	Ser	Trp	Gly	Ala	Gly	Phe	Val	Asn	Ser	Leu	Ile	Gln	Thr	
								145			150			155		
Gly	Leu	Ala	Met	Ala	Met	Pro	Leu	Cys	Gly	His	Arg	Leu	Asn	His	Phe	
								165			170			175		
Phe	Cys	Glu	Met	Pro	Val	Phe	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	Glu	
								180			185			190		
Gly	Thr	Glu	Ala	Lys	Met	Phe	Val	Ala	Arg	Val	Ile	Val	Val	Ala	Val	
								195			200			205		
Pro	Ala	Ala	Leu	Ile	Leu	Gly	Ser	Tyr	Val	His	Ile	Ala	His	Ala	Val	
								210			215			220		
Leu	Arg	Val	Lys	Ser	Thr	Ala	Gly	Arg	Arg	Lys	Ala	Phe	Gly	Thr	Cys	
								225			230			235		
Gly	Ser	His	Leu	Leu	Val	Val	Phe	Leu	Phe	Tyr	Gly	Ser	Ala	Ile	Tyr	
								245			250			255		
Thr	Tyr	Leu	Gln	Ser	Ile	His	Asn	Tyr	Ser	Glu	Arg	Glu	Gly	Lys	Phe	
								260			265			270		
Val	Ala	Leu	Phe	Tyr	Thr	Ile	Ile	Thr	Pro	Ile	Leu	Asn	Pro	Leu	Ile	
								275			280			285		
Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly	Ala	Leu	Trp	Lys	Val	Leu	
								290			295			300		
Trp	Arg	Gly	Arg	Asp	Ser	Gly										
								305			310					

**<210> 1289**

**<211> 311**

<212> PRT

<213> Unknown (H38g206 protein)

**<220>**

<223> Synthetic construct

**<400> 1289**

Met	Lys	Ile	Lys	Asn	His	Thr	Pro	Val	Thr	Glu	Val	Pro	Leu	Met	Gly
1				5					10					15	
Ile	Pro	His	Thr	Lys	Gly	Met	Glu	Asn	Val	Leu	Phe	Val	Leu	Phe	Leu
			20					25					30		
Ala	Phe	Tyr	Leu	Phe	Thr	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala
		35					40					45			
Val	Leu	Thr	Phe	Ser	Asn	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly
	50					55					60				
Asn	Leu	Ser	Val	Phe	Asp	Ile	Phe	Phe	Pro	Ser	Val	Ser	Ser	Pro	Lys
65				70						75					80
Met	Met	Leu	Cys	Leu	Val	Gly	Gln	Ser	Cys	Thr	Ile	Ser	Phe	Gln	Gly
			85						90					95	
Cys	Ala	Ser	Gln	Leu	Phe	Phe	His	His	Phe	Leu	Gly	Cys	Thr	Glu	Cys
			100					105					110		
Phe	Leu	Tyr	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Ala	Ala	Ile	Cys	His
		115					120					125			
Pro	Leu	Pro	Tyr	Thr	Val	Ile	Met	Lys	Arg	Arg	Val	Cys	Ala	Leu	Leu
		130				135					140				
Thr	Leu	Gly	Thr	Trp	Thr	Gly	Ser	Cys	Leu	His	Ala	Ser	Val	Leu	Thr
145				150						155				160	
Leu	Leu	Ile	Phe	Lys	Leu	Ser	Tyr	Cys	Gly	Pro	Asn	Glu	Val	Asp	Asn
			165						170					175	

Phe Phe Cys Asp Ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp Thr  
 180 185 190  
 Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala Leu  
 195 200 205  
 Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile Ser  
 210 215 220  
 Ile Leu Lys Ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile Val  
 245 250 255  
 Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val Val  
 260 265 270  
 Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu Ile  
 290 295 300  
 Gln Gly Val His Asn Cys Gly  
 305 310

<210> 1290

<211> 298

<212> PRT

<213> Unknown (H38g207 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400> 1290

Val Arg Gly Ser Lys Gln Leu Arg Asn Gly Thr Leu Val Ser Gln Phe  
 1 5 10 15  
 Leu Leu Lys Gly Leu Arg Asp Ser Lys Ala Trp Arg Pro Leu Leu Phe  
 20 25 30  
 Thr Thr Phe Leu Leu Ile Tyr Ile Val Val Val Val Gly Ser His Met  
 35 40 45  
 Phe Thr Val Asp Tyr Arg Arg His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Gly His Ser Leu Met Asp Ala Ala Cys Ile Ser Asn Met Val Thr Gln  
 65 70 75 80  
 Val Leu Val His Leu Leu Ala Pro Val Gly Pro Val Leu Tyr Cys Ala  
 85 90 95  
 Cys Leu Ile Gln Ile Cys Phe Leu His Phe Leu Ala Pro Xaa Glu Ser  
 100 105 110  
 Phe Leu Leu Thr Ala Val Ala Tyr Asp Ser Met Leu Ala Ile Cys Gln  
 115 120 125  
 Pro Leu His Tyr Phe Val Leu Val Gly Arg Leu Thr His Thr Gly Leu  
 130 135 140  
 Thr Ser Ile Ser Cys Leu Leu Ala Leu Ala Asn Ala Phe Thr Tyr Ser  
 145 150 155 160  
 Ile Leu Thr Ala Leu Pro Lys Phe Cys Arg Pro Cys Leu Ile Thr His  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Ser Leu Leu Arg Leu Ser Cys Phe Ser Thr  
 180 185 190  
 Arg Thr Asn Glu Leu Ala Leu Phe Phe Ser Phe Leu Val Ala Leu Ala  
 195 200 205  
 His Cys Val Leu Val Val Val Ser Tyr Gly His Val Val Ala Ala Val  
 210 215 220  
 Gln Ile His Ser Thr Gln Gly Xaa Arg Lys Ala Phe Ser Thr Cys Val

225		230		235		240									
Ala	His	Leu	Ala	Met	Ile	Gly	Leu	Phe	Tyr	Val	Thr	Ser	Val	Pro	Cys
			245						250					255	
Tyr	Ile	Leu	Pro	Asn	Ser	Ala	Tyr	Ser	Gly	Leu	Gly	Asp	Trp	Val	Leu
			260					265					270		
Ser	Val	Leu	Cys	Val	Val	Leu	Thr	His	Met	Leu	Asn	Pro	Ile	Phe	Pro
		275					280					285			
Ser	Met	Leu	Gly	Xaa	Gln	Cys	Met	Ser	His						
	290					295									

&lt;210&gt; 1291

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g208 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1291

Met	Gly	Val	Lys	Asn	His	Ser	Thr	Val	Thr	Glu	Phe	Leu	Leu	Ser	Gly
1				5					10					15	
Leu	Thr	Glu	Gln	Ala	Glu	Leu	Gln	Leu	Pro	Leu	Phe	Cys	Leu	Phe	Leu
			20					25					30		
Gly	Ile	Tyr	Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Ser	Met	Ile	Ser	Ile
		35					40					45			
Ile	Arg	Leu	Asn	Arg	Gln	Leu	His	Thr	Pro	Met	Tyr	Tyr	Phe	Leu	Ser
	50					55					60				
Ser	Leu	Ser	Phe	Leu	Asp	Phe	Cys	Tyr	Ser	Ser	Val	Ile	Thr	Pro	Lys
65					70					75				80	
Met	Leu	Ser	Gly	Phe	Leu	Cys	Arg	Asp	Arg	Ser	Ile	Ser	Tyr	Ser	Gly
				85					90					95	
Cys	Met	Ile	Gln	Leu	Phe	Phe	Phe	Cys	Val	Cys	Val	Ile	Ser	Glu	Cys
			100					105					110		
Tyr	Met	Leu	Ala	Ala	Met	Ala	Cys	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser
	115						120					125			
Pro	Leu	Leu	Tyr	Arg	Val	Ile	Met	Ser	Pro	Arg	Val	Cys	Ser	Leu	Leu
	130					135					140				
Val	Ala	Ala	Val	Phe	Ser	Val	Gly	Phe	Thr	Asp	Ala	Val	Ile	His	Gly
145					150					155				160	
Gly	Cys	Ile	Leu	Arg	Leu	Ser	Phe	Cys	Gly	Ser	Asn	Ile	Ile	Lys	His
			165						170					175	
Tyr	Phe	Cys	Asp	Ile	Val	Pro	Leu	Ile	Lys	Leu	Ser	Cys	Ser	Ser	Thr
			180						185					190	
Tyr	Ile	Asp	Glu	Leu	Leu	Ile	Phe	Val	Ile	Gly	Gly	Phe	Asn	Met	Val
	195						200					205			
Ala	Thr	Ser	Leu	Thr	Ile	Ile	Ser	Tyr	Ala	Phe	Ile	Leu	Thr	Ser	
	210					215					220				
Ile	Leu	Arg	Ile	His	Ser	Lys	Lys	Gly	Arg	Cys	Lys	Ala	Phe	Ser	Thr
225					230					235				240	
Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Leu	Met	Phe	Tyr	Gly	Ser	Leu	Met
				245					250					255	
Ser	Met	Tyr	Leu	Lys	Pro	Ala	Ser	Ser	Ser	Ser	Leu	Thr	Gln	Glu	Lys
			260					265					270		
Val	Ser	Ser	Val	Phe	Tyr	Thr	Thr	Val	Ile	Leu	Met	Leu	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Asn	Glu	Val	Arg	Asn	Ala	Leu	Met	Lys	Leu
	290					295					300				
Leu	Arg	Arg	Lys	Ile	Ser	Leu	Ser								
305					310										

&lt;210&gt; 1292



<211> 251  
 <212> PRT  
 <213> Unknown (H38g209 protein)

<220>  
 <223> Synthetic construct

<400> 1292

```

Met Tyr Tyr Phe Leu Ser His Leu Ala Phe Val Asp Leu Cys Tyr Ser
 1          5          10          15
Ser Ala Ile Thr Pro Lys Met Met Val Asn Phe Val Val Glu Arg Asn
          20          25          30
Thr Ile Pro Phe His Ala Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr
          35          40          45
Phe Met Ile Thr Glu Cys Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys
          50          55          60
Tyr Val Ala Ile Cys Ser Pro Leu His Tyr Ser Thr Leu Met Ser Arg
          65          70          75          80
Arg Val Cys Ile Gln Leu Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu
          85          90          95
Val Ala Leu Phe His Thr Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly
          100          105          110
Pro Asn Leu Ile Asn His Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala
          115          120          125
Leu Ser Cys Ser Asp Thr His Met Lys Glu Ile Leu Ile Phe Ala Phe
          130          135          140
Ala Gly Phe Asp Met Ile Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr
          145          150          155          160
Ile Phe Ile Ile Ala Ala Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln
          165          170          175
His Lys Ala Ile Ser Thr Cys Gly Ser His Met Val Thr Val Thr Ile
          180          185          190
Phe Tyr Gly Thr Leu Ile Phe Met Tyr Leu Gln Pro Lys Ser Asn His
          195          200          205
Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile
          210          215          220
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
          225          230          235          240
Asp Ala Ser Lys Lys Ala Leu Asp Lys Gly Cys
          245          250

```

<210> 1293  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g210 protein)

<220>  
 <223> Synthetic construct

<400> 1293

```

Met Ser Asn Ala Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1          5          10          15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
          20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35          40          45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
          50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
          65          70          75          80
Met Thr Leu Val Ser Pro Ser Gly Arg Thr Ile Ser Phe His Ser Cys

```

				85						90						95		
Val	Ala	Gln	Leu	Tyr	Phe	Phe	His	Phe	Leu	Gly	Ser	Thr	Glu	Cys	Phe			
			100					105					110					
Leu	Tyr	Thr	Val	Met	Ser	Tyr	Asp	Arg	Tyr	Leu	Ala	Ile	Ser	Tyr	Pro			
		115					120					125						
Leu	Arg	Tyr	Thr	Asn	Met	Met	Thr	Gly	Arg	Ser	Cys	Ala	Leu	Leu	Ala			
	130					135					140							
Thr	Gly	Thr	Trp	Leu	Ser	Gly	Ser	Leu	His	Ser	Ala	Val	Gln	Thr	Ile			
145					150					155					160			
Leu	Thr	Phe	His	Leu	Pro	Tyr	Cys	Gly	Pro	Asn	Gln	Ile	Gln	His	Tyr			
			165					170					175					
Phe	Cys	Asp	Ala	Pro	Pro	Ile	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	Ser			
		180					185					190						
Ala	Asn	Glu	Met	Val	Ile	Phe	Val	Asn	Ile	Gly	Leu	Val	Ala	Ser	Gly			
	195					200					205							
Cys	Phe	Val	Leu	Ile	Val	Leu	Ser	Tyr	Val	Ser	Ile	Val	Cys	Ser	Ile			
	210					215					220							
Leu	Arg	Ile	Arg	Thr	Ser	Glu	Gly	Arg	His	Arg	Ala	Phe	Gln	Thr	Cys			
225					230					235					240			
Ala	Ser	His	Cys	Ile	Val	Val	Leu	Cys	Phe	Phe	Gly	Pro	Gly	Leu	Phe			
		245					250					255						
Ile	Tyr	Leu	Arg	Pro	Gly	Ser	Arg	Asp	Ala	Leu	His	Gly	Val	Val	Ala			
		260					265					270						
Val	Phe	Tyr	Thr	Thr	Leu	Thr	Pro	Leu	Phe	Asn	Pro	Val	Val	Tyr	Thr			
	275					280					285							
Leu	Arg	Asn	Lys	Glu	Val	Lys	Lys	Ala	Leu	Leu	Lys	Leu	Lys	Asn	Gly			
	290					295					300							
Ser	Val	Phe	Ala	Gln	Gly	Glu												
305					310													

**<210> 1294**

**<211> 278**

<212> PRT

<213> Unknown (H38g211 protein)

**<220>**

<223> Synthetic construct

## <221> VARIANT

<222> (1) ... (278)

<223> Xaa = Any Amino Acid

**<400> 1294**

His 1	Ser	Ser	Leu	Leu	Phe	Ala	Val	Phe	Leu	Leu	Thr	Tyr	Ser	Val	Thr
				5					10					15	
Leu	Val	Gly	Asn	Leu	Gly	Met	Thr	Asp	Leu	Ile	Cys	Gln	Ser	Arg	Thr
			20					25					30		
Ser	Ser	Ala	Leu	His	Thr	Pro	Met	Cys	Phe	Leu	Leu	Ser	Val	Phe	Ser
		35					40					45			
Phe	Leu	Asp	Ile	Cys	Ser	Ser	Ser	Ile	Val	His	Pro	Arg	Leu	Leu	Ile
	50					55					60				
His	Phe	Leu	Thr	Thr	Arg	Pro	Ser	Ile	Ser	Phe	Ala	Gly	Gly	Ile	Ile
65					70				75					80	
Gln	Met	Ala	Leu	Met	Thr	Phe	Tyr	Gly	Thr	Gly	Glu	Cys	Leu	Leu	Leu
				85					90					95	
Ala	Ile	Val	Ala	Tyr	Asp	Xaa	Val	Val	Ala	Ile	Cys	His	Pro	Phe	Pro
			100					105					110		
Xaa	His	Ile	Ile	Met	Ser	Lys	Gly	Leu	Cys	Ala	Gln	Leu	Val	Val	Val
		115					120					125			
Thr	Ser	Ala	Val	Gly	Val	Leu	Ile	Ser	Ala	His	Arg	Gln	Asp	Ala	Phe
	130					135					140				

```

Ile Ser Pro Tyr Arg Gly Leu Asn Ile Ile Asp His Tyr Tyr Cys Ser
145          150          155          160
Val Thr Phe Pro Thr Pro Met Leu Gln Leu Ala Cys Ser Asp Ala Thr
          165          170          175
Val Ala Asn Met Ile Leu Phe Val Ser Ser Ala Leu Ile Thr Ile Pro
          180          185          190
Thr Ile Ser Val Ile Leu Val Ser Tyr Thr Tyr Ile Leu Val Asn Leu
          195          200          205
Val Arg Met Arg Ser Leu Asp Ala Gln Cys Lys Ala Phe Ser Thr Arg
          210          215          220
Ala Ser His Leu Thr Ala His Cys Leu Phe Tyr Gly Phe Val Phe Leu
225          230          235          240
Val Tyr Ile Pro Pro Asn Pro Glu Met Ala Ser Ala Tyr Asn Lys Ile
          245          250          255
Leu Phe Thr Val Val Ile Pro Met Leu Asn Leu Leu Val Xaa Gly Leu
          260          265          270
Arg Asn Lys Asp Val Lys
          275

```

&lt;210&gt; 1295

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g212 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1295

```

Ser Val Ala Lys Gly Asn His Ser Thr Val Tyr Glu Phe Ile Leu Leu
1      5      10      15
Gly Leu Thr Asp Asn Ala Glu Leu Gln Val Thr Leu Phe Gly Ile Phe
          20      25      30
Leu Val Val Tyr Leu Ala Ser Phe Met Gly Asn Phe Gly Leu Ile Met
          35      40      45
Leu Ile Gln Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu
          50      55      60
Ser His Leu Ala Phe Val Asp Phe Ser Phe Thr Ser Ser Val Ala Pro
65      70      75      80
Asn Thr Leu Val Asn Phe Leu Cys Glu Val Lys Ser Ile Thr Phe Tyr
          85      90      95
Ala Cys Ala Ile Gln Val Cys Cys Phe Ile Thr Phe Val Val Cys Glu
          100     105     110
Leu Tyr Leu Leu Ser Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115     120     125
Asn Pro Leu Leu Tyr Val Ile Leu Ile Pro Arg Lys Cys Ile Lys Leu
130     135     140
Ile Ala Ser Thr Tyr Val Tyr Gly Phe Thr Val Gly Leu Val Gln Thr
145     150     155     160
Val Ala Thr Ser Tyr Leu Ser Phe Cys Asp Ser Asn Val Ile Asn His
          165     170     175
Phe Tyr His Asp Asp Val Pro Leu Val Ala Leu Ala Cys Ser Asp Thr
          180     185     190
His Val Lys Glu Leu Met Leu Leu Ile Ala Gly Phe Asn Thr Leu
          195     200     205
Cys Ser Leu Val Ile Val Leu Ile Ser Tyr Gly Phe Ile Phe Phe Ala
210     215     220
Ile Leu Arg Ile His Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225     230     235     240
Ser Ala Ser His Leu Thr Ser Ile Thr Ile Phe Tyr Gly Thr Ile Ile
          245     250     255
Phe Met Tyr Pro Gln Pro Lys Ser Ser His Ser Leu Asn Met Asp Lys

```

260 265 270  
 Val Ala Ser Val Phe Asn Val Val Val Ile Pro Thr Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Leu Lys Arg Ile  
 290 295 300  
 Ile Glu Lys Leu Cys Leu Ala Val  
 305 310

<210> 1296  
 <211> 232  
 <212> PRT  
 <213> Unknown (H38g213 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(232)  
 <223> Xaa = Any Amino Acid

<400> 1296  
 Ser Gly Leu Val Pro Lys Ser Phe Pro Gly Cys Leu Thr Gln Leu Phe  
 1 5 10 15  
 Phe Leu His Tyr Ser Phe Val Leu Asp Ser Ala Ile Leu Leu Ala Met  
 20 25 30  
 Ala Phe Asp Arg Tyr Met Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr  
 35 40 45  
 Ile Leu Thr Pro Lys Thr Ile Val Lys Ile Ala Val Gly Ile Cys Phe  
 50 55 60  
 Arg Ser Phe Cys Val Phe Val Pro Cys Val Phe Leu Val Asn Arg Leu  
 65 70 75 80  
 Pro Phe Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys Glu His Ile  
 85 90 95  
 Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Ile Trp Cys  
 100 105 110  
 Gly Phe Cys Val Pro Ile Met Thr Val Met Thr Asp Val Ile Leu Ile  
 115 120 125  
 Ala Val Ser Tyr Thr Leu Ile Leu Cys Ala Val Phe Cys Leu Pro Ser  
 130 135 140  
 Gln Asp Ala Arg Gln Lys Ala Leu Cys Ser Cys Gly Ser His Val Cys  
 145 150 155 160  
 Val Ile Leu Ile Phe Tyr Ile Pro Ala Phe Phe Ser Ile Leu Ala His  
 165 170 175  
 Cys Phe Gly His Asn Val Pro His Thr Phe His Ile Met Phe Ala Asn  
 180 185 190  
 Leu Tyr Val Ile Ile Pro Pro Ala Leu Asn Ser Ile Val Tyr Arg Ile  
 195 200 205  
 Lys Thr Lys Gln Ile Gln Asn Arg Ile Leu Leu Leu Phe Pro Lys Gly  
 210 215 220  
 Ser Gln Xaa Xaa Val Pro Glu Leu  
 225 230

<210> 1297  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g214 protein)

<220>  
 <223> Synthetic construct

<400> 1297

```

Met Ser Asn Ala Ser Leu Leu Thr Ala Phe Ile Leu Met Gly Leu Pro
 1          5          10          15
His Ala Pro Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val
          20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35          40          45
Val Asp Ser His Leu His Thr Thr Met Tyr Tyr Phe Leu Thr Asn Leu
          50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Leu Leu
          65          70          75          80
Met Thr Leu Val Phe Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85          90          95
Met Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Gly Thr Glu Cys Phe
          100          105          110
Leu Tyr Arg Val Met Ser Cys Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Thr Gly Arg Ser Cys Thr Leu Leu Ala
          130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Ala Ile
          145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Trp Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Ile Glu Thr Val Ile Phe Val Thr Val Gly Ile Val Ala Ser Gly
          195          200          205
Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
          210          215          220
Leu Arg Ile Arg Thr Ser Glu Gly Lys His Arg Ala Phe Gln Thr Cys
          225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Gly Pro Gly Leu Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Lys Ala Val Asp Gly Val Val Ala
          260          265          270
Val Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Leu Lys Leu Lys Asp Lys
          290          295          300
Val Ala His Ser Gln Ser
          305          310

```

&lt;210&gt; 1298

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g215 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1298

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Leu Gln Ile Leu Leu Phe Thr Leu Phe Leu Ala
          20          25          30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Val Leu Ile
          35          40          45
Gln Ala Asn Ala Trp Leu His Met Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
          65          70          75          80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys

```

```
<210> 1299
<211> 315
<212> PRT
<213> Unknown (H38g216 protein)
```

<220>  
<223> Synthetic construct

<400> 1299															
Met	Leu	Leu	Ser	Asn	Ile	Thr	Gln	Phe	Ser	Pro	Ile	Phe	Tyr	Leu	Thr
1				5					10					15	
Ser	Phe	Pro	Gly	Leu	Glu	Gly	Ile	Lys	His	Trp	Ile	Phe	Ile	Pro	Phe
			20					25					30		
Phe	Phe	Met	Tyr	Met	Val	Ala	Ile	Ser	Gly	Asn	Cys	Phe	Ile	Leu	Ile
		35					40					45			
Ile	Ile	Lys	Thr	Asn	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Tyr	Leu	Leu
	50					55					60				
Ser	Leu	Leu	Ala	Leu	Thr	Asp	Leu	Gly	Leu	Cys	Val	Ser	Thr	Leu	Pro
65					70					75					80
Thr	Thr	Met	Gly	Ile	Phe	Trp	Phe	Asn	Ser	Gln	Ser	Ile	Tyr	Phe	Gly
				85					90					95	
Ala	Cys	Gln	Ile	Gln	Met	Phe	Cys	Ile	His	Ser	Phe	Ser	Phe	Met	Glu
			100					105					110		
Ser	Ser	Val	Leu	Leu	Met	Met	Ser	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys
		115					120					125			
His	Pro	Leu	Arg	Tyr	Ser	Val	Ile	Ile	Thr	Gly	Gln	Gln	Val	Val	Arg
	130					135					140				
Ala	Gly	Leu	Ile	Val	Ile	Phe	Arg	Gly	Pro	Val	Ala	Thr	Ile	Pro	Ile
145					150					155					160
Val	Leu	Leu	Leu	Lys	Ala	Phe	Pro	Tyr	Cys	Gly	Ser	Val	Val	Leu	Ser
				165					170						175

```

His Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp
      180                      185                      190
Thr Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val
      195                      200                      205
Met Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His
      210                      215                      220
Thr Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln
      225                      230                      235                      240
Thr Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met
      245                      250                      255
Met Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala
      260                      265                      270
Ile His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu
      275                      280                      285
Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile
      290                      295                      300
Ile Lys Leu Leu Gly Leu Lys Lys Ala Ser Lys
      305                      310                      315

```

&lt;210&gt; 1300

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g217 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1300

```

Met Asn Pro Glu Asn Trp Thr Gln Val Thr Ser Phe Val Leu Leu Gly
  1                      5                      10                      15
Phe Pro Ser Ser His Leu Ile Gln Phe Leu Val Phe Leu Gly Leu Met
      20                      25                      30
Val Thr Tyr Ile Val Thr Ala Thr Gly Lys Leu Leu Ile Ile Val Leu
      35                      40                      45
Ser Trp Ile Asp Gln Arg Leu His Ile Gln Met Tyr Phe Phe Leu Arg
      50                      55                      60
Asn Phe Ser Phe Leu Glu Leu Leu Leu Val Thr Val Val Val Pro Lys
      65                      70                      75                      80
Met Leu Val Val Ile Leu Thr Gly Asp His Thr Ile Ser Phe Val Ser
      85                      90                      95
Cys Ile Ile Gln Ser Tyr Leu Tyr Phe Phe Leu Gly Thr Thr Asp Phe
      100                      105                      110
Phe Leu Leu Ala Val Met Ser Leu Asp Arg Tyr Leu Ala Ile Cys Arg
      115                      120                      125
Pro Leu Arg Tyr Glu Thr Leu Met Asn Gly His Val Cys Ser Gln Leu
      130                      135                      140
Val Leu Ala Ser Trp Leu Ala Gly Phe Leu Trp Val Leu Cys Pro Thr
      145                      150                      155                      160
Val Leu Met Ala Ser Leu Pro Phe Cys Gly Pro Asn Gly Ile Asp His
      165                      170                      175
Phe Phe Arg Asp Ser Trp Pro Leu Leu Arg Leu Ser Cys Gly Asp Thr
      180                      185                      190
His Leu Leu Lys Leu Val Ala Phe Met Leu Ser Thr Leu Val Leu Leu
      195                      200                      205
Gly Ser Leu Ala Leu Thr Ser Val Ser Tyr Ala Cys Ile Leu Ala Thr
      210                      215                      220
Val Leu Arg Ala Pro Thr Ala Ala Glu Arg Arg Lys Ala Phe Ser Thr
      225                      230                      235                      240
Cys Ala Ser His Leu Thr Val Val Val Ile Ile Tyr Gly Ser Ser Ile
      245                      250                      255
Phe Leu Tyr Ile Arg Met Ser Glu Ala Gln Ser Lys Leu Leu Asn Lys

```

<400>	1301															
Met	Met	Gly	Glu	Ala	Arg	Asn	Arg	Thr	Val	Val	Gln	Glu	Phe	Ile	Leu	
1				5					10					15		
Glu	Gly	Phe	Pro	Ala	Val	Gln	His	Leu	Gly	Asn	Val	Leu	Phe	Leu	Val	
			20					25					30			
His	Leu	Leu	Ala	Tyr	Leu	Ala	Ser	Ile	Met	Ala	Asn	Met	Leu	Ile	Ile	
		35					40					45				
Thr	Ile	Thr	Trp	Ala	Asp	His	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	
	50				55						60					
Leu	Asn	Ser	Phe	Ser	Phe	Cys	Glu	Cys	Cys	Phe	Ile	Thr	Thr	Val	Ile	
65					70					75					80	
Pro	Lys	Leu	Leu	Val	Ile	Phe	Leu	Ser	Gly	Arg	Gln	Ile	Ile	Pro	Phe	
				85					90					95		
Thr	Thr	Cys	Leu	Met	Gln	Ser	Phe	Ser	Phe	Leu	Phe	Leu	Gly	Ser	Thr	
			100					105					110			
Val	Phe	Phe	Leu	Met	Ala	Val	Met	Ser	Leu	Asp	Xaa	Tyr	Leu	Ala	Ile	
		115					120					125				
Cys	Lys	Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Leu	Arg	Thr	Ser	Phe	
	130					135					140					
His	Leu	Val	Thr	Val	Cys	Phe	Val	Val	Gly	Phe	Thr	Leu	Ile	Thr	Gly	
145					150					155					160	
Leu	Met	Val	Lys	Val	Ser	Gln	Leu	Ser	Phe	Cys	Gly	Pro	His	Val	Ile	
				165					170					175		
Pro	His	Phe	Phe	Arg	Asp	Leu	Gly	Pro	Leu	Ile	Gln	Leu	Ser	Cys	Ser	
			180					185					190			
Asp	Thr	Arg	Ser	Thr	Glu	Thr	Leu	Ala	Phe	Val	Leu	Val	Ser	Phe	Val	
	195						200					205				
Leu	Phe	Thr	Ser	Leu	Ile	Ile	Thr	Ile	Ile	Ala	Tyr	Gly	Asn	Ile	Val	
	210					215					220					
Val	Thr	Ile	Val	Arg	Leu	Pro	Ser	Ala	Lys	Glu	Arg	Gln	Lys	Ala	Phe	
225					230					235					240	
Ser	Thr	Cys	Ser	Ser	His	Leu	Ile	Val	Leu	Ser	Leu	Val	Tyr	Gly	Ser	
				245					250					255		
Cys	Val	Phe	Ile	Tyr	Val	Lys	Pro	Lys	Gln	Met	Asp	Arg	Leu	Asp	Ser	
			260					265					270			
Asn	Arg	Met	Ala	Ala	Leu	Val	Asn	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn	
	275						280					285				
Pro	Ile	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Gln	Val	His	Gln	Ala	Leu	Arg	
	290					295					300					



Asp Ala Gln Ser Arg Met Lys Leu Xaa Lys Gln Asn His Asn Leu Gln  
 305 310 315 320  
 Xaa Arg Asn Ala Pro Phe Leu Asp Leu Ile Gln Ser Phe Ser Cys Phe  
 325 330 335  
 Trp Asn

<210> 1302  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g219 protein)

<220>  
 <223> Synthetic construct

<400> 1302  
 Met Ala Ser Thr Ser Asn Val Thr Glu Leu Ile Phe Thr Gly Leu Phe  
 1 5 10 15  
 Gln Asp Pro Ala Val Gln Ser Val Cys Phe Val Val Phe Leu Pro Val  
 20 25 30  
 Tyr Leu Ala Thr Val Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser  
 35 40 45  
 Ile Ser Lys Ser Leu Asp Ser Pro Met Tyr Phe Phe Leu Ser Cys Leu  
 50 55 60  
 Ser Leu Val Glu Ile Ser Tyr Ser Ser Thr Ile Ala Pro Lys Phe Ile  
 65 70 75 80  
 Ile Asp Leu Leu Ala Lys Ile Lys Thr Ile Ser Leu Glu Gly Cys Leu  
 85 90 95  
 Thr Gln Ile Phe Phe Phe His Phe Phe Gly Val Ala Glu Ile Leu Leu  
 100 105 110  
 Ile Val Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Met Asn Ile Ile Ser Arg Gln Leu Cys His Leu Leu Val Ala  
 130 135 140  
 Gly Ser Trp Leu Gly Gly Phe Cys His Ser Ile Ile Gln Ile Leu Val  
 145 150 155 160  
 Ile Ile Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Tyr Phe  
 165 170 175  
 Cys Asp Leu Gln Pro Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Met  
 180 185 190  
 Glu Gly Val Ile Val Leu Ala Asn Ser Gly Leu Phe Ser Val Phe Ser  
 195 200 205  
 Phe Leu Ile Leu Val Ser Ser Tyr Ile Val Ile Leu Val Asn Leu Arg  
 210 215 220  
 Asn His Ser Ala Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ala Ser  
 225 230 235 240  
 His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Ala Ile Phe Leu Tyr  
 245 250 255  
 Met Arg Pro Ser Ser Thr Phe Thr Glu Asp Lys Leu Val Ala Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ala Glu Val Lys Ile Ala Ile Arg Arg Leu Trp Ser Lys Lys Glu  
 290 295 300  
 Asn Pro Gly Arg Glu  
 305

<210> 1303  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g220 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1303

```

Met Ala Lys Gly Asn His Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr Asp Asn Gln Glu Leu Gln Val Ile Leu Phe Gly Val Phe Leu
          20          25          30
Leu Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Val Leu
          35          40          45
Ile His Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ala Phe Val Asp Phe Tyr Gly Thr Ser Ala Ile Thr Pro Asn
 65          70          75          80
Thr Leu Val Asn Ser Leu His Glu Ile Lys Ser Met Ser Phe Tyr Ala
          85          90          95
Cys Ala Thr Gln Val Cys Cys Phe Ile Thr Leu Ser Val Trp Glu Val
          100          105          110
Ile Val Ala Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Val Val Leu Met Pro Arg Arg Leu Cys Ile Gln Met Val
          130          135          140
Thr Gly Leu Tyr Ile Tyr Gly Phe Thr Met Gly Leu Ile Gln Ala Val
          145          150          155          160
Ala Thr Phe His Met Ser Phe Cys Asp Ser Asn Val Val Asn Gln Phe
          165          170          175
Tyr Cys Asp Asp Val Pro Leu Ile Ala Leu Ala Cys Ser Asp Thr Gln
          180          185          190
Val Lys Glu Leu Met Leu Phe Ile Ile Ala Ala Phe Asn Val Phe Cys
          195          200          205
Ser Leu Ile Ile Val Leu Ile Ser Tyr Val Phe Ile Val Phe Ala Ile
          210          215          220
Leu Arg Ile His Ser Ala Val Gly Arg Gln Lys Ala Phe Ser Thr Cys
          225          230          235          240
Ala Ser His Met Phe Ser Ile Ser Ile Tyr Tyr Gly Thr Leu Ser Phe
          245          250          255
Met Tyr Leu Gln Pro Lys Ser Ser His Ser Leu Asp Lys Asp Lys Phe
          260          265          270
Ala Ser Val Phe Tyr Ala Val Val Ile Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Met Lys Lys Ile Ile
          290          295          300
Glu Lys Met Cys Ser Ser Asn Gln Gln Xaa Asn Leu Leu Val Leu Lys
          305          310          315          320
Glu Ile

```

&lt;210&gt; 1304

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g221 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1304

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
 1          5          10          15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
          20          25          30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
          35          40          45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
          50          55          60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
65          70          75          80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
          85          90          95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly
130          135          140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145          150          155          160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
          165          170          175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
          180          185          190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Leu Ile
195          200          205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
210          215          220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225          230          235          240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
          245          250          255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
          260          265          270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
          275          280          285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
290          295          300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305          310          315

```

&lt;210&gt; 1305

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g222 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1305

```

Met Asn Pro Ala Asn His Ser Gln Val Ala Gly Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Gln Val Trp Glu Leu Arg Phe Val Phe Phe Thr Val Phe Ser
          20          25          30
Ala Val Tyr Phe Met Thr Val Val Gly Asn Leu Leu Ile Val Val Ile
          35          40          45
Val Thr Ser Asp Pro His Leu His Thr Thr Met Tyr Phe Leu Leu Gly
          50          55          60
Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Ile Thr Ala Pro Arg
65          70          75          80
Met Leu Val Asp Leu Leu Ser Gly Asn Pro Thr Ile Ser Phe Gly Gly

```

```

      85              90              95
Cys Leu Thr Gln Leu Phe Phe Phe His Phe Ile Gly Gly Ile Lys Ile
      100              105              110
Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
      115              120              125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Thr Val Cys Ala Leu Leu
      130              135              140
Met Ala Ala Ser Trp Val Gly Gly Phe Ile His Ser Ile Val Gln Ile
      145              150              155              160
Ala Leu Thr Ile Gln Leu Pro Phe Cys Gly Pro Asp Lys Leu Asp Asn
      165              170              175
Phe Tyr Cys Asp Val Pro Gln Leu Ile Lys Leu Ala Cys Thr Asp Thr
      180              185              190
Phe Val Leu Glu Leu Leu Met Val Ser Asn Asn Gly Leu Val Thr Leu
      195              200              205
Met Trp Phe Leu Val Leu Leu Gly Ser Tyr Thr Ala Leu Leu Val Met
      210              215              220
Leu Arg Ser His Ser Arg Glu Gly Arg Ser Lys Ala Leu Ser Thr Cys
      225              230              235              240
Ala Ser His Ile Ala Val Val Thr Leu Ile Phe Val Pro Cys Ile Tyr
      245              250              255
Val Tyr Thr Arg Pro Phe Arg Thr Phe Pro Met Asp Lys Ala Val Ser
      260              265              270
Val Leu Tyr Thr Ile Val Thr Pro Met Leu Asn Pro Ala Ile Tyr Thr
      275              280              285
Leu Arg Asn Lys Glu Val Ile Met Ala Met Lys Lys Leu Trp Arg Arg
      290              295              300
Lys Lys Asp Pro Ile Gly Pro Leu Glu His Arg
      305              310              315

```

&lt;210&gt; 1306

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g223 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1306

```

Met Ser Phe Leu Asn Gly Thr Ser Leu Thr Pro Ala Ser Phe Ile Leu
  1              5              10              15
Asn Gly Ile Pro Gly Leu Glu Asp Val His Leu Trp Ile Ser Phe Pro
      20              25              30
Leu Cys Thr Met Tyr Ser Ile Ala Ile Thr Gly Asn Phe Gly Leu Met
      35              40              45
Tyr Leu Ile Tyr Cys Asp Glu Ala Leu His Arg Pro Met Tyr Val Phe
      50              55              60
Leu Ala Leu Leu Ser Phe Thr Asp Val Leu Met Cys Thr Ser Thr Leu
      65              70              75              80
Pro Asn Thr Leu Phe Ile Leu Trp Phe Asn Leu Lys Glu Ile Asp Phe
      85              90              95
Lys Ala Cys Leu Ala Gln Met Phe Phe Val His Thr Phe Thr Gly Met
      100              105              110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp His Cys Val Ala Ile
      115              120              125
Cys Phe Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Ser Val Ile Ala
      130              135              140
Lys Ala Gly Phe Leu Thr Phe Leu Arg Gly Val Met Leu Val Ile Pro
      145              150              155              160
Ser Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Lys Gly Asn Val Ile
      165              170              175

```

```

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly
      180      185      190
Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile
      195      200      205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
      210      215      220
Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
      225      230      235      240
Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro
      245      250      255
Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro
      260      265      270
Leu His Ile His Ile Ile Met Ala Asn Leu Tyr Leu Leu Met Pro Pro
      275      280      285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Arg Gln Val Arg Glu
      290      295      300
Ser Val Ile Arg Phe Phe Leu Lys Gly Lys Asp Asn Ser His Asn Phe
      305      310      315      320

```

&lt;210&gt; 1307

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g224 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1307

```

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
  1      5      10      15
Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
      20      25      30
Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
      35      40      45
Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
      50      55      60
Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
      65      70      75      80
Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
      85      90      95
Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
      100      105      110
Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
      130      135      140
Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
      145      150      155      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
      165      170      175
Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
      180      185      190
Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
      195      200      205
Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
      210      215      220
Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser
      225      230      235      240
His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
      245      250      255
Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe

```

260 265 270  
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg  
 275 280 285  
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val  
 290 295 300  
 Ile  
 305

<210> 1308  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g225 protein)

<220>  
 <223> Synthetic construct

<400> 1308  
 Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly  
 1 5 10 15  
 Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu  
 20 25 30  
 Val Leu Tyr Gly Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu  
 35 40 45  
 Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln  
 50 55 60  
 His Leu Ala Leu Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys  
 65 70 75 80  
 Met Leu Ile Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu  
 85 90 95  
 Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val  
 100 105 110  
 Ile Met Leu Ala Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu  
 130 135 140  
 Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser  
 145 150 155 160  
 Ser Tyr Val Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His  
 165 170 175  
 Phe Tyr Cys Asp Asn Val Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr  
 180 185 190  
 Tyr Leu Pro Glu Thr Val Val Phe Ile Ser Ala Ala Thr Asn Val Val  
 195 200 205  
 Gly Ser Leu Ile Ile Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser  
 210 215 220  
 Ile Leu Lys Ile Cys Ser Ser Glu Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Met Met Ala Val Thr Ile Phe Tyr Gly Thr Leu Leu  
 245 250 255  
 Phe Met Tyr Val Gln Pro Arg Ser Asn His Ser Leu Asp Thr Asp Asp  
 260 265 270  
 Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Thr Ala Leu Gln Arg  
 290 295 300  
 Phe Met Thr Asn Leu Cys Tyr Ser Phe  
 305 310

<210> 1309  
 <211> 326  
 <212> PRT

<213> Unknown (H38g226 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1309

```

Met Lys Ile Ser Asn Asn Ser Leu Gly Phe Leu Pro Thr Thr Phe Ile
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Ser Glu His Leu Trp Ile Ser Val
          20           25           30
Pro Phe Ser Leu Ile Tyr Ile Ile Ile Phe Leu Gly Asn Gly Ile Ile
          35           40           45
Leu His Val Ile Arg Thr Asp Ile Ala Leu His Gln Pro Met Tyr Leu
          50           55           60
Phe Leu Ala Met Leu Ala Leu Ala Glu Val Arg Val Ser Ala Ser Thr
65           70           75           80
Leu Pro Thr Val Leu Gly Ile Phe Leu Phe Gly Asn Thr Glu Ile Ser
          85           90           95
Leu Glu Ala Phe Phe Phe Gln Met Phe Ser Ile His Ser Leu Ser Met
          100          105          110
Met Glu Ser Ala Val Leu Leu Ala Met Ser Leu Asp Arg Phe Ile Ala
          115          120          125
Ile Tyr Ser Pro Leu Ser Tyr Thr Ala Ile Leu Thr Leu Pro Arg Val
          130          135          140
Phe Gly Thr Gly Ala Ile Ile Val Leu Lys Ser Ile Met Leu Met Ala
145          150          155          160
Pro Leu Pro Ile Leu Leu Trp Arg Leu Pro Phe Cys Gly His Asn Ala
          165          170          175
Leu Ser His Ser Tyr Cys Leu His Pro Asn Leu Ile Tyr Leu Ser Cys
          180          185          190
Gly Asn Ile Ser Val Asn Asn Ile Tyr Gly Ile Phe Ile Val Thr Ser
          195          200          205
Thr Phe Gly Leu Asp Ser Leu Leu Ile Val Ile Ser Tyr Gly Leu Ile
          210          215          220
Leu His Thr Val Leu Gly Ile Ala Thr Gly Glu Gly Arg Lys Lys Ala
225          230          235          240
Leu Asn Thr Cys Gly Ser His Val Cys Ala Val Leu Ala Tyr Tyr Val
          245          250          255
Pro Met Ile Gly Leu Ser Ile Val His Arg Leu Gly His Arg Val Ser
          260          265          270
Pro Leu Leu Gln Ala Met Met Ala Asn Ala Tyr Leu Phe Phe Pro Pro
          275          280          285
Val Val Asn Pro Ile Val Tyr Ser Ile Lys Thr Lys Glu Ile His Gly
          290          295          300
Ala Ile Val Arg Met Leu Leu Glu Lys Arg Arg Arg Val Xaa Pro Lys
305          310          315          320
Thr Ile Val Gly Arg Asn
          325

```

<210> 1310

<211> 311

<212> PRT

<213> Unknown (H38g227 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1310

```

Met Ser Lys Thr Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1          5          10          15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
      20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
      35          40          45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
      50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
      65          70          75          80
Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
      85          90          95
Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
      100          105          110
Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
      115          120          125
Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
      130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
      145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
      165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
      180          185          190
Ala Asn Glu Met Val Ile Phe Val Asp Ile Gly Leu Val Ala Ser Gly
      195          200          205
Cys Phe Leu Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
      210          215          220
Leu Arg Ile His Thr Ser Glu Gly Arg His Arg Ala Phe Gln Thr Cys
      225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Phe
      245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Asp Val Val Asp Gly Val Val Ala
      260          265          270
Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
      275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
      290          295          300
Val Ala His Ser Gln Gly Glu
305          310

```

&lt;210&gt; 1311

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g228 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1311

```

Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
      20          25          30
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
      35          40          45
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
      50          55          60
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
      65          70          75          80

```



```
<210> 1312
<211> 303
<212> PRT
<213> Unknown (H38g229 protein)
```

<220>  
<223> Synthetic construct

627

```
<210> 1313
<211> 316
<212> PRT
<213> Unknown (H38g230 protein)
```

<400> 1313																
Leu	Ile	Ala	Thr	Gly	Asn	Trp	Thr	Arg	Ile	Ser	Glu	Phe	Ile	Leu	Met	
1				5					10					15		
Ser	Phe	Ser	Ser	Leu	Pro	Thr	Glu	Ile	Gln	Ser	Leu	Leu	Phe	Leu	Thr	
			20					25					30			
Phe	Leu	Thr	Ile	Tyr	Leu	Val	Thr	Leu	Met	Gly	Asn	Cys	Leu	Ile	Ile	
		35					40					45				
Leu	Val	Thr	Leu	Ala	Asp	Pro	Met	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	
	50					55					60					
Leu	Arg	Asn	Leu	Ser	Phe	Leu	Glu	Ile	Gly	Phe	Asn	Leu	Val	Ile	Val	
65					70					75					80	
Pro	Lys	Met	Leu	Gly	Thr	Leu	Leu	Ala	Gln	Asp	Thr	Thr	Ile	Ser	Phe	
				85					90					95		
Leu	Gly	Cys	Ala	Thr	Gln	Met	Tyr	Phe	Phe	Phe	Phe	Phe	Gly	Val	Ala	
			100					105					110			
Glu	Cys	Phe	Leu	Gln	Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	
		115					120					125				
Cys	Ser	Pro	Leu	His	Tyr	Pro	Val	Ile	Met	Asn	Gln	Arg	Thr	Arg	Ala	
	130					135					140					
Lys	Leu	Ala	Ala	Ala	Ser	Trp	Phe	Pro	Gly	Phe	Pro	Val	Ala	Thr	Val	
145					150					155					160	
Gln	Thr	Thr	Trp	Leu	Phe	Ser	Phe	Pro	Phe	Cys	Gly	Thr	Asn	Lys	Val	
			165						170					175		
Asn	His	Phe	Phe	Cys	Asp	Ser	Pro	Pro	Val	Leu	Arg	Leu	Val	Cys	Ala	
		180						185					190			
Asp	Thr	Ala	Leu	Phe	Glu	Ile	Tyr	Ala	Ile	Val	Gly	Thr	Ile	Leu	Val	
		195					200					205				
Val	Met	Ile	Pro	Cys	Leu	Leu	Ile	Leu	Cys	Ser	Tyr	Thr	Arg	Ile	Ala	
	210					215					220					
Ala	Ala	Ile	Leu	Lys	Ile	Pro	Ser	Ala	Lys	Gly	Lys	Asn	Lys	Ala	Phe	
225					230					235					240	
Ser	Thr	Cys	Ser	Ser	His	Leu	Leu	Val	Val	Ser	Leu	Phe	Tyr	Ile	Ser	
			245						250					255		
Leu	Ser	Leu	Thr	Tyr	Phe	Arg	Pro	Lys	Ser	Asn	Asn	Ser	Pro	Glu	Gly	
			260					265					270			

Thr Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn  
           275                          280                          285  
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser  
           290                          295                          300  
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu  
 305                          310                          315

&lt;210&gt; 1314

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g231 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1314

Met Pro Asn Phe Thr Asp Val Thr Glu Phe Thr Leu Leu Gly Leu Thr  
   1                  5                  10                  15  
 Cys Arg Gln Glu Leu Gln Val Leu Phe Phe Val Val Phe Leu Ala Val  
           20                  25                  30  
 Tyr Met Ile Thr Leu Leu Gly Asn Ile Gly Met Ile Ile Leu Ile Ser  
           35                  40                  45  
 Ile Ser Pro Gln Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His Leu  
   50                  55                  60  
 Ser Phe Ala Asp Val Cys Phe Ser Ser Asn Val Thr Pro Lys Met Leu  
   65                  70                  75                  80  
 Glu Asn Leu Leu Ser Glu Thr Lys Thr Ile Ser Tyr Val Gly Cys Leu  
           85                  90                  95  
 Val Gln Cys Tyr Phe Phe Ile Ala Val Val His Val Glu Val Tyr Ile  
           100                  105                  110  
 Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Gly Cys Asn Pro Leu  
           115                  120                  125  
 Leu Tyr Gly Ser Lys Met Ser Arg Thr Val Cys Val Arg Leu Ile Ser  
   130                  135                  140  
 Val Pro Tyr Val Tyr Gly Phe Ser Val Ser Leu Ile Cys Thr Leu Trp  
   145                  150                  155                  160  
 Thr Tyr Gly Leu Tyr Phe Cys Gly Asn Phe Glu Ile Asn His Phe Tyr  
           165                  170                  175  
 Cys Ala Asp Pro Pro Leu Ile Gln Ile Ala Cys Gly Arg Val His Ile  
           180                  185                  190  
 Lys Glu Ile Thr Met Ile Val Ile Ala Gly Ile Asn Phe Thr Tyr Ser  
           195                  200                  205  
 Leu Ser Val Val Leu Ile Ser Tyr Thr Leu Ile Val Val Ala Val Leu  
   210                  215                  220  
 Arg Met Arg Ser Ala Asp Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly  
   225                  230                  235                  240  
 Ser His Leu Thr Ala Val Ser Met Phe Tyr Gly Thr Pro Ile Phe Met  
           245                  250                  255  
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val  
           260                  265                  270  
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr  
           275                  280                  285  
 Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Val Asn Lys Ala Ile Thr  
   290                  295                  300  
 Lys Thr Tyr Val Arg  
 305

&lt;210&gt; 1315

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g232 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1315

```

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1           5           10           15
Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Ile Leu
 35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
 50           55           60
Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
          85           90           95
Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
          100          105          110
Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
          130          135          140
Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
          145          150          155          160
Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
          180          185          190
Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
          195          200          205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val
          210          215          220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
          225          230          235          240
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
          245          250          255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
          260          265          270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
          275          280          285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
          290          295          300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
          305          310          315          320

```

&lt;210&gt; 1316

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g233 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1316

```

Met Glu Gln His Asn Leu Thr Thr Val Asn Glu Phe Ile Leu Thr Gly
 1           5           10           15
Ile Thr Asp Ile Ala Glu Leu Gln Ala Pro Leu Phe Ala Leu Phe Leu
          20           25           30
Met Ile Tyr Val Ile Ser Val Met Gly Asn Leu Gly Met Ile Val Leu
          35           40           45

```

Thr Lys Leu Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 His Leu Ala Phe Met Asp Leu Gly Tyr Ser Thr Val Gly Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Val Val Asp Lys Asn Ile Ile Ser Tyr Tyr Phe  
 85 90 95  
 Cys Ala Thr Gln Leu Ala Phe Phe Leu Val Phe Ile Gly Ser Glu Leu  
 100 105 110  
 Phe Ile Leu Ser Ala Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ile Met Ser Arg Arg Val Cys Gln Val Leu  
 130 135 140  
 Val Ala Ile Pro Tyr Leu Tyr Cys Thr Phe Ile Ser Leu Leu Val Thr  
 145 150 155 160  
 Ile Lys Ile Phe Thr Leu Ser Phe Cys Gly Tyr Asn Val Ile Ser His  
 165 170 175  
 Phe Tyr Cys Asp Ser Leu Pro Leu Leu Pro Leu Leu Cys Ser Asn Thr  
 180 185 190  
 His Glu Ile Glu Leu Ile Ile Leu Ile Phe Ala Ala Ile Asp Leu Ile  
 195 200 205  
 Ser Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala  
 210 215 220  
 Ile Leu Arg Met Asn Ser Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe  
 245 250 255  
 Met Tyr Val Gln Pro Lys Ser Ser His Ser Phe Asp Thr Asp Lys Val  
 260 265 270  
 Ala Ser Ile Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Arg Arg Thr Trp  
 290 295 300  
 Asn Asn Leu Cys Asn Ile Phe Val  
 305 310

&lt;210&gt; 1317

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g234 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1317

Met Met Trp Glu Asn Trp Thr Ile Val Ser Glu Phe Val Leu Val Ser  
 1 5 10 15  
 Phe Ser Ala Leu Ser Thr Glu Leu Gln Ala Leu Leu Phe Leu Leu Phe  
 20 25 30  
 Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Val Leu Ile Ile Leu  
 35 40 45  
 Val Thr Ile Ala Asp Ser Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro  
 65 70 75 80  
 Lys Met Leu Gly Thr Leu Ile Ile Gln Asp Thr Thr Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Ala Ala Glu  
 100 105 110  
 Cys Cys Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asp Pro Leu His Tyr Pro Val Ile Met Gly His Ile Ser Cys Ala Gln

```

130          135          140
Leu Ala Ala Ala Ser Trp Phe Ser Gly Phe Ser Val Ala Thr Val Gln
145          150          155          160
Thr Thr Trp Ile Phe Ser Phe Pro Phe Cys Gly Pro Asn Arg Val Asn
          165          170          175
His Phe Phe Cys Asp Ser Pro Pro Val Ile Ala Leu Val Cys Ala Asp
          180          185          190
Thr Ser Val Phe Glu Leu Glu Ala Leu Thr Ala Thr Val Pro Phe Ile
          195          200          205
Leu Phe Pro Phe Leu Leu Ile Leu Gly Ser Tyr Val Arg Ile Leu Ser
          210          215          220
Thr Ile Phe Arg Met Pro Ser Ala Glu Gly Lys His Gln Ala Phe Ser
225          230          235          240
Thr Cys Ser Ala His Leu Leu Val Val Ser Leu Phe Tyr Ser Thr Ala
          245          250          255
Ile Leu Thr Tyr Phe Arg Pro Gln Ser Ser Ala Ser Ser Glu Ser Lys
          260          265          270
Lys Leu Leu Ser Leu Ser Ser Thr Val Val Thr Pro Met Leu Asn Pro
          275          280          285
Ile Ile Tyr Ser Ser Arg Asn Lys Glu Val Lys Ala Ala Leu Lys Arg
          290          295          300
Leu Ile His Arg Thr Leu Gly Ser Gln Lys Leu
305          310          315

```

&lt;210&gt; 1318

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g235 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1318

```

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
1      5      10      15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
          20      25      30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
          35      40      45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
          50      55      60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ser Ile Thr Pro Asn
65      70      75      80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
          85      90      95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
          100     105     110
Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115     120     125
Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
          130     135     140
Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
145     150     155     160
Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
          165     170     175
Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
          180     185     190

```

His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe  
           195                          200                          205  
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val  
           210                          215                          220  
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala  
 225                          230                          235                          240  
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly  
                           245                          250                          255  
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp  
                           260                          265                          270  
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile  
           275                          280                          285  
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met  
           290                          295                          300  
 Glu Asn Leu Cys Leu Thr  
 305                          310

&lt;210&gt; 1319

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g236 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(184)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1319

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr  
   1                  5                  10                  15  
 His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile  
                   20                  25                  30  
 Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser  
                   35                  40                  45  
 His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu  
   50                  55                  60  
 Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys  
 65                  70                  75                  80  
 Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His  
                   85                  90                  95  
 Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile  
                   100                  105                  110  
 Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His  
           115                  120                  125  
 Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val  
   130                  135                  140  
 Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys  
 145                  150                  155                  160  
 Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr  
                   165                  170                  175  
 Val Tyr Leu Gln Pro Asp Phe Phe  
                   180

&lt;210&gt; 1320

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g237 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1320

```

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1           5           10           15
Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro
      20           25           30
Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
      35           40           45
Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
 50           55           60
Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
65           70           75           80
Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
      85           90           95
Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
      100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
130          135          140
Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
145          150          155          160
Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
      165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
      180          185          190
Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
      195          200          205
Gly Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu
210          215          220
Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230          235          240
Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
      245          250          255
Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
      260          265          270
Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
      275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
      290          295          300
Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
305          310          315          320
Lys

```

&lt;210&gt; 1321

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g238 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(134)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1321

```

Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1           5           10           15

```



Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg  
                   20                  25                  30  
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln  
                   35                  40                  45  
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser  
                   50                  55                  60  
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly  
 65                  70                  75                  80  
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln  
                   85                  90                  95  
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser  
                   100                  105                  110  
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Gly Lys Xaa Ser Gly Glu Arg  
                   115                  120                  125  
 Ser Ser Phe Pro Arg Glu  
                   130

&lt;210&gt; 1322

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g239 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1322

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr  
   1                  5                  10                  15  
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro  
                   20                  25                  30  
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn  
                   35                  40                  45  
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro  
                   50                  55                  60  
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser  
 65                  70                  75                  80  
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys  
                   85                  90                  95  
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val  
                   100                  105                  110  
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg  
                   115                  120                  125  
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro  
                   130                  135                  140  
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile  
 145                  150                  155                  160  
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser  
                   165                  170                  175  
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala  
                   180                  185                  190  
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe  
                   195                  200                  205  
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr  
                   210                  215                  220  
 Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg  
 225                  230                  235                  240  
 Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val

				245					250					255	
Phe	Tyr	Gly	Thr	Leu	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Arg	Ser	Asn	His
			260					265					270		
Ser	Leu	Asp	Thr	Asp	Lys	Met	Ala	Ser	Val	Phe	Tyr	Thr	Leu	Val	Ile
		275					280					285			
Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asn	Val	Lys
		290				295					300				
Asp	Ala	Leu	Lys	Arg	Phe	Leu	Asp	Asn	Pro	Cys	Arg	Ser	Leu		
305					310					315					

**<210> 1323**

**<211> 315**

<212> PRT

<213> Unknown (H38g240 protein)

**<220>**

**<223> Synthetic construct**

**<400> 1323**

Met 1	Leu	Ser	Pro	Asn 5	His	Thr	Ile	Val 10	Thr	Glu	Phe	Ile	Leu 15	Leu	Gly
Leu	Thr	Asp 20	Asp	Pro	Val	Leu	Glu 25	Lys	Ile	Leu	Phe	Gly 30	Val	Phe	Leu
Ala	Ile	Tyr 35	Leu	Ile	Thr	Leu	Ala 40	Gly	Asn	Leu	Cys	Met 45	Ile	Leu	Leu
Ile	Arg 50	Thr	Asn	Ser	Gln 55	Leu	Gln	Thr	Pro	Met 60	Tyr	Phe	Phe	Leu	Gly
His 65	Leu	Ser	Phe	Val 70	Asp	Ile	Cys	Tyr	Ser	Ser 75	Asn	Val	Thr	Pro	Asn 80
Met	Leu	His	Asn 85	Phe	Leu	Ser	Glu	Gln 90	Thr	Ile	Ser	Tyr 95	Ala	Gly	
Cys	Phe	Thr 100	Gln	Cys	Leu	Leu	Phe 105	Ile	Ala	Leu	Val	Ile 110	Thr	Glu	Phe
Tyr	Phe	Leu 115	Ala	Ser	Met	Ala	Leu 120	Asp	Arg	Tyr	Val	Ala 125	Ile	Cys	Ser
Pro	Leu	His 130	Tyr	Ser	Ser 135	Arg	Met	Ser	Lys	Asn 140	Ile	Cys	Ile	Ser	Leu
Val 145	Thr	Val	Pro	Tyr 150	Met	Tyr	Gly	Phe	Leu	Asn 155	Gly	Leu	Ser	Gln	Thr 160
Leu	Leu	Thr 165	Phe	His	Leu	Ser	Phe 170	Cys	Gly	Ser	Leu	Glu 175	Ile	Asn	His 180
Phe	Tyr	Cys 180	Ala	Asp	Pro	Pro	Leu 185	Ile	Met	Leu	Ala	Cys 190	Ser	Asp	Thr
Arg	Val	Lys 195	Lys	Met	Ala	Met	Phe 200	Val	Val	Ala	Gly	Phe 205	Thr	Leu	Ser
Ser	Ser	Leu 210	Phe	Ile	Ile	Leu	Leu 215	Ser	Tyr	Leu	Phe	Ile 220	Phe	Ala	Ala
Ile 225	Phe	Arg	Ile	Arg 230	Ser	Ala	Glu	Gly	Arg	His 235	Lys	Ala	Phe	Ser	Thr 240
Cys	Ala	Ser	His 245	Leu	Thr	Ile	Val	Thr	Leu	Phe 250	Tyr	Gly	Thr	Leu	Phe 255
Cys	Met	Tyr 260	Val	Arg	Pro	Pro	Ser 265	Glu	Lys	Ser	Val	Glu 270	Glu	Ser	Lys
Ile	Ile	Ala 275	Val	Phe	Tyr	Thr	Phe 280	Leu	Ser	Pro	Met	Leu 285	Asn	Pro	Leu
Ile	Tyr	Ser 290	Leu	Arg	Asn 295	Arg	Asp	Val	Ile	Leu	Ala 300	Ile	Gln	Gln	Met
Ile 305	Arg	Gly	Lys	Ser 310	Phe	Cys	Lys	Ile	Ala	Val 315					

**<210> 1324**

<211> 313  
 <212> PRT  
 <213> Unknown (H38g241 protein)

<220>  
 <223> Synthetic construct

<400> 1324  
 Met Pro Ile Ala Asn Asp Thr Gln Phe His Thr Ser Ser Phe Leu Leu  
 1 5 10 15  
 Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Phe Pro  
 20 25 30  
 Phe Phe Ser Val Tyr Leu Ile Ala Leu Leu Gly Asn Ala Ala Ile Phe  
 35 40 45  
 Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Cys  
 50 55 60  
 Leu Ala Met Leu Asp Ser Ile Asp Leu Ser Leu Ser Thr Ala Thr Ile  
 65 70 75 80  
 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Ile Lys Glu Ile Ser Phe  
 85 90 95  
 Gly Gly Tyr Leu Ser Gln Met Phe Phe Ile His Phe Phe Thr Val Met  
 100 105 110  
 Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile  
 115 120 125  
 Cys Lys Pro Leu Trp Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser  
 130 135 140  
 Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Ile Pro  
 145 150 155 160  
 Leu Val Phe Leu Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile  
 165 170 175  
 Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala  
 180 185 190  
 Ser Ile Lys Val Asn Ile Met Phe Gly Leu Gly Ser Ile Ser Leu Leu  
 195 200 205  
 Leu Leu Asp Val Leu Leu Ile Ile Leu Ser His Ile Arg Ile Leu Tyr  
 210 215 220  
 Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Ser Thr Pro Ala  
 245 250 255  
 Phe Phe Ser Phe Phe Thr His Cys Phe Gly His Asp Ile Pro Gln Tyr  
 260 265 270  
 Ile His Ile Phe Leu Ala Asn Leu Tyr Val Val Val Pro Pro Thr Leu  
 275 280 285  
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys His Ile Arg Glu Thr Val  
 290 295 300  
 Leu Arg Ile Phe Phe Lys Thr Asp His  
 305 310

<210> 1325  
 <211> 328  
 <212> PRT  
 <213> Unknown (H38g242 protein)

<220>  
 <223> Synthetic construct

<400> 1325  
 Met His Ile Phe Lys Phe Val Leu Asp Phe Asn Met Lys Asn Val Thr  
 1 5 10 15  
 Glu Val Thr Leu Phe Val Leu Lys Gly Phe Thr Asp Asn Leu Glu Leu

```

      20      25      30
Gln Thr Ile Phe Phe Phe Leu Phe Leu Ala Ile Tyr Leu Phe Thr Leu
      35      40      45
Met Gly Asn Leu Gly Leu Ile Leu Val Val Ile Arg Asp Ser Gln Leu
      50      55      60
His Lys Pro Met Tyr Tyr Phe Leu Ser Met Leu Ser Ser Val Asp Ala
      65      70      75      80
Cys Tyr Ser Ser Val Ile Thr Pro Asn Met Leu Val Asp Phe Thr Thr
      85      90      95
Lys Asn Lys Val Ile Ser Phe Leu Gly Cys Val Ala Gln Val Phe Leu
      100      105      110
Ala Cys Ser Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala
      115      120      125
Tyr Asp Arg Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser
      130      135      140
Met Ser Pro Arg Val Tyr Met Pro Leu Ile Asn Ala Ser Tyr Val Ala
      145      150      155      160
Gly Ile Leu His Ala Thr Ile His Thr Val Ala Thr Phe Ser Leu Ser
      165      170      175
Phe Cys Gly Ala Asn Glu Ile Arg Arg Val Phe Cys Asp Ile Pro Pro
      180      185      190
Leu Leu Ala Ile Ser Tyr Ser Asp Thr His Thr Asn Gln Leu Leu Leu
      195      200      205
Phe Tyr Phe Val Gly Ser Ile Glu Leu Val Thr Ile Leu Ile Val Leu
      210      215      220
Ile Ser Tyr Gly Leu Ile Leu Leu Ala Ile Leu Lys Met Tyr Ser Ala
      225      230      235      240
Glu Gly Arg Arg Lys Val Phe Ser Thr Cys Gly Ala His Leu Thr Gly
      245      250      255
Val Ser Ile Tyr Tyr Gly Thr Ile Leu Phe Met Tyr Val Arg Pro Ser
      260      265      270
Ser Ser Tyr Ala Ser Asp His Asp Met Ile Val Ser Ile Phe Tyr Thr
      275      280      285
Ile Val Ile Pro Leu Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys
      290      295      300
Asp Val Lys Asp Ser Met Lys Lys Met Phe Gly Lys Asn Gln Val Ile
      305      310      315      320
Asn Lys Val Tyr Phe His Thr Lys
      325

```

&lt;210&gt; 1326

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g243 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1326

```

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu
      1      5      10      15
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro
      20      25      30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile
      35      40      45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe
      50      55      60

```

```

Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val
65          70          75          80
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe
          85          90          95
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met
          100         105         110
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
          115         120         125
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr
          130         135         140
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro
145          150         155         160
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile
          165         170         175
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly
          180         185         190
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile
          195         200         205
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile
          210         215         220
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230         235         240
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro
          245         250         255
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro
          260         265         270
His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
          275         280         285
Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
          290         295         300
Gly Val Ile Lys Leu Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
305          310         315         320
Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
          325

```

&lt;210&gt; 1327

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g244 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(301)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1327

```

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
1          5          10          15
Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
          20          25          30
Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
          35          40          45
Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
          50          55          60
Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
65          70          75          80
Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
          85          90          95
Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro

```

100	105	110
Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr		
115	120	125
Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe		
130	135	140
Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val		
145	150	155
Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp		
165	170	175
Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly		
180	185	190
Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile		
195	200	205
Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser		
210	215	220
Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val		
225	230	235
Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr		
245	250	255
Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu		
260	265	270
Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met		
275	280	285
Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu		
290	295	300

&lt;210&gt; 1328

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g245 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1328

Gly Ser Xaa Lys Gln Xaa Lys Ser Xaa Pro Pro Ile Phe Phe Leu Thr		
1	5	10
Gly Ile Pro Gly Leu Glu Ala Gln His Gly Trp Leu Ser Ile Pro Phe		
20	25	30
Phe Thr Met Tyr Ile Val Ala Ile Val Gly Asn Ile Leu Ile Met Ala		
35	40	45
Ala Val Gln Glu Asp Ser Ala Leu His Glu Pro Met Tyr Leu Phe Leu		
50	55	60
Ser Met Leu Ala Val Thr Glu Val Gly Val Ser Val Ser Thr Leu Pro		
65	70	75
Thr Val Thr Gly Ile Leu Trp Phe Asp Ala His Arg Val Asp Phe Asp		
85	90	95
Gly Cys Leu Ala Gln Met Phe Phe Ile His Thr Phe Ser Cys Met Glu		
100	105	110
Ser Gly Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Tyr		
115	120	125
Asn Leu Leu Arg Tyr Thr Ala Ile Leu Thr Leu Pro Arg Ile Ile Cys		
130	135	140
Met Gly Leu Gly Ile Thr Leu Lys Ser Val Ala Leu Met Ala Pro Leu		
145	150	155
Pro Ile Leu Leu Arg Gln Leu Pro Tyr Cys His Thr Asn Val Leu Ser		
165	170	175

```

His Ser Tyr Cys Leu His Ser Asp Leu Ile Gln Leu Pro Cys Ala Asp
      180      185      190
Thr Lys Leu Asn Ser Ile Leu Gly Leu Ala Ile Val Leu Ala Asn Phe
      195      200      205
Gly Leu Asp Ser Leu Leu Ile Val Val Ser Tyr Val Leu Ile Leu Tyr
      210      215      220
Thr Val Met Gly Ile Ala Ser Gly Glu Gly Arg Trp Lys Ala Leu Asn
      225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Tyr Tyr Val Pro Met
      245      250      255
Ile Gly Val Ser Val Met His Arg Ala Ala Lys His Ala Ser Pro Ile
      260      265      270
Val His Thr Leu Met Ser Ser Ile Cys Leu Leu Val Pro Pro Val Leu
      275      280      285
Asn Pro Ile Ile Tyr Ser Val Lys Thr Gln Thr Ile Arg Gln Gly Ile
      290      295      300
Leu Thr Leu Phe Ser Cys Lys Arg Glu Leu Leu Xaa Ile Thr Ala Arg
      305      310      315      320
Ser Gln Glu Leu

```

&lt;210&gt; 1329

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g246 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(292)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1329

```

Thr Leu Phe Ile Ile Ser Lys Phe Gln Gly Cys Xaa Lys Val Gly Leu
  1      5      10      15
Tyr Thr Gln Ser Leu Tyr Leu Leu Ala Glu Tyr Phe His Arg Gly Gln
      20      25      30
Leu Met Lys Met Leu Thr Ser Thr Asn Leu Ser Leu Ser Val Val Thr
      35      40      45
Ile Gly Ile Phe Gln Phe Asn Val Arg Glu Ile Val Phe Gly Ala Phe
      50      55      60
Leu Val Tyr Ile Gln Met Phe Met Thr Tyr Leu Cys Thr Gly Leu Glu
      65      70      75      80
Ser Gly Val Leu Ile Ile Leu Ala Ile Asp His Tyr Val Val Ile Arg
      85      90      95
Asn Pro Leu Arg Tyr Thr Met Ile Leu Met Asn Asn Val Val Ala Ile
      100      105      110
Leu Gly Val Met Ile Ile Arg Ser Leu Ile Phe Ile Ile Pro Phe Glu
      115      120      125
Phe Leu Ile Leu Leu Leu Ser Phe Cys Ala Ala His Ile Ile Pro His
      130      135      140
Thr Lys Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ala Ser Val
      145      150      155      160
Arg Ala Asn Asn Met Phe Gly Met Val Ala Phe Ser Val Gly Phe Ile
      165      170      175
Asp Leu Ile Ala Ile Gly Phe Ser Tyr Val Lys Lys Leu Arg Ala Leu
      180      185      190
Phe His Leu Pro Pro Trp Asn Gly Gln Phe Glu Ala Leu Asn Thr Cys
      195      200      205
Gly Ser His Val Cys Met Leu Ile Phe Tyr Ile Pro Val Phe Phe Phe

```

210		215		220
Xaa Tyr Thr Ala Trp	Xaa Lys His Pro Cys	Tyr Ile Arg Ile Phe Leu		
225	230	235	240	
Ala Asn Val Tyr Thr	Val Val Leu Pro Val Phe	Asn Pro Val Ile Tyr		
	245	250	255	
Gly Ile Arg Lys Lys Gln	Ile Pro Asp Xaa Gly	Ile Asp L u Lys Thr		
	260	265	270	
Phe Asp Asp Gln Ser Leu	Leu Val Met Met Ile Tyr	Ile Leu Gly Tyr		
	275	280	285	
Ile Cys Lys Tyr				
290				

&lt;210&gt; 1330

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g247 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1330

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly	
1	5 10 15
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Phe Leu Phe Ser	
	20 25 30
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr	
	35 40 45
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala	
	50 55 60
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys	
65	70 75 80
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly	
	85 90 95
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met	
	100 105 110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys	
	115 120 125
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe	
	130 135 140
Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu	
145	150 155 160
Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser	
	165 170 175
Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr	
	180 185 190
Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu	
	195 200 205
Ala Ser Phe Leu Ile Leu Ile Ile Ser Tyr Ile Phe Ile Leu Val Thr	
	210 215 220
Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu	
225	230 235 240
Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe	
	245 250 255
Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala	
	260 265 270
Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr	
	275 280 285
Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Cys Ser Gln	
	290 295 300
Phe Val Asn Tyr Ser Lys Ile Phe	
305	310



<210> 1331  
 <211> 168  
 <212> PRT  
 <213> Unknown (H38g248 protein)

<220>  
 <223> Synthetic construct

<400> 1331  
 Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu  
 1 5 10 15  
 Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu  
 20 25 30  
 Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met  
 35 40 45  
 Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile  
 65 70 75 80  
 Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu  
 85 90 95  
 Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala  
 100 105 110  
 Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile  
 115 120 125  
 Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His  
 130 135 140  
 Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe  
 145 150 155 160  
 Thr Met Ala Leu Ala Ala Pro Leu  
 165

<210> 1332  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g249 protein)

<220>  
 <223> Synthetic construct

<400> 1332  
 Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu  
 1 5 10 15  
 Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro  
 20 25 30  
 Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu  
 35 40 45  
 Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile  
 65 70 75 80  
 Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe  
 85 90 95  
 Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met  
 100 105 110  
 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala  
 130 135 140  
 Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro

```

145          150          155          160
Phe Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu
          165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly
          180          185          190
Asn Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
          195          200          205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
          210          215          220
Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
225          230          235          240
Asn Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro
          245          250          255
Ala Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro
          260          265          270
Pro Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp
290          295          300
Cys Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser
305          310          315          320
Met

```

&lt;210&gt; 1333

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g250 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1333

```

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
1          5          10          15
Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
          20          25          30
Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
          35          40          45
Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
          50          55          60
Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr
65          70          75          80
Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
          85          90          95
Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
          100          105          110
Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
          115          120          125
Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
130          135          140
Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
145          150          155          160
Leu Pro Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn
          165          170          175
Val Ile Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser
          180          185          190
Cys Asp Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp
          195          200          205
Thr Leu Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe
210          215          220

```

```

Ile Leu Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys
225                230                235                240
Ala Leu Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser
                245                250                255
Thr Ile Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val
                260                265                270
Ser Pro Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro
                275                280                285
Ala Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys
                290                295                300
Gln Gly Met Gln Arg Leu Leu Lys Lys Gly Cys
305                310                315

```

&lt;210&gt; 1334

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g251 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(302)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1334

```

Leu Ser Ser Met Cys Leu Thr Ile Val Met His Cys Glu Phe Phe Leu
1          5          10          15
Met Asp Leu Thr Asp Asp Pro Gln Leu His Pro Thr Phe Ser Ala Leu
                20          25          30
Phe Leu Pro Ile Tyr Val Val Met Val Met Ala Asn Leu Gly Leu Leu
                35          40          45
Ala Phe Ile Val Val Ser Pro Gln Phe Leu Thr Pro Met Tyr Phe Phe
                50          55          60
Leu Ser Asn Trp Ser Ser Val Asp Phe Cys Tyr Ser Ser Val Thr Val
65          70          75          80
Pro Lys Ile Ser Met Gly Phe Phe Ser Asp Cys Gln Val Phe Ser Phe
                85          90          95
Ser Gly Cys Met Ala Gln Leu Ser Cys Phe Xaa Ile Phe Ala Asp Thr
                100          105          110
Glu Phe Phe Leu Leu Ala Ser Met Val Tyr Tyr Arg Xaa Glu Ala Val
                115          120          125
Cys Asn Pro Leu Leu Tyr His Ile Thr Met Ser Pro Lys Leu Cys Leu
                130          135          140
Gln Leu Val Ala Thr Ser Met Asn Met Val Leu Pro Ser Ser Thr Ile
145          150          155          160
Phe His Leu Ile Phe Cys Lys Ser Arg Ala Ile Ile His Xaa Phe Cys
                165          170          175
Tyr Phe Ser Pro Pro Pro Arg Leu Xaa Lys Leu Ser Cys Ser Asp Met
                180          185          190
Gln Gly Leu Gln Leu Leu Thr Phe Ala Ser Ser Ser Phe Asn Val Ser
                195          200          205
Val Ser Arg Thr Ile Phe Leu Val Ser Tyr Leu Ile Met Arg Met Pro
                210          215          220
Ser Val Xaa Gly Lys His Cys Ala Ser His Leu Thr Ala Val Ser Leu
225          230          235          240
Cys Tyr Gly Thr Thr Val Phe Leu His Leu His Leu Ser Leu Lys Cys
                245          250          255
Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
                260          265          270
Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys

```

	275		280		285
Thr	Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu				
	290		295		300

<210> 1335  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g252 protein)

<220>  
 <223> Synthetic construct

<400> 1335  
 Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr  
 1 5 10 15  
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His  
 20 25 30  
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val  
 35 40 45  
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His  
 50 55 60  
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu  
 65 70 75 80  
 Leu Thr Cys Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe  
 85 90 95  
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe  
 100 105 110  
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala  
 115 120 125  
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr  
 130 135 140  
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg  
 145 150 155 160  
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro  
 165 170 175  
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser  
 180 185 190  
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly  
 195 200 205  
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser  
 210 215 220  
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser  
 225 230 235 240  
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala  
 245 250 255  
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg  
 260 265 270  
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn  
 275 280 285  
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val  
 290 295 300  
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp  
 305 310 315 320  
 Lys Gly Ala Gly

<210> 1336  
 <211> 274  
 <212> PRT  
 <213> Unknown (H38g253 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(274)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1336

```

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1           5           10           15
Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
          20           25           30
Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
          35           40           45
Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
 50           55           60
Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
65           70           75           80
Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
          85           90           95
Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
          100          105          110
Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
          115          120          125
Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
130          135          140
Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
145          150          155          160
Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
          165          170          175
Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
          180          185          190
Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
          195          200          205
Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
210          215          220
Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
225          230          235          240
Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
          245          250          255
Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
          260          265          270
Ile Leu

```

&lt;210&gt; 1337

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g254 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1337

```

Met Ser Ser Leu Asn Val Thr Glu Pro His Leu Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Ala Ala Gln Arg Trp Leu Gly Phe Pro

```

```

      20      25      30
Phe Cys Val Val Tyr Leu Ile Ala Leu Val Gly Asn Leu Ile Ile Leu
      35      40      45
Phe Val Ile Trp Thr Asp Lys Asn Leu His Gln Pro Met Phe Tyr Phe
      50      55      60
Leu Ala Met Leu Ser Val Ile Asp Leu Ser Leu Ser Thr Ser Thr Ile
      65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Gln Glu Leu Cys Phe
      85      90      95
Gly Cys Cys Val Ala Gln Val Phe Phe Ile His Phe Phe Ser Val Met
      100      105      110
Glu Ser Ile Val Leu Leu Val Met Gly Phe Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Phe Arg Xaa Thr Lys Ile Leu Thr Asn Arg Ile Thr Gly
      130      135      140
Val Ile Ala Met Val Val Val Leu Arg Ser Leu Cys Met Ile Ala Pro
      145      150      155      160
Ile Ile Phe Leu Leu Met Arg Leu Pro Tyr Cys Gly His Arg Ile Ile
      165      170      175
Pro Tyr Thr Tyr Cys Glu His Met Gly Val Ala Arg Leu Ala Cys Ala
      180      185      190
Ser Ile Ser Val Asn Val Ser His Gly Leu Gly Asn Ile Phe Ile Leu
      195      200      205
Phe Leu Asp Met Phe Leu Ile Ile Ile Ser Tyr Ala Arg Ile Leu Cys
      210      215      220
Thr Val Phe His Leu Pro Ser Gln Glu Ala His Leu Lys Ala Leu Asn
      225      230      235      240
Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala Phe Phe Gly Pro Ala
      245      250      255
Leu Phe Ser Phe Leu Thr His Arg Phe Gly His Gly Ile Pro Gln Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Ile Val Val Ile Pro Pro Ala
      275      280      285
Leu Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Glu Arg
      290      295      300
Val Glu Ser Leu Phe Thr Lys Asn Xaa Leu Asn
      305      310      315

```

&lt;210&gt; 1338

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g255 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1338

```

Val Glu Asn Ser Pro Met Val Thr Asp Phe Ile Phe Leu Gly Met Thr
  1              5              10              15
Asp Asn Ser Gln Leu Glu Val Leu Leu Phe Gly Val Phe Leu Ile Ala
      20      25      30
Tyr Ile Ile Thr Val Leu Glu Asn Leu Gly Leu Val Val Leu Ile Arg
      35      40      45
Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Gln
      50      55      60
Ser Phe Leu Asp Val Cys Phe Ser Ser Ile Thr Ile Pro Gln Asn Leu
      65      70      75      80

```

Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr  
                             85                            90                            95  
 Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe  
                             100                            105                            110  
 Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu  
                             115                            120                            125  
 Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala  
                             130                            135                            140  
 Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser  
                             145                            150                            155                            160  
 Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe  
                             165                            170                            175  
 Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile  
                             180                            185                            190  
 Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr  
                             195                            200                            205  
 Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile  
                             210                            215                            220  
 Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys  
                             225                            230                            235                            240  
 Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr  
                             245                            250                            255  
 Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile  
                             260                            265                            270  
 Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile  
                             275                            280                            285  
 Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu  
                             290                            295                            300  
 Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile  
                             305                            310                            315                            320  
 Leu Xaa Arg

&lt;210&gt; 1339

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g256 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1339

Trp Leu Asp Glu Lys Lys Gln Asp Ser Asn Val Thr Glu Leu Val Leu  
   1                            5                            10                            15  
 Leu Gly Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Leu Leu Leu  
                             20                            25                            30  
 Phe Leu Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val  
                             35                            40                            45  
 Val Thr Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr  
                             50                            55                            60  
 Phe Leu Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr  
                             65                            70                            75                            80  
 Leu Pro Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser  
                             85                            90                            95  
 Phe Ser Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala  
                             100                            105                            110  
 Ser Glu Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala  
                             115                            120                            125  
 Ile Cys Asn Pro Leu Arg Tyr Leu Ile Ile Met Asn Pro Gln Leu Cys  
                             130                            135                            140  
 Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile

```

145          150          155          160
Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro Asn Glu
          165          170          175
Leu Asp Asn Phe Tyr Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys
          180          185          190
Met Asp Thr Tyr Val Val Glu Val Leu Met Ile Ala Asn Ser Gly Leu
          195          200          205
Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala Val Ile
          210          215          220
Leu Ile Thr Leu Arg Thr His Phe Gly Gln Gly Gln Asn Lys Phe Leu
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe Met Pro
          245          250          255
Cys Ile Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val Asp Lys
          260          265          270
Ile Phe Ser Met Phe Tyr Thr Val Met Thr Pro Met Leu Ser Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Ala Asp Met Lys Thr Ala Met Lys Lys Leu
          290          295          300
Arg Ile Lys Pro Cys Asp Ile
305          310

```

&lt;210&gt; 1340

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g257 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1340

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1      5      10      15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
20     25     30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35     40     45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50     55     60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65     70     75     80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85     90     95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100    105    110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
115    120    125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
130    135    140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145    150    155    160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
165    170    175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
180    185    190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195    200    205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210    215    220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225    230    235    240

```



```
<210> 1341
<211> 320
<212> PRT
<213> Unknown (H38g258 protein)
```

```
<221> VARIANT
<222> (1)...(320)
<223> Xaa = Any Amino Acid
```

651

290		295		300
Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile				
305		310		315
				320

&lt;210&gt; 1342

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g259 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1342

Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr				
1	5	10	15	
Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile				
	20	25	30	
Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile				
	35	40	45	
Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu				
	50	55	60	
Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu				
	65	70	75	80
Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile				
	85	90	95	
Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu				
	100	105	110	
Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu				
	115	120	125	
Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile				
	130	135	140	
Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met				
	145	150	155	160
Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe				
	165	170	175	
Cys Asp Val Lys Pro Leu Leu Lys Leu Ser Leu Ile Ser Gly Trp Leu				
	180	185	190	
Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu				
	195	200	205	
Leu Ser Tyr Phe Tyr Ile Ile Thr His Leu Phe Phe Lys Thr His Ser				
	210	215	220	
Phe Ser Met Leu Arg Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met				
	225	230	235	240
Val Val Ile Leu Leu Tyr Ala Pro Val Leu Phe Thr Tyr Ile His His				
	245	250	255	
Ala Ser Gly Thr Ser Met Asp Gln Asp Arg Ile Thr Ala Ile Met Tyr				
	260	265	270	
Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn				
	275	280	285	
Lys Glu Val Lys Gly Ala Phe Asn Arg Ala Met Lys Arg Trp Leu Trp				
	290	295	300	
Pro Lys Glu Ile Leu				
305				

&lt;210&gt; 1343

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g260 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1343

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Val Phe Val Leu Val Leu
      20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
      65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
      115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
      145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
      210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
      225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
      245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
      260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
      275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
      290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Arg Lys Ile Asp Cys
      305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
      325          330

```

&lt;210&gt; 1344

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g261 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1344

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
 1           5           10           15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val

```

```

      20      25      30
Phe Thr Ala Val Tyr Val Phe Ile Ile Ile Gly Asn Met Leu Ile Ile
      35      40      45
Val Ala Val Val Ser Ser Gln Arg Leu His Lys Pro Met Tyr Ile Phe
      50      55      60
Leu Ala Asn Leu Ser Phe Leu Asp Ile Leu Tyr Thr Ser Ala Val Met
      65      70      75      80
Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser Val Ala
      85      90      95
Gly Cys Leu Leu Gln Phe Phe Ile Phe Gly Ser Leu Ala Thr Ala Glu
      100      105      110
Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
      115      120      125
Tyr Pro Leu His Tyr Pro Leu Leu Met Gly Pro Arg Arg Tyr Met Gly
      130      135      140
Leu Val Val Thr Thr Trp Leu Ser Gly Phe Val Val Asp Gly Leu Val
      145      150      155      160
Val Ala Leu Val Ala Gln Leu Arg Phe Cys Gly Pro Asn His Ile Asp
      165      170      175
Gln Phe Tyr Cys Asp Phe Met Leu Phe Val Gly Leu Ala Cys Ser Asp
      180      185      190
Pro Arg Val Ala Gln Val Thr Thr Leu Ile Leu Ser Val Phe Cys Leu
      195      200      205
Thr Ile Pro Phe Gly Leu Ile Leu Thr Ser Tyr Ala Arg Ile Val Val
      210      215      220
Ala Val Leu Arg Val Pro Ala Gly Ala Ser Arg Arg Arg Ala Phe Ser
      225      230      235      240
Thr Cys Ser Ser His Leu Ala Val Val Thr Thr Phe Tyr Gly Thr Leu
      245      250      255
Met Ile Phe Tyr Val Ala Pro Ser Ala Val His Ser Gln Leu Leu Ser
      260      265      270
Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Phe Asn Pro
      275      280      285
Val Ile Tyr Thr Met Arg Asn Lys Glu Val His Gln Ala Leu Arg Lys
      290      295      300
Ile Leu Cys Ile Lys Gln Thr Glu Thr Leu Asp
      305      310      315

```

&lt;210&gt; 1345

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g262 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1345

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
      1      5      10      15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
      20      25      30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Leu Val
      35      40      45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
      50      55      60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
      65      70      75      80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
      85      90      95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
      100      105      110

```

```

Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
   115               120               125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
   130               135               140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
  145               150               155               160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
               165               170               175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
               180               185               190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
   195               200               205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
   210               215               220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
  225               230               235               240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
               245               250               255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
               260               265               270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
   275               280               285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
   290               295               300
Gln Lys Thr Val Pro Met Glu Ile
  305               310

```

&lt;210&gt; 1346

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g263 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1346

```

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
  1               5               10               15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
               20               25               30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val
   35               40               45
Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu
   50               55               60
Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
   65               70               75               80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser
               85               90               95
Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
               100               105               110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
               115               120               125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
   130               135               140
Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser
  145               150               155               160
Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu
               165               170               175
Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr
               180               185               190
Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro

```

```

      195              200              205
Leu S r Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu
 210              215              220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
 225              230              235              240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245              250              255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
      260              265              270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
      275              280              285
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
      290              295              300
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
 305              310              315

```

&lt;210&gt; 1347

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g264 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1347

```

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile
 1              5              10              15
Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe
      20              25              30
Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met
      35              40              45
Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe
      50              55              60
Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile
      65              70              75              80
Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr
      85              90              95
Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr
      100              105              110
Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile
      115              120              125
Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val
      130              135              140
Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile
      145              150              155              160
Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu
      165              170              175
Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile
      180              185              190
Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile
      195              200              205
Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser
      210              215              220
Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser
      225              230              235              240
Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val
      245              250              255

```

Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile  
                   260                  265                  270  
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr  
                   275                  280                  285  
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys  
                   290                  295                  300  
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile  
 305                  310                  315

&lt;210&gt; 1348

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g265 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1348

Met Ser Pro Arg Met Cys Leu Ser Phe Leu Ala Val Ala Trp Thr Leu  
   1                  5                  10                  15  
 Gly Val Ser His Ser Leu Phe Gln Leu Ala Phe Leu Val Asn Leu Pro  
                   20                  25                  30  
 Phe Cys Gly Pro Asn Val Leu Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
                   35                  40                  45  
 Leu Leu Arg Leu Ala Cys Thr Asp Thr Tyr Arg Leu Gln Phe Met Val  
                   50                  55                  60  
 Thr Val Asn Ser Gly Phe Ile Cys Val Gly Thr Phe Phe Ile Leu Leu  
 65                  70                  75                  80  
 Ile Ser Tyr Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly  
                   85                  90                  95  
 Gly Ser Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ser Thr Ala Val  
                   100                  105                  110  
 Leu Leu Phe Phe Gly Pro Pro Met Phe Val Tyr Thr Trp Pro His Pro  
                   115                  120                  125  
 Asn Ser Gln Met Asp Lys Phe Leu Ala Ile Phe Asp Ala Val Leu Thr  
                   130                  135                  140  
 Pro Phe Leu Asn Pro Val Val Tyr Thr Phe Arg Asn Lys Glu Met Lys  
 145                  150                  155                  160  
 Ala Ala Ile Lys Arg Val Cys Lys Gln Leu Val Ile Tyr Lys Lys Ile  
                   165                  170                  175  
 Ser

&lt;210&gt; 1349

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g266 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1349

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Lys Phe Leu Leu Leu Gly  
   1                  5                  10                  15  
 Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu  
                   20                  25                  30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Leu Ala  
                   35                  40                  45  
 Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
                   50                  55                  60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

65          70          75          80
Met Leu Val Ser Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
          85          90          95
Cys Leu Thr Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu
          130          135          140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145          150          155          160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
          165          170          175
Phe Phe Cys Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr
          180          185          190
Leu Leu Asn Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
          195          200          205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
          210          215          220
Leu Met Gly Met Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
          245          250          255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
          260          265          270
Thr Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu Arg Leu
          290          295          300
Leu Ser Arg Ala Asp Ser Cys Pro Leu Thr Asn Gln Gly Leu Arg Thr
305          310          315          320
Lys Arg

```

&lt;210&gt; 1350

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g267 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1350

```

Tyr Thr Glu Pro Glu Asn Leu Thr Gly Val Leu Glu Phe Leu Leu Leu
1          5          10          15
Gly Leu Pro Asp Asp Pro Glu Leu Gln Pro Val Leu Phe Gly Leu Phe
          20          25          30
Leu Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Val Ser Ser Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Ala Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ala His Ser Arg Leu Ile Ser Tyr Val
          85          90          95
Gly Cys Leu Thr Gln Met Ser Phe Leu Ile Phe Phe Ala Cys Met Glu
          100          105          110

```



```

Ser Leu Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
    115                120                125
His Pro Leu His Tyr Gln Val Ile Met Ser Pro Arg Leu Cys Gly Phe
    130                135                140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
    145                150                155                160
Asn Leu Ile Val Leu Gln Leu Thr Cys Phe Asn Asp Val Glu Ile Ser
    165                170                175
Asn Phe Phe Cys Asp Pro Ser Xaa Leu Leu Lys Leu Ala Cys Ser Asp
    180                185                190
Thr Ser Ile Asn Asn Met Val Val Tyr Phe Ile Gly Ala Ile Phe Gly
    195                200                205
Phe Leu Pro Leu Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
    210                215                220
Ser Ile Leu Arg Val Leu Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser
    225                230                235                240
Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Leu Tyr Gly Thr Ala
    245                250                255
Leu Gly Gly Tyr Leu Ser Ser Ala Val Ser Leu Ser Ser Arg Lys Gly
    260                265                270
Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met Leu Asn Pro
    275                280                285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Gln Arg
    290                295                300
Leu His Gly Arg Ile Met Xaa Ser Pro Tyr Leu Leu His Leu Phe Cys
    305                310                315                320
Ser Ile

```

&lt;210&gt; 1351

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g268 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1351

```

Met Arg Gln Ile Asn Gln Thr Gln Val Thr Glu Phe Leu Leu Leu Gly
  1          5          10          15
Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
    20          25          30
Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu
    35          40          45
Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
    50          55          60
Asn Leu Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln
    65          70          75          80
Ala Leu Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu
    85          90          95
Cys Ala Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
    100         105         110
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn
    115         120         125
Pro Leu Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu
    130         135         140
Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
    145         150         155         160
Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
    165         170         175
Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr

```

```

      180      185      190
His Ala Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu
      195      200      205
Ile Pro Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr
      210      215      220
Val Val Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr
225      230      235      240
Cys Gly Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile
      245      250      255
Ile Thr Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val
      260      265      270
Ser Val Phe Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Leu Ile Tyr
      275      280      285
Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Val Ala Thr
      290      295      300
Arg Asn Phe Pro
305

```

&lt;210&gt; 1352

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g269 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1352

```

Met Pro Ile Leu Met Ala Ile Gly Asn Trp Thr Glu Ile Ser Glu Phe
  1      5      10      15
Ile Leu Met Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu
      20      25      30
Phe Leu Thr Phe Leu Thr Ile Tyr Leu Val Thr Leu Lys Gly Asn Ser
      35      40      45
Leu Ile Ile Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met
      50      55      60
Tyr Phe Phe Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu
      65      70      75      80
Val Ile Val Pro Lys Met Leu Gly Thr Leu Leu Ala Gln Asp Thr Thr
      85      90      95
Ile Ser Phe Leu Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Phe
      100      105      110
Gly Val Ala Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
      115      120      125
Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
      130      135      140
Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
      145      150      155      160
Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
      165      170      175
Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Lys Leu
      180      185      190
Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
      195      200      205
Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
      210      215      220
Arg Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys His
      225      230      235      240
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
      245      250      255
Tyr Ile Ser Ser Ser Leu Thr Tyr Phe Trp Pro Lys Ser Asn Asn Ser
      260      265      270

```

Pro Glu Ser Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro  
                   275                                  280                                  285  
 Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ser Glu Val Lys Asn  
                   290                                  295                                  300  
 Ala Leu Ser Arg Thr Phe His Lys Val Leu Ala Leu Arg Asn Cys Ile  
 305                                  310                                  315                                  320  
 Pro

&lt;210&gt; 1353

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g270 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(260)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1353

Ala His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro  
   1                                  5                                  10                                  15  
 Gln Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met  
                   20                                  25                                  30  
 Gly Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu  
                   35                                  40                                  45  
 Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys  
                   50                                  55                                  60  
 Lys Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly  
 65                                  70                                  75                                  80  
 Leu Val Ser Val Thr Trp Ser Cys Trp Gly Gly Gln Leu Leu Gly His  
                                   85                                  90                                  95  
 Val Ser Trp Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp  
                   100                                  105                                  110  
 His Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser  
                   115                                  120                                  125  
 Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly Val Val  
                   130                                  135                                  140  
 Leu Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg  
 145                                  150                                  155                                  160  
 Ala Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly  
                   165                                  170                                  175  
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile  
                   180                                  185                                  190  
 Ile Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly  
                   195                                  200                                  205  
 Met Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro  
                   210                                  215                                  220  
 Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg  
 225                                  230                                  235                                  240  
 Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu Xaa Arg His Leu His  
                   245                                  250                                  255  
 Leu Thr Ser Leu  
                   260

&lt;210&gt; 1354

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g271 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1354

Glu Glu Ile Leu Xaa Ile Ile Ser Gln His Val His Thr Gly Cys Val  
 1 5 10 15  
 Gln Asn Xaa Glu Leu Gln Pro Ile Leu Phe Gly Leu Phe Leu Ser Met  
 20 25 30  
 Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Val Ser  
 35 40 45  
 Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Leu Ala Asp Ile Gly Phe Pro Ser Thr Thr Val Pro Lys Met Ile  
 65 70 75 80  
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu  
 85 90 95  
 Thr Gln Ile Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu  
 100 105 110  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu  
 115 120 125  
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 130 135 140  
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Phe Gln Leu His Asn Trp Ile  
 145 150 155 160  
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Ser Phe Phe  
 165 170 175  
 Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr  
 180 185 190  
 Asn Asn Ile Val Met Tyr Phe Leu Ala Ala Ile Leu Gly Phe Leu Pro  
 195 200 205  
 Ile Ser Gly Ile Phe Tyr Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu  
 210 215 220  
 Lys Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly  
 245 250 255  
 Tyr Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala  
 260 265 270  
 Ser Val Met Tyr Thr Val Val Ala Pro Met Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Ser Leu Arg Lys Arg Asp Ile Lys Ser Ala Leu Gln Gln Leu His Gly  
 290 295 300  
 Arg Ile Val Xaa Ser His Asp Leu Ile Ile Gly Ser Ile Leu Xaa Pro  
 305 310 315 320  
 Trp Val Gly Lys Gly Ser Lys Val Lys  
 325

&lt;210&gt; 1355

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g272 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1355

```

Met Glu Ser Pro Asn His Thr Asp Val Asp Pro Ser Val Phe Phe Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Gln Phe His Leu Trp Leu Ser Leu Pro
          20          25          30
Val Cys Gly Leu Gly Thr Ala Thr Ile Val Gly Asn Ile Thr Ile Leu
          35          40          45
Val Val Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val
          65          70          75          80
Pro Lys Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala
          85          90          95
Ser Ala Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met
          100          105          110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala
          130          135          140
His Ile Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro
          145          150          155          160
Cys Pro Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile
          165          170          175
Leu His Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly
          180          185          190
Asp Thr Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val
          195          200          205
Ile Gly Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala
          210          215          220
Gln Ala Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu
          225          230          235          240
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro
          245          250          255
Ala Leu Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val
          260          265          270
His Ile His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala
          275          280          285
Leu Asn Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Lys Arg
          290          295          300
Val Val Arg Val Phe Gln Ser Gly Gln Gly Met Gly Ile Lys Ala Ser
          305          310          315          320
Glu

```

&lt;210&gt; 1356

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g273 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1356

```

Met Thr Trp Ser Gly Gly Thr Ile Val Gly Glu Xaa Gly Glu Phe Val
 1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Leu Phe Ala
          20          25          30
Leu Leu Leu Leu Ala Tyr Val Leu Val Leu Thr Glu Asn Thr Leu Ile

```

<400> 1357															
Met	Glu	Ala	Gly	Asn	Gln	Thr	Gly	Phe	Leu	Glu	Phe	Ile	Leu	Leu	Gly
1				5				10						15	
Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Phe	Ile	Phe	Gly	Leu	Phe	Leu
			20					25					30		
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala
		35					40					45			
Ile	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
Asn	Leu	Ser	Trp	Val	Asp	Ile	Cys	Phe	Ser	Thr	Cys	Ile	Val	Pro	Lys
65					70					75					80
Met	Leu	Val	Asn	Ile	Gln	Thr	Glu	Asn	Lys	Ala	Ile	Ser	Tyr	Met	Asp
			85					90						95	
Cys	Leu	Thr	Gln	Val	Tyr	Phe	Ser	Met	Phe	Phe	Pro	Ile	Leu	Asp	Thr
			100					105					110		

Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His  
 115 120 125  
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu  
 130 135 140  
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile  
 145 150 155 160  
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val  
 195 200 205  
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser  
 210 215 220  
 Ile Arg Lys Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Val His Phe Thr Ser Ala Val Thr His Ser Ser Gln Lys Ile Ser  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Ser Leu  
 290 295 300  
 Leu Ser Arg Ala Ala Ser Cys Leu  
 305 310

&lt;210&gt; 1358

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g275 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1358

Met Thr Ala Cys Asn Ala Ser Gln Gly His Pro Ser Phe Phe Ile Leu  
 1 5 10 15  
 Gln Gly Ile Pro Gly Met Glu Asp Lys His Arg Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Ser Ser Met Tyr Phe Ile Met Val Leu Gly Asn Cys Thr Ile Leu  
 35 40 45  
 Leu Thr Ile Ser Thr Glu Arg Ser Leu His Lys Pro Met Phe Leu Leu  
 50 55 60  
 Leu Cys Leu Leu Ala Leu Thr Asp Leu Gly Met Ser Thr Thr Thr Ile  
 65 70 75 80  
 Pro Lys Val Leu Cys Ile Phe Trp Phe Gly Gln Ser Glu Ile Ser Tyr  
 85 90 95  
 Glu Gly Cys Leu Val Gln Leu Phe Phe Ile His Ser Ile Ser Ala Met  
 100 105 110  
 Gln Ser Ala Val Leu Met Thr Met Ala Phe Asp His Tyr Val Ala Ile  
 115 120 125  
 Cys Lys Pro Leu Arg Tyr Ala Thr Ile Leu Ser Asn Ser Cys Thr Gly  
 130 135 140  
 Leu Ile Gly Leu Val Ser Leu Val Arg Ala Ile Leu Phe Ile Leu Pro  
 145 150 155 160  
 Met Pro Ile Leu Leu Gln Gln Met Pro Tyr His Ala Asn Arg Val Ile

```

          165          170          175
Pro Thr Thr Ser Cys Glu His Met Ala Val Val Lys Met Val Cys Val
          180          185          190
Asp Thr Thr Val Asn Arg Ile Tyr Gly Leu Val Val Ala Leu Leu Val
          195          200          205
Ala Gly Tyr Asp Leu Ser Ala Ile Ala Ser Ser Tyr Val Leu Ile Ile
          210          215          220
Gln Ala Ile Met His Leu Ser Ser Lys Glu Ala His His Lys Ala Val
          225          230          235          240
Asn Thr Cys Thr Thr His Ile Cys Val Met Leu Ile Ser Tyr Thr Pro
          245          250          255
Ser Leu Phe Ser Phe Leu Ala His Arg Phe Gly Gln Gly Ile Pro Pro
          260          265          270
His Val His Ile Ile Leu Gly Asn Leu Tyr Phe Leu Val Pro Pro Met
          275          280          285
Leu Ser Pro Ile Ile Tyr Gly Val Lys Thr Lys Glu Phe Trp Asp Lys
          290          295          300
Val Thr Lys Xaa Val Ala Gly Lys Lys Asn Pro Gln Pro Leu Thr Met
          305          310          315          320

```

&lt;210&gt; 1359

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g276 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1359

```

Met Glu Leu Trp Asn Phe Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
  1          5          10          15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Ile Thr
          20          25          30
Ile Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Ala
          35          40          45
Ile Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
          50          55          60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
          65          70          75          80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
          85          90          95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp
          100          105          110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met
          130          135          140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr
          145          150          155          160
Val Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His
          165          170          175
Leu Leu Cys Glu Ile Pro His Leu Leu Lys Val Ala Cys Ala Asp Thr
          180          185          190
Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
          195          200          205
Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr
          210          215          220
Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
          225          230          235          240
Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
          245          250          255

```



Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn  
                           260                          265                          270  
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
                           275                          280                          285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val  
                           290                          295                          300  
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu  
 305                          310                          315

&lt;210&gt; 1360

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g277 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1360

Met Lys Ala Gly Asn Phe Ser Asp Thr Pro Glu Phe Phe Leu Leu Gly  
 1                          5                          10                          15  
 Leu Ser Gly Asp Pro Glu Leu Gln Pro Ile Leu Phe Met Leu Phe Leu  
                           20                          25                          30  
 Ser Met Tyr Leu Ala Thr Met Leu Gly Asn Leu Leu Ile Ile Leu Ala  
                           35                          40                          45  
 Val Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
                           50                          55                          60  
 Ile Leu Ser Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Met Pro Lys  
 65                          70                          75                          80  
 Met Leu Val Asn Ile Gln Ala Gln Ala Gln Ser Ile Asn Tyr Thr Gly  
                           85                          90                          95  
 Cys Leu Thr Gln Ile Cys Phe Val Leu Val Phe Val Gly Leu Glu Asn  
                           100                          105                          110  
 Gly Ile Leu Val Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
                           115                          120                          125  
 Pro Leu Arg Tyr Asn Val Ile Met Asn Pro Lys Leu Cys Gly Leu Leu  
                           130                          135                          140  
 Leu Leu Leu Ser Phe Ile Val Ser Val Leu Asp Ala Leu Leu His Thr  
 145                          150                          155                          160  
 Leu Met Val Leu Gln Leu Thr Phe Cys Ile Asp Leu Glu Ile Pro His  
                           165                          170                          175  
 Phe Phe Cys Glu Leu Ala His Ile Leu Lys Leu Ala Cys Ser Asp Val  
                           180                          185                          190  
 Leu Ile Asn Asn Ile Leu Val Tyr Leu Val Thr Ser Leu Leu Gly Val  
                           195                          200                          205  
 Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr Arg Ile Val Ser Ser  
                           210                          215                          220  
 Val Met Lys Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Ile  
 225                          230                          235                          240  
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Gly Phe  
                           245                          250                          255  
 Gly Val Tyr Leu Ser Ser Gly Ala Thr His Ser Ser Arg Lys Gly Ala  
                           260                          265                          270  
 Ile Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu  
                           275                          280                          285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Met Leu Lys Ala Leu Arg Lys Leu  
                           290                          295                          300  
 Ile Ser Arg Ile Pro Ser Phe His  
 305                          310

&lt;210&gt; 1361

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g278 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1361

```

Lys Ile Ser Asn Ser Ser Lys Phe Gln Val Ser Glu Phe Ile Leu Leu
 1           5           10           15
Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu
      20           25           30
Ala Leu Leu Tyr Leu Ser Ala Leu Ala Ala Asn Thr Leu Ile Leu Ile
      35           40           45
Ile Ile Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu
      50           55           60
Gly Ile Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro
65           70           75           80
Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro
      85           90           95
Glu Cys Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu
      100          105          110
Ser Gly Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu Arg Tyr Pro Ser Ile Val Thr Ser Ser Leu Ile Leu Lys
      130          135          140
Ala Thr Leu Phe Met Val Leu Arg Asn Gly Leu Phe Val Thr Pro Val
145          150          155          160
Pro Val Leu Ala Ala Gln Arg Asp Tyr Cys Ser Lys Asn Glu Ile Glu
      165          170          175
His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp
      180          185          190
Arg Arg Pro Asn Ser Ile Cys Gln Leu Val Leu Ala Trp Leu Gly Met
      195          200          205
Gly Ser Asp Leu Ser Leu Ile Ile Leu Ser Tyr Ile Leu Ile Leu Tyr
      210          215          220
Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Ala Lys Ala Leu Ser
225          230          235          240
Thr Cys Ser Ser His Leu Thr Leu Ile Leu Phe Phe Tyr Thr Ile Val
      245          250          255
Val Val Ile Ser Val Thr His Leu Thr Glu Met Lys Ala Thr Leu Ile
      260          265          270
Pro Val Leu Leu Asn Val Leu His Asn Ile Ile Pro Pro Ser Leu Asn
      275          280          285
Pro Thr Val Tyr Ala Leu Gln Thr Lys Glu Leu Arg Ala Ala Phe Gln
      290          295          300
Lys Val Leu Phe Ala Leu Thr Lys Glu Ile Arg Ser Xaa Arg Pro Ser
305          310          315          320
Pro Xaa Cys Thr Xaa Thr Ser Ala
      325

```

&lt;210&gt; 1362

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g279 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1362

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
1      5      10      15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
20      25      30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
35      40      45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
50      55      60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
65      70      75      80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
85      90      95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
100     105     110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115     120     125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
130     135     140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
145     150     155     160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
165     170     175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
180     185     190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
195     200     205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
210     215     220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
225     230     235     240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
245     250     255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
260     265     270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
275     280     285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
290     295     300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
305     310     315

```

&lt;210&gt; 1363

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g280 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1363

```

Met Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro
1      5      10      15
Leu Ala Leu Leu Tyr Leu Leu Ala Leu Ser Ala Asn Ile Leu Ile Leu
20      25      30
Ile Ile Ile Asn Lys Glu Ala Ala Leu His Gln Pro Met Tyr Tyr Phe
35      40      45
Leu Gly Ile Leu Ala Met Ala Asp Ile Gly Leu Ala Thr Thr Ile Met
50      55      60
Pro Lys Ile Leu Ala Ile Leu Trp Phe Asn Ala Lys Thr Ile Ser Leu

```

```

65          70          75          80
Leu Glu Cys Phe Ala Gln Met Tyr Ala Ile His Cys Phe Val Ala Met
      85          90          95
Glu Ser Ser Thr Phe Val Cys Met Ala Ile Asp Arg Tyr Val Ala Ile
      100         105         110
Cys Arg Pro Leu Arg Tyr Pro Ser Ile Ile Thr Glu Ser Phe Val Phe
      115         120         125
Lys Ala Asn Gly Phe Met Ala Leu Arg Asn Ser Leu Cys Leu Ile Ser
      130         135         140
Val Pro Leu Leu Ala Ala Gln Arg His Tyr Cys Ser Gln Asn Gln Ile
      145         150         155         160
Glu His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ser Cys Asp
      165         170         175
Asp Arg Arg Ile Asn Ser Ile Asn Gln Val Leu Leu Ala Trp Thr Leu
      180         185         190
Met Gly Ser Asp Leu Gly Leu Ile Ile Leu Ser Tyr Ala Leu Ile Leu
      195         200         205
Tyr Ser Val Leu Lys Leu Asn Ser Pro Glu Ala Ala Ser Lys Ala Leu
      210         215         220
Ser Thr Cys Thr Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Val
      225         230         235         240
Ile Ile Val Ile Ser Ile Thr Arg Ser Thr Gly Met Arg Val Pro Leu
      245         250         255
Ile Pro Val Leu Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu
      260         265         270
Asn Pro Met Val Tyr Ala Leu Lys Asn Lys Glu Leu Arg Gln Gly Leu
      275         280         285
Tyr Lys Val Leu Arg Leu Gly Val Lys Gly Thr
      290         295

```

&lt;210&gt; 1364

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g281 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1364

```

Met Thr Trp Ser Gly Gly Thr Leu Val Gly Glu Xaa Gly Glu Phe Val
1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Ser Phe Ala
      20          25          30
Arg Xaa Ser Ala Ala Tyr Ala Leu Val Leu Thr Glu Asn Thr Leu Ile
      35          40          45
Ile Met Ala Ser Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
      50          55          60
Val Leu Ala Asn Met Ser Ser Leu Glu Ile Trp Tyr Val Thr Val Thr
      65          70          75          80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85          90          95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100         105         110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115         120         125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130         135         140

```

Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe  
 145 150 155 160  
 Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys  
 165 170 175  
 Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu  
 180 185 190  
 Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile  
 195 200 205  
 Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser  
 210 215 220  
 Tyr Val Ala Ile Thr Gly Ala Val Met His Thr Ser Ser Ala Ala Gly  
 225 230 235 240  
 Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile  
 245 250 255  
 Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu  
 260 265 270  
 Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile  
 275 280 285  
 Val Pro Leu Leu Asn Pro Ile Tyr Cys Leu Arg Asn Gln Glu Val  
 290 295 300  
 Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro  
 305 310 315 320  
 Asp Pro Lys Lys Ala Ser Arg  
 325

&lt;210&gt; 1365

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g282 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1365

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr

180										185			190				
Tyr	Arg	Leu	Gln	Phe	Met	Val	Thr	Val	Asn	Ser	Gly	Phe	Ile	Cys	Val		
195							200			205							
Gly	Thr	Phe	Phe	Ile	Leu	Leu	Ile	Ser	Tyr	Val	Phe	Ile	Leu	Phe	Thr		
210							215			220							
Val	Trp	Lys	His	Ser	Ser	Gly	Gly	Ser	Ser	Lys	Ala	Leu	Ser	Thr	Leu		
225	230					235					240						
Ser	Ala	His	Ser	Thr	Ala	Val	Leu	Leu	Phe	Gly	Pro	Pro	Met	Phe			
245							250					255					
Val	Tyr	Thr	Trp	Pro	His	Pro	Asn	Ser	Gln	Met	Asp	Lys	Phe	Leu	Ala		
260							265					270					
Ile	Phe	Asp	Ala	Val	Leu	Thr	Pro	Phe	Leu	Asn	Pro	Val	Val	Tyr	Thr		
275							280					285					
Phe	Arg	Asn	Lys	Glu	Met	Lys	Ala	Ala	Ile	Lys	Arg	Val	Cys	Lys	Gln		
290							295					300					
Leu	Val	Ile	Tyr	Lys	Lys	Ile	Ser	Xaa	Met	Ile	Gln	Xaa	Ala	Leu	Leu		
305	310					315					320						
Val	Lys	His	Asp	Met	Ala	Leu	Cys	Phe	Phe	Leu	Xaa	Tyr					
325							330										

**<210> 1366**

**<211> 280**

<212> PRT

<213> Unknown (H38g283 protein)

**<220>**

<223> Synthetic construct

<400> 1366

Met 1	Leu	Leu	Gly	Asn 5	Leu	Ala	Ile	Ile	Ser 10	Phe	Ile	Cys	Leu	Asp 15	Ser
Arg	Leu	His	Ser 20	Pro	Met	Tyr	Phe	Phe 25	Leu	Cys	Asn	Phe	Ser 30	Leu	Met
Glu	Met	Val 35	Val	Thr	Ser	Thr	Val 40	Val	His	Arg	Met	Leu 45	Ala	Asp	Leu
Leu	Ser 50	Thr	His	Lys	Thr	Met 55	Ser	Leu	Ala	Lys	Cys 60	Leu	Thr	Gln	Ser
Phe 65	Phe	Tyr	Phe	Ser 70	Leu	Gly	Ser	Ala	Asn 75	Phe	Leu	Ile	Leu	Met 80	Val
Met	Ala	Phe	Asp 85	Arg	Tyr	Val	Ala	Ile 90	Cys	His	Pro	Leu	Arg 95	Tyr	Pro
Thr	Ile	Thr	Asn 100	Gly	Pro	Val	Cys 105	Val	Lys	Leu	Val	Val 110	Ala	Cys	Trp
Val	Val 115	Gly	Phe	Leu	Ser	Ile 120	Val	Ser	Pro	Thr	Leu	Gln 125	Lys	Thr	Arg
Leu	Trp 130	Phe	Cys	Gly	Pro	Asn 135	Ile	Ile	Gly	His	Tyr 140	Phe	Cys	Asp	Ser
Ala 145	Pro	Leu	Leu	Lys 150	Leu	Ala	Cys	Ser	Asp 155	Thr	Arg	His	Ile	Glu	Arg 160
Met	Asp	Leu	Phe 165	Leu	Ser	Leu	Leu	Phe	Val 170	Leu	Thr	Thr 175	Met	Leu	Leu
Ile	Ile	Leu	Ser 180	Tyr	Ile	Leu	Ile	Val 185	Ala	Ala	Val	Leu 190	His	Ile	Pro
Ser	Ser 195	Ser	Gly	Cys	Gln	Lys	Ala 200	Phe	Ser	Thr	Cys 205	Ala	Ser	His	Leu
Thr	Val 210	Val	Val	Leu	Gly	Tyr 215	Gly	Ser	Ala	Ile	Phe 220	Ile	Tyr	Val	Arg
Pro 225	Gly	Lys	Gly	His 230	Ser	Thr	Tyr	Leu	Asn 235	Lys	Ala	Val	Ala	Met	Val 240
Thr	Ala	Met	Val 245	Thr	Pro	Phe	Leu	Asn 250	Pro	Phe	Ile	Phe 255	Thr	Phe	Arg

Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe  
                   260                  265                  270  
 Leu Gly Asp Pro Ala Ala Cys Arg  
                   275                  280

<210> 1367  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g284 protein)

<220>  
 <223> Synthetic construct

<400> 1367  
 Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly  
   1                  5                  10                  15  
 Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu  
                   20                  25                  30  
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr  
                   35                  40                  45  
 Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala  
                   50                  55                  60  
 Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu  
  65                  70                  75                  80  
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly  
                   85                  90                  95  
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met  
                  100                 105                 110  
 Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg  
                  115                 120                 125  
 Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu  
  130                 135                 140  
 Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val  
  145                 150                 155                 160  
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser  
                  165                 170                 175  
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr  
                  180                 185                 190  
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val  
                  195                 200                 205  
 Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu  
                  210                 215                 220  
 Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser  
  225                 230                 235                 240  
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser  
                  245                 250                 255  
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val  
                  260                 265                 270  
 Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile  
                  275                 280                 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val  
                  290                 295                 300  
 Thr Lys Tyr Ile Leu Cys Lys Glu Lys  
  305                 310

<210> 1368  
 <211> 214  
 <212> PRT  
 <213> Unknown (H38g285 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 1368

```

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1           5           10           15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
 20           25           30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
 35           40           45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
 50           55           60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
 65           70           75           80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
 85           90           95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
 100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
 115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
 130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
 145          150          155          160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
 165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
 180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
 195          200          205
Gly Lys Ile Ser Cys His
 210

```

<210> 1369

<211> 330

<212> PRT

<213> Unknown (H38g286 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1369

```

Met Cys Leu Leu Thr Leu Gln Val Thr Gly Pro Met Asn Val Ser Glu
 1           5           10           15
Pro Asn Ser Ser Phe Ala Leu Val Asn Glu Phe Ile Leu Gln Asp Leu
 20           25           30
Ser Phe Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe Thr Thr
 35           40           45
Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Cys Ala Leu
 50           55           60
Trp Cys Asp Arg Arg Arg His Thr Pro Met Tyr Met Phe Leu Gly Asn
 65           70           75           80
Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro Lys Met
 85           90           95

```



```

Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys
      100      105      110
Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu Cys Leu
      115      120      125
Ile Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Val Ile Cys His Pro
      130      135      140
Leu His Tyr Pro Asn Ile Ile Met Thr Gly His Leu Cys Ala Lys Leu
      145      150      155      160
Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Thr
      165      170      175
Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Asn Asp His
      180      185      190
Val Val Cys Asp Pro Gly Pro Leu Phe Ala Leu Ala Cys Val Ser Ala
      195      200      205
Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile Phe
      210      215      220
Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys Ala
      225      230      235      240
Val Leu Gly Met Pro Ser Ser Thr Gly Lys His Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
      260      265      270
Val Met Cys Val Ser Pro Gly Leu Gly His Ser Met Gly Met Gln Lys
      275      280      285
Ile Lys Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro Leu
      290      295      300
Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys Val
      305      310      315      320
Leu Gly Ser Ser Asn Ile Ile Xaa Ala Ile
      325      330

```

&lt;210&gt; 1370

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g287 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1370

```

Met Met Asp Asn His Ser Ser Ala Thr Glu Phe His Leu Leu Gly Phe
  1      5      10      15
Pro Gly Ser Gln Gly Leu His His Ile Leu Phe Ala Ile Phe Phe Phe
      20      25      30
Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Val Ile Val
      35      40      45
Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ser Thr Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Met Met
      65      70      75      80
Leu Trp Gly Leu Leu Phe Leu Gly Cys Arg Gln Tyr Leu Ser Leu His
      85      90      95
Val Ser Leu Asn Phe Ser Cys Gly Thr Met Glu Phe Ala Leu Leu Gly
      100      105      110
Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg Tyr
      115      120      125
Asn Ile Ile Met Asn Ser Ser Thr Cys Ile Trp Val Val Ile Val Ser
      130      135      140
Trp Val Phe Gly Phe Leu Ser Glu Ile Trp Pro Ile Tyr Ala Thr Phe
      145      150      155      160
Gln Phe Thr Phe Arg Lys Ser Asn Ser Leu Asp His Phe Tyr Cys Asp

```

Met	Ser	Asn	Thr	Asn	Gly	Ser	Ala	Ile	Thr	Glu	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Leu	Thr	Asp	Cys	Pro	Glu	Leu	Gln	Ser	Leu	Leu	Phe	Val	Leu	Phe	Leu
		20						25					30		
Val	Val	Tyr	Leu	Val	Thr	Leu	Leu	Gly	Asn	Leu	Gly	Met	Ile	Met	Leu
		35					40					45			
Met	Arg	Leu	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr
	50					55					60				
Asn	Leu	Ala	Phe	Val	Asp	Leu	Cys	Tyr	Thr	Ser	Asn	Ala	Thr	Pro	Gln
65					70					75				80	
Met	Ser	Thr	Asn	Ile	Val	Ser	Glu	Lys	Thr	Ile	Ser	Phe	Ala	Gly	Cys
			85						90					95	
Phe	Thr	Gln	Cys	Tyr	Ile	Phe	Ile	Ala	Leu	Leu	Leu	Thr	Glu	Phe	Tyr
			100					105					110		
Met	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Tyr	Asp	Pro
		115					120					125			
Leu	Arg	Tyr	Ser	Val	Lys	Thr	Ser	Arg	Arg	Val	Cys	Ile	Cys	Leu	Ala
		130				135					140				
Thr	Phe	Pro	Tyr	Val	Tyr	Gly	Phe	Ser	Asp	Gly	Leu	Phe	Gln	Ala	Ile
145					150					155				160	
Leu	Thr	Phe	Arg	Leu	Thr	Phe	Cys	Arg	Ser	Ser	Val	Ile	Asn	His	Phe
			165						170					175	
Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Lys	Leu	Ser	Cys	Ser	Asp	Thr	Tyr
			180					185					190		
Val	Lys	Glu	His	Ala	Met	Phe	Ile	Ser	Ala	Gly	Phe	Asn	Leu	Ser	Ser
		195					200					205			
Ser	Leu	Thr	Ile	Val	Leu	Val	Ser	Tyr	Ala	Phe	Ile	Leu	Ala	Ala	Ile
						215					220				
Leu	Arg	Ile	Lys	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr	Cys
225					230					235				240	
Gly	Ser	His	Met	Met	Ala	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe	Cys
				245					250					255	

Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile  
                   260                  265                  270  
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu  
                   290                  295                  300  
 Arg  
 305

<210> 1372

<211> 313

<212> PRT

<213> Unknown (H38g289 protein)

<220>

<223> Synthetic construct

<400> 1372

Met Ala Asn Leu Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser  
   1                  5                  10                  15  
 Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu  
                   20                  25                  30  
 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile  
                   35                  40                  45  
 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe  
                   50                  55                  60  
 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu  
   65                  70                  75                  80  
 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met  
                   85                  90                  95  
 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile  
                   100                  105                  110  
 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu  
                   115                  120                  125  
 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly  
                   130                  135                  140  
 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser  
   145                  150                  155                  160  
 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe  
                   165                  170                  175  
 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu  
                   180                  185                  190  
 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser  
                   195                  200                  205  
 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu  
                   210                  215                  220  
 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly  
   225                  230                  235                  240  
 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu  
                   245                  250                  255  
 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val  
                   260                  265                  270  
 Ala Leu Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu  
                   275                  280                  285  
 Thr Phe Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln  
                   290                  295                  300  
 Arg Leu Lys Gly Leu Cys Lys Ala Gln  
   305                  310

<210> 1373

<211> 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g290 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1373

```

Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
      20           25           30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
      65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
      115          120          125
Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
      145          150          155          160
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
      210          215          220
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
      225          230          235          240
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
      245          250          255
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
      260          265          270
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
      275          280          285
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
      290          295          300
His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
      305          310          315

```

&lt;210&gt; 1374

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g291 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(345)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1374

```

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
          20           25           30
Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35           40           45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
          50           55           60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
65           70           75           80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
          85           90           95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
130          135          140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
145          150          155          160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
          165          170          175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
          180          185          190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
195          200          205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
210          215          220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
225          230          235          240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
          245          250          255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
260          265          270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
275          280          285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
290          295          300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
305          310          315          320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
          325          330          335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
          340          345

```

&lt;210&gt; 1375

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g292 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(238)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1375

```

Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1           5           10           15
Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp

```

```

      20      25      30
Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser
      35      40      45
Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser
      50      55      60
Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr
      65      70      75      80
Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu
      85      90      95
Leu Pro His Phe Leu Leu Val Asn Phe Phe Phe His Leu Met Arg Leu
      100      105      110
Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln
      115      120      125
Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser
      130      135      140
Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp
      145      150      155      160
Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser
      165      170      175
Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys
      180      185      190
Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp Ala Ala Glu Xaa Asn
      195      200      205
Lys Val Val Phe Leu Phe Ile Phe Leu Leu Thr Pro Phe Leu Asn Leu
      210      215      220
Leu Thr Gly Gln Ile Tyr Xaa Pro Lys Ser Val Leu Gly Gly
      225      230      235

```

&lt;210&gt; 1376

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g293 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1376

```

Pro Met Lys Val Ala Asn Asn Val Thr Glu Phe Ile Phe Leu Gly Leu
      1      5      10      15
Ser Gln Asp Ser Gly Met Gln Leu Met Phe Phe Val Leu Phe Leu Leu
      20      25      30
Phe Tyr Val Val Ile Met Val Gly Asn Leu Leu Ile Leu Leu Met Val
      35      40      45
Phe Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50      55      60
Leu Ser Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met
      65      70      75      80
Ile Glu Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys
      85      90      95
Ile Thr Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe
      100      105      110
Val Leu Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro
      115      120      125
Leu Arg Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala
      130      135      140
Ser Leu Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu
      145      150      155      160

```

Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr  
 165 170 175  
 Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr  
 180 185 190  
 Leu Val Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly  
 195 200 205  
 Cys Phe Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu  
 210 215 220  
 Gln Lys Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile  
 245 250 255  
 Tyr Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe  
 260 265 270  
 Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Glu Glu Val Lys Asn Ala Met Arg Arg Leu Trp Ser Ser Lys Ile  
 290 295 300  
 Ser Leu Lys Glu Lys Gln Arg  
 305 310

&lt;210&gt; 1377

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g294 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1377

Met Glu Ile Leu Ser Asn Ser Thr Ser Lys Phe Pro Thr Phe Leu Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Ala His Val Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Cys Cys Phe Tyr Ala Ile Ala Leu Ser Gly Asn Ser Val Ile Leu  
 35 40 45  
 Phe Val Ile Ile Thr Gln Gln Ser Leu His Glu Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Thr Val Ser Ser Leu  
 65 70 75 80  
 Ser Thr Thr Leu Gly Ile Leu Trp Phe Glu Ala Arg Glu Ile Ser Leu  
 85 90 95  
 Tyr Ser Cys Ile Val Gln Met Phe Phe Leu His Gly Phe Thr Phe Met  
 100 105 110  
 Glu Ser Gly Val Leu Val Ala Thr Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asp Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ser Arg Ile Ile  
 130 135 140  
 Gln Met Gly Leu Leu Met Ile Thr Arg Ala Ile Val Leu Ile Leu Pro  
 145 150 155 160  
 Leu Leu Leu Leu Leu Lys Pro Leu Tyr Phe Cys Arg Met Asn Ala Leu  
 165 170 175  
 Ser His Ser Tyr Cys Tyr His Pro Asp Val Ile Gln Leu Ala Cys Ser  
 180 185 190  
 Asp Ile Arg Ala Asn Ser Ile Cys Gly Leu Ile Asp Leu Ile Leu Thr  
 195 200 205  
 Thr Gly Ile Asp Thr Pro Cys Ile Val Leu Ser Tyr Ile Leu Ile Ile

```

      210              215              220
Arg Phe Val Leu Arg Ile Ala Ser Pro Glu Glu Trp His Lys Val Phe
225              230              235              240
Ser Thr Cys Val Ser His Val Gly Ala Val Ala Phe Phe Tyr Ile His
      245              250              255
Met Leu Ser Leu Ser Leu Val Tyr Arg Tyr Gly Arg Ser Ala Pro Arg
      260              265              270
Val Val His Ser Val Met Ala Asn Val Tyr Leu Leu Leu Pro Pro Val
      275              280              285
Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Lys Ala
      290              295              300
Met Leu Ser Leu Leu Leu Thr Lys Xaa Thr Asp Ile Val Leu Phe Asp
305              310              315              320
Thr Asn Leu

```

&lt;210&gt; 1378

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g295 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1378

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser
      20              25              30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35              40              45
Ile Leu Ala Val Cys Ser Asp Ser Pro Leu His Thr Pro Arg Tyr Phe
      50              55              60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65              70              75              80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Thr Ser
      85              90              95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100              105              110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115              120              125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130              135              140
Val Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
      145              150              155              160
His Ser Trp Ile Val Leu Gln Phe Thr Ile Val Xaa Asn Leu Glu Ile
      165              170              175
Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
      180              185              190
Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
      195              200              205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Ile
      210              215              220
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
      225              230              235              240
Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr
      245              250              255

```



Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Gln Pro Pro Arg Asn  
                   260                  265                  270  
 Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro M t Leu Asn  
                   275                  280                  285  
 Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu Trp  
                   290                  295                  300  
 Arg Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe  
 305                  310                  315                  320  
 Ser

<210> 1379

<211> 325

<212> PRT

<213> Unknown (H38g296 protein)

<220>

<223> Synthetic construct

<400> 1379

Met Ala Ile Phe Asn Asn Thr Thr Ser Ser Ser Ser Asn Phe Leu Leu  
 1                  5                  10                  15  
 Thr Ala Phe Pro Gly Leu Glu Cys Ala His Val Trp Ile Ser Ile Pro  
                   20                  25                  30  
 Val Cys Cys Leu Tyr Thr Ile Ala Leu Leu Gly Asn Ser Met Ile Phe  
                   35                  40                  45  
 Leu Val Ile Ile Thr Lys Arg Arg Leu His Lys Pro Met Tyr Tyr Phe  
                   50                  55                  60  
 Leu Ser Met Leu Ala Ala Val Asp Leu Cys Leu Thr Ile Thr Thr Leu  
 65                  70                  75                  80  
 Pro Thr Val Leu Gly Val Leu Trp Phe His Ala Arg Glu Ile Ser Phe  
                   85                  90                  95  
 Lys Ala Cys Phe Ile Gln Met Phe Phe Val His Ala Phe Ser Leu Leu  
                   100                  105                  110  
 Glu Ser Ser Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
                   115                  120                  125  
 Cys Asn Pro Leu Asn Tyr Ala Thr Ile Leu Thr Asp Arg Met Val Leu  
                   130                  135                  140  
 Val Ile Gly Leu Val Ile Cys Ile Arg Pro Ala Val Phe Leu Leu Pro  
 145                  150                  155                  160  
 Leu Leu Val Ala Ile Asn Thr Val Ser Phe His Gly Gly His Glu Leu  
                   165                  170                  175  
 Ser His Pro Phe Cys Tyr His Pro Glu Val Ile Lys Tyr Thr Tyr Ser  
                   180                  185                  190  
 Lys Pro Trp Ile Ser Ser Phe Trp Gly Leu Phe Leu Gln Leu Tyr Leu  
                   195                  200                  205  
 Asn Gly Thr Asp Val Leu Phe Ile Leu Phe Ser Tyr Val Leu Ile Leu  
                   210                  215                  220  
 Arg Thr Val Leu Gly Ile Val Ala Arg Lys Lys Gln Gln Lys Ala Leu  
 225                  230                  235                  240  
 Ser Thr Cys Val Cys His Ile Cys Ala Val Thr Ile Phe Tyr Val Pro  
                   245                  250                  255  
 Leu Ile Ser Leu Ser Leu Ala His Arg Leu Phe His Ser Thr Pro Arg  
                   260                  265                  270  
 Val Leu Cys Ser Thr Leu Ala Asn Ile Tyr Leu Leu Leu Pro Pro Val  
                   275                  280                  285  
 Leu Asn Pro Ile Ile Tyr Ser Leu Lys Thr Lys Thr Ile Arg Gln Ala  
                   290                  295                  300  
 Met Phe Gln Leu Leu Gln Ser Lys Gly Ser Trp Gly Phe Asn Val Arg  
 305                  310                  315                  320  
 Gly Leu Arg Gly Arg

325

&lt;210&gt; 1380

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g297 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1380

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
          20           25           30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
          165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly
          210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
305          310          315

```

&lt;210&gt; 1381

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g298 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1381

```

Met Ser Pro Leu Asn Gln Thr Thr Glu Asn His Gln Ser Phe Phe Thr
 1          5          10          15
Leu Thr Gly Ile Pro Gly Met Pro Glu Lys Asp Leu Trp Met Ala Leu
 20          25          30
Pro Leu Cys Leu Leu Tyr Ser Thr Thr Ile Leu Gly Asn Val Thr Ile
 35          40          45
Leu Val Val Ile Lys Val Glu Gln Ser Leu His Glu Pro Met Tyr Tyr
 50          55          60
Phe Leu Ala Met Leu Ala Ala Thr Asp Leu Ser Leu Ser Leu Ser Ser
 65          70          75          80
Met Pro Thr Met Val Ser Val His Trp Phe Asn Trp Arg Ser Ile Thr
 85          90          95
Phe Asn Gly Cys Leu Ile Gln Met Phe Phe Ile His Thr Phe Gly Gly
100          105          110
Val Glu Ser Gly Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala
115          120          125
Ile Arg Phe Pro Leu His Tyr Ala Thr Ile Leu Thr His Ser Val Ile
130          135          140
Ser Lys Ile Ala Ala Ala Ile Leu Leu Arg Ser Val Gly Ala Val Leu
145          150          155          160
Pro Val Pro Phe Leu Ile Lys Arg Leu Pro Phe Cys His Ser Asn Val
165          170          175
Leu Ser His Ala Tyr Cys Leu His Gln Asp Ala Met Arg Leu Ala Cys
180          185          190
Ala Asp Thr Gly Val Asn Ser Ile Tyr Gly Leu Leu Ala Val Ile Phe
195          200          205
Ile Ile Val Leu Asp Ala Leu Ile Leu Leu Ala Ser Tyr Ile Leu Ile
210          215          220
Leu Gln Ala Val Leu Ser Ile Ala Ser Gln Glu Asp Arg Leu Lys Ala
225          230          235          240
Leu Asn Thr Cys Leu Ser His Met Ser Ala Val Leu Leu Phe Tyr Val
245          250          255
Pro Leu Ile Gly Met Thr Leu Ile His Arg Tyr Gly Lys His Leu Ser
260          265          270
Pro Leu Ile His Thr Phe Met Ala Asn Ile Tyr Leu Leu Pro Pro
275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Xaa Xaa
290          295          300
Gln Ile Val Gln Ala Phe Cys Gly Ala Arg Val Ser Pro Xaa Trp His
305          310          315          320
Leu Leu Phe

```

&lt;210&gt; 1382

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g299 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1382

```

Met Ser Val Leu Asn Asn Ser Glu Val Lys Leu Phe Leu Leu Ile Gly
 1          5          10          15
Ile Pro Gly Leu Glu His Ala His Ile Trp Phe Ser Ile Pro Ile Cys
 20          25          30
Leu Met Tyr Leu Leu Ala Ile Met Gly Asn Cys Thr Ile Leu Phe Ile

```

```

      35              40              45
Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala
  50              55              60
M t Leu Ala Val Ser Asp Met Gly Leu Ser Leu Ser Ser Leu Pro Thr
  65              70              75              80
Met Leu Arg Val Phe Leu Phe Asn Ala Met Gly Ile Ser Pro Asn Ala
      85              90              95
Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Val Met Glu Ser
      100              105              110
Ser Val Leu Leu Ile Met Ser Leu Asp Arg Phe Leu Ala Ile His Asn
      115              120              125
Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Asn Arg Val Ala Lys Met
      130              135              140
Gly Leu Ile Leu Ala Ile Arg Ser Ile Leu Leu Val Ile Pro Phe Pro
  145              150              155              160
Phe Thr Leu Arg Arg Leu Lys Tyr Cys Gln Lys Asn Leu Leu Ser His
      165              170              175
Ser Tyr Cys Leu His Gln Asp Thr Met Lys Leu Ala Cys Ser Asp Asn
      180              185              190
Lys Thr Asn Val Ile Tyr Gly Phe Phe Ile Ala Leu Cys Thr Met Leu
      195              200              205
Asp Leu Ala Leu Ile Val Leu Ser Tyr Val Leu Ile Leu Lys Thr Ile
      210              215              220
Leu Ser Ile Ala Ser Leu Ala Glu Arg Leu Lys Ala Leu Asn Thr Cys
  225              230              235              240
Val Ser His Ile Cys Ala Val Leu Thr Phe Tyr Val Pro Ile Ile Thr
      245              250              255
Leu Ala Ala Met His His Phe Ala Lys His Lys Ser Pro Leu Val Val
      260              265              270
Ile Leu Ile Ala Asp Met Phe Leu Leu Val Pro Pro Leu Met Asn Pro
      275              280              285
Ile Val Tyr Cys Val Lys Thr Arg Gln Ile Trp Glu Lys Ile Leu Gly
      290              295              300
Lys Leu Leu Asn Val Cys Gly Arg
  305              310

```

&lt;210&gt; 1383

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g300 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(308)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1383

```

Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
  1              5              10              15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
      20              25              30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
      35              40              45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
      50              55              60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
  65              70              75              80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
      85              90              95

```

```

Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
      100      105      110
Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
      115      120      125
Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
      130      135      140
Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
      145      150      155      160
Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
      165      170      175
Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
      180      185      190
Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
      195      200      205
Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
      210      215      220
Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
      225      230      235      240
Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
      245      250      255
Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
      260      265      270
Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
      275      280      285
Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
      290      295      300
Trp Lys Asp Ser
305

```

&lt;210&gt; 1384

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g301 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1384

```

Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe Leu
      20      25      30
Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
      35      40      45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
      65      70      75      80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
      85      90      95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
      100      105      110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser Asp
      115      120      125
Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
      130      135      140
Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln Thr
      145      150      155      160
Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp His
      165      170      175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

```

180								185				190			
Ser	Ser	Asn	Glu	Ala	Ala	Ile	Met	Val	Ser	Ser	Ile	Val	Leu	Leu	Met
		195					200					205			
Thr	Pro	Phe	Cys	Leu	Val	Leu	Leu	Ser	Tyr	Ile	Arg	Ile	Ile	Ser	Thr
		210					215					220			
Ile	Leu	Lys	Ile	Gln	Ser	Arg	Glu	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr
225					230					235					240
Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ala	Leu	Cys	Tyr	Gly	Thr	Thr	Ile
				245						250					255
Phe	Thr	Tyr	Ile	Gln	Pro	His	Ser	Gly	Pro	Ser	Val	Leu	Gln	Glu	Lys
				260									270		
Leu	Ile	Ser	Val	Phe	Tyr	Ala	Ile	Val	Met	Pro	Leu	Leu	Asn	Pro	Val
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Trp	His	Lys	Leu
		290				295					300				
Leu	Glu	Lys	Phe	Ser	Gly	Leu	Thr	Ser	Lys	Leu	Gly	Thr			
305					310					315					

**<210> 1385**

**<211> 306**

<212> PRT

<213> Unknown (H38g302 protein)

**<220>**

**<223> Synthetic construct**

**<400> 1385**

Met 1	Glu	Gly	Lys	Asn 5	Gln	Thr	Asn	Ile	Ser 10	Glu	Phe	Leu	Leu	Leu 15	Gly
Phe	Ser	Ser	Trp	Gln	Gln	Gln	Gln	Val	Leu	Leu	Phe	Ala	Leu	Phe	Leu
			20					25					30		
Cys	Leu	Tyr	Leu	Thr	Gly	Leu	Phe	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala
		35					40					45			
Ile	Gly	Ser	Asp	His	Cys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Leu	Cys	Leu	Pro	Ser	Ala	Thr	Val	Pro	Lys
65				70					75					80	
Met	Leu	Leu	Asn	Ile	Gln	Thr	Gln	Thr	Gln	Thr	Ile	Ser	Tyr	Pro	Gly
			85						90					95	
Cys	Leu	Ala	Gln	Met	Tyr	Phe	Cys	Met	Met	Phe	Ala	Asn	Met	Asp	Asn
			100					105					110		
Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
		115					120					125			
Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ala	Leu	Arg	Leu	Cys	Ala	Ser	Leu
	130					135					140				
Val	Ala	Ala	Pro	Trp	Val	Ile	Ala	Ile	Leu	Asn	Pro	Leu	Leu	His	Thr
145				150					155					160	
Leu	Met	Met	Ala	His	Leu	His	Phe	Cys	Ser	Asp	Asn	Val	Ile	His	His
			165					170					175		
Phe	Phe	Cys	Asp	Ile	Asn	Ser	Leu	Leu	Pro	Leu	Ser	Cys	Ser	Asp	Thr
		180					185					190			
Ser	Leu	Asn	Gln	Leu	Ser	Val	Leu	Ala	Thr	Val	Gly	Leu	Ile	Phe	Val
		195					200					205			
Val	Pro	Ser	Val	Cys	Ile	Leu	Val	Ser	Tyr	Ile	Leu	Ile	Val	Ser	Ala
	210					215					220				
Val	Met	Lys	Val	Pro	Ser	Ala	Gln	Gly	Lys	Leu	Lys	Ala	Phe	Ser	Thr
225				230					235					240	
Cys	Gly	Ser	His	Leu	Ala	Leu	Val	Ile	Leu	Phe	Tyr	Gly	Ala	Asn	Thr
			245					250					255		
Gly	Val	Tyr	Met	Ser	Pro	Leu	Ser	Asn	His	Ser	Thr	Glu	Lys	Asp	Ser
		260						265				270			

Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr  
 290 295 300  
 Leu Ser  
 305

<210> 1386

<211> 311

<212> PRT

<213> Unknown (H38g303 protein)

<220>

<223> Synthetic construct

<400> 1386

Met Gly Pro Arg Asn Gln Thr Ala Val Ser Glu Phe Leu Leu Met Lys  
 1 5 10 15  
 Val Thr Glu Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala  
 35 40 45  
 Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys  
 65 70 75 80  
 Ile Leu Val Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser  
 100 105 110  
 Cys Phe Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu  
 130 135 140  
 Ile Leu Leu Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser  
 145 150 155 160  
 Leu Met Val Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu  
 165 170 175  
 Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser Ser Val Phe Gly Ala  
 195 200 205  
 Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser Gln Ile Val Thr Ser  
 210 215 220  
 Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe Tyr Gly Thr Ala Phe  
 245 250 255  
 Gly Val Tyr Ile Ser Ser Ala Val Ala Glu Ser Ser Arg Ile Thr Ala  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Pro Gln Met Met Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Lys Ala Leu Arg Lys Leu  
 290 295 300  
 Ile Gly Arg Leu Phe Pro Phe  
 305 310

<210> 1387

<211> 313

<212> PRT

<213> Unknown (H38g304 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1387

```

Met Glu Ala Arg Asn Gln Thr Ala Ile Ser Lys Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ile Glu Asp Pro Glu Leu Gln Pro Val Leu Phe Ser Leu Phe Leu
      20           25           30
Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
      35           40           45
Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Leu Ser Thr Thr Thr Ile Pro Lys
65           70           75           80
Met Leu Val Asn Ile Gln Ala Gln Asn Arg Ser Ile Thr Tyr Ser Gly
      85           90           95
Cys Leu Thr Gln Ile Cys Phe Val Leu Phe Phe Ala Gly Leu Glu Asn
      100          105          110
Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
      130          135          140
Ile Leu Leu Ser Leu Leu Thr Ser Val Val Asn Ala Leu Leu Leu Ser
145          150          155          160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Leu
      165          170          175
Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu Thr Cys Ser Asp Thr
      180          185          190
Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala Cys Ile Phe Gly Gly
      195          200          205
Val Pro Leu Ser Gly Ile Ile Leu Ser Tyr Thr Gln Ile Thr Ser Cys
      210          215          220
Val Leu Arg Met Pro Ser Ala Ser Gly Lys His Lys Ala Val Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Ile Val Leu Leu Phe Tyr Gly Ala Gly Leu
      245          250          255
Gly Val Tyr Ile Ser Ser Val Val Thr Asp Ser Pro Arg Lys Ala Ala
      260          265          270
Val Ala Ser Val Met Tyr Ser Val Phe Pro Gln Met Val Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Thr Leu Arg Lys Phe
      290          295          300
Ile Gly Arg Ile Pro Ser Leu Leu Trp
305          310

```

&lt;210&gt; 1388

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g305 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1388

```

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
      20           25           30
Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
      35           40           45

```



```

Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
          85          90          95
Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
          100          105          110
Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
          130          135          140
Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
145          150          155          160
Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
          165          170          175
Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
          180          185          190
Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
          195          200          205
Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
          210          215          220
Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
          245          250          255
Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
          260          265          270
Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
          290          295          300
Val Asn Arg Lys Ile Thr Ser Ser Ser
305          310

```

&lt;210&gt; 1389

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g306 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1389

```

Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1          5          10          15
Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
          20          25          30
Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
          35          40          45
Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe Leu
          50          55          60
Ala Met Leu Ala Ala Ile Asp Gln Leu Ser Ile Ser Ser Ala Leu Pro
65          70          75          80
Pro Gly Gln Thr Val Phe Trp Phe Thr Asp Gln Lys Asn Lys Pro Phe
          85          90          95
Ala Gly

```

&lt;210&gt; 1390

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g307 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1390

```

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1              5              10              15
Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
      20              25              30
Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
      35              40              45
Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
 50              55              60
Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
 65              70              75              80
Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
      85              90              95
Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
      100              105              110
His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
      115              120              125
Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
 130              135              140
Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
 145              150              155              160
Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
      165              170              175
Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
      180              185              190
Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
      195              200              205
Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
 210              215              220
Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Glu
 225              230              235              240
Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
      245              250              255
Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
      260              265              270
Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
      275              280              285
Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
      290              295              300
Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
 305              310              315              320

```

&lt;210&gt; 1391

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g308 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1391

```

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1              5              10              15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
      20              25              30

```

Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser  
           35                          40                          45  
 Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
           50                          55                          60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys  
 65                          70                          75                          80  
 Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly  
                           85                          90                          95  
 Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn  
                           100                          105                          110  
 Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His  
           115                          120                          125  
 Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu  
           130                          135                          140  
 Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr  
 145                          150                          155                          160  
 Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His  
                           165                          170                          175  
 Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr  
                           180                          185                          190  
 His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile  
                           195                          200                          205  
 Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr  
           210                          215                          220  
 Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr  
 225                          230                          235                          240  
 Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile  
                           245                          250                          255  
 Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr  
                           260                          265                          270  
 Met Ala Thr Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
           275                          280                          285  
 Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val  
           290                          295                          300  
 Val Gly Arg Val Val Phe Ser Val  
 305                          310

&lt;210&gt; 1392

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g309 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1392

Met Tyr Phe Phe Leu Arg Gln Leu Ser Val Val Glu Leu Phe Tyr Thr  
   1                          5                          10                          15  
 Thr Asp Ile Val Pro Arg Thr Leu Ala Asn Leu Gly Ser Pro His Pro  
           20                          25                          30  
 Gln Ala Ile Ser Phe Gln Gly Cys Ala Ala His Met Tyr Val Phe Ile  
           35                          40                          45  
 Val Leu Gly Ile Ser Glu Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp  
           50                          55                          60  
 Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser  
 65                          70                          75                          80  
 Pro Arg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile  
                           85                          90                          95  
 Ile Thr Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg  
           100                          105                          110  
 Ser His Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu

```

      115              120              125
Arg Leu Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr
 130              135              140
Ala Thr Ile Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser
145              150              155              160
Tyr Ile Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser
      165              170              175
Arg Arg Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser
      180              185              190
Leu Phe Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly
 195              200              205
Ser Ser Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile
 210              215              220
Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val
225              230              235              240
Arg Arg Ala Leu Arg His Leu Val Lys Arg Gln Arg Pro Ser
      245              250

```

&lt;210&gt; 1393

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g310 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1393

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1              5              10              15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
      20              25              30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35              40              45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val
 50              55              60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
65              70              75              80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
      85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100              105              110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
 115              120              125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130              135              140
Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu
145              150              155              160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
      165              170              175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
      180              185              190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195              200              205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
 210              215              220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225              230              235              240

```

Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu  
 305 310 315 320  
 Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr  
 325 330

&lt;210&gt; 1394

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g311 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1394

Met Glu Glu Tyr Asn Thr Ser Ser Thr Asp Phe Thr Phe Met Gly Leu  
 1 5 10 15  
 Phe Asn Arg Lys Glu Thr Ser Gly Leu Ile Phe Ala Ile Ile Ser Ile  
 20 25 30  
 Ile Phe Phe Thr Ala Leu Met Ala Asn Gly Val Met Ile Phe Leu Ile  
 35 40 45  
 Gln Thr Asp Leu Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His  
 50 55 60  
 Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys  
 85 90 95  
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe  
 100 105 110  
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 115 120 125  
 Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile  
 130 135 140  
 Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro  
 145 150 155 160  
 Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe  
 165 170 175  
 Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala  
 180 185 190  
 Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile  
 195 200 205  
 Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val  
 210 215 220  
 Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr  
 245 250 255  
 Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val  
 260 265 270  
 Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala Leu  
 290 295 300  
 Gly Arg Phe Lys Gly Pro Gln

305

310

&lt;210&gt; 1395

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g312 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(295)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1395

```

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr
 1           5           10           15
Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu
      20           25           30
Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile
      35           40           45
Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
      50           55           60
Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
65           70           75           80
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu
      85           90           95
Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
      100          105          110
Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile
      115          120          125
Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
      130          135          140
Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
145          150          155          160
Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro
      165          170          175
Ile Ser Gly Thr Phe Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
      180          185          190
Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly
      195          200          205
Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly
      210          215          220
Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala
225          230          235          240
Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
      245          250          255
Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg
      260          265          270
Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val
      275          280          285
Xaa Val Arg Lys Gly Ser Lys
      290          295

```

&lt;210&gt; 1396

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g313 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1396

```

Met Thr Leu Gly Ser Leu Gly Asn Ser Ser Ser Val Ser Ala Thr
 1              5              10              15
Phe Leu Leu Ser Gly Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile
      20              25              30
Ser Ile Pro Leu Cys Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys
      35              40              45
Thr Ile Leu Phe Ile Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met
      50              55              60
Tyr Leu Phe Leu Ser Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu
65              70              75              80
Cys Thr Leu Pro Thr Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu
      85              90              95
Ile Ser His Asp Ala Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe
      100              105              110
Ser Phe Leu Glu Ser Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe
      115              120              125
Val Ala Ile Cys His Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr
      130              135              140
Val Ile Gly Arg Ile Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu
145              150              155              160
Ile Phe Pro Leu Pro Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser
      165              170              175
Pro Val Leu Ser His Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu
      180              185              190
Ala Cys Ala Asp Met Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile
      195              200              205
Val Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala
      210              215              220
Leu Ile Leu Arg Thr Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe
225              230              235              240
Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe
      245              250              255
Tyr Thr Pro Met Ile Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln
      260              265              270
Ala Pro His Leu Val Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe
      275              280              285
Pro Pro Val Met Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
      290              295              300
Arg Asp Arg Val Thr His Ala Phe Cys Tyr
305              310

```

&lt;210&gt; 1397

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g314 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1397

```

Met Gly Leu Phe Arg Gln Ser Lys His Pro Met Ala Asn Ile Thr Trp
 1              5              10              15
Met Ala Asn His Thr Gly Trp Ser Asp Phe Ile Leu Leu Gly Leu Phe
      20              25              30
Arg Gln Ser Lys His Pro Ala Leu Cys Val Val Ile Phe Val Val
      35              40              45
Phe Leu Met Ala Leu Ser Gly Asn Ala Val Leu Ile Leu Leu Ile His
      50              55              60
Cys Asp Ala His Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln Leu

```

```

65          70          75          80
Ser Leu Met Asp Met Ala Tyr Ile Ser Val Thr Val Pro Lys Met Leu
          85          90          95
Leu Asp Gln Val Met Gly Val Asn Lys Ile Ser Ala Pro Glu Cys Gly
          100          105          110
Met Gln Met Phe Phe Tyr Val Thr Leu Ala Gly Ser Glu Phe Phe Leu
          115          120          125
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
          130          135          140
Arg Tyr Pro Val Leu Met Asn His Arg Val Cys Leu Phe Leu Ser Ser
          145          150          155          160
Gly Cys Trp Phe Leu Gly Ser Val Asp Gly Phe Thr Phe Thr Pro Ile
          165          170          175
Thr Met Thr Phe Pro Phe Arg Gly Ser Arg Glu Ile His His Phe Phe
          180          185          190
Cys Glu Val Pro Ala Val Leu Asn Leu Ser Cys Ser Asp Thr Ser Leu
          195          200          205
Tyr Glu Ile Phe Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile Pro
          210          215          220
Val Val Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Ile His
          225          230          235          240
Gly Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser
          245          250          255
Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Ile Tyr Thr
          260          265          270
Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met Val
          275          280          285
Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Val Asn Pro Leu Ile Tyr
          290          295          300
Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu Thr
          305          310          315          320
Val Glu Pro Ala Phe Gln Lys Ala Met Glu
          325          330

```

&lt;210&gt; 1398

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g315 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(197)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1398

```

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu
1          5          10          15
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly
          20          25          30
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr
          35          40          45
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp
          50          55          60
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp
65          70          75          80
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu
          85          90          95
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr
          100          105          110

```



Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His  
           115                          120                          125  
 Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu  
           130                          135                          140  
 Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val  
 145                          150                          155                          160  
 Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu  
                           165                          170                          175  
 Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys  
                           180                          185                          190  
 Leu Leu Pro Xaa Gly  
           195

<210> 1399

<211> 313

<212> PRT

<213> Unknown (H38g316 protein)

<220>

<223> Synthetic construct

<400> 1399

Met Met Thr Leu Lys Asn Cys Thr Val Phe Thr Asp Phe Ile Phe Leu  
   1                          5                          10                          15  
 Gly Leu Ser Gly Thr Gln Asp Ile Gln Gln Gly Leu Phe Val Leu Phe  
           20                          25                          30  
 Phe Leu Ile Tyr Gly Ile Thr Val Ile Val Asn Leu Gly Met Ile Leu  
           35                          40                          45  
 Leu Ile Lys Met Asp Leu Arg Leu His Thr Pro Val Tyr Tyr Phe Leu  
           50                          55                          60  
 Ser Asn Leu Ser Phe Cys Asp Val Cys Tyr Ser Ser Ser Val Ser Pro  
 65                          70                          75                          80  
 Arg Met Leu Ala Asp Phe Leu Ser Asp Gln Lys Trp Ile Pro Tyr Asn  
                           85                          90                          95  
 Leu Cys Ala Ile Gln Met Tyr Leu Phe Gly Val Phe Ala Asp Val Glu  
                           100                          105                          110  
 Cys Leu Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
           115                          120                          125  
 Asn Pro Leu Leu Tyr Thr Ile Thr Met Pro Arg Arg Ile Cys Thr Gln  
           130                          135                          140  
 Leu Val Ala Leu Ala Tyr Val Val Gly Leu Val Asp Ser Ala Ile His  
 145                          150                          155                          160  
 Thr Cys Cys Thr Phe Arg Leu Ser Phe Cys Asn Ser Asn Val Ile Asn  
                           165                          170                          175  
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Asn Pro Thr Ile  
                           180                          185                          190  
 Asn Ser Ile Asn Glu Ile Val Met Phe Thr Phe Val Gly Cys Val Ala  
           195                          200                          205  
 Gly Cys Ser Ile Val Thr Val Phe Leu Ser Tyr Ser Tyr Ile Ile Ile  
           210                          215                          220  
 Thr Ile Leu Lys Met Ser Ser Ala Glu Gly Arg Arg Lys Ala Phe Ser  
 225                          230                          235                          240  
 Thr Cys Thr Ser His Leu Met Ala Val Ala Val Phe His Gly Thr Leu  
                           245                          250                          255  
 Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Met Glu Thr Asp  
                           260                          265                          270  
 Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
           275                          280                          285  
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Lys Gly Ala Leu Lys Lys  
           290                          295                          300  
 Ala Ile Ser Thr Lys Leu Tyr Ser Val

305

310

<210> 1400  
 <211> 323  
 <212> PRT  
 <213> Unknown (H38g317 protein)

<220>  
 <223> Synthetic construct

<400> 1400  
 Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met  
 1 5 10 15  
 Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro  
 20 25 30  
 Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu  
 35 40 45  
 Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His  
 50 55 60  
 Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly  
 65 70 75 80  
 Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly  
 85 90 95  
 Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile  
 100 105 110  
 His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile  
 115 120 125  
 Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu  
 130 135 140  
 Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys  
 145 150 155 160  
 Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr  
 165 170 175  
 Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val  
 180 185 190  
 Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe  
 195 200 205  
 Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser  
 210 215 220  
 Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp  
 225 230 235 240  
 Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu  
 245 250 255  
 Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu  
 260 265 270  
 Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe  
 275 280 285  
 Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys  
 290 295 300  
 Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly  
 305 310 315 320  
 Gly Ala Gln

<210> 1401  
 <211> 128  
 <212> PRT  
 <213> Unknown (H38g318 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(128)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1401

```

Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1           5           10           15
Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
          20           25           30
Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
          35           40           45
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
          50           55           60
Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
65           70           75           80
Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
          85           90           95
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
          100          105          110
Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
          115          120          125

```

&lt;210&gt; 1402

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g319 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1402

```

Met Phe Leu Leu Asn Thr Ser Glu Val Glu Val Ser Thr Phe Leu Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Ile Pro
          20           25           30
Ile Cys Leu Met Tyr Leu Met Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35           40           45
Phe Val Ile Arg Thr Glu His Ser Leu Gln Glu Pro Met Tyr Tyr Phe
          50           55           60
Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser Phe Ser Ser Leu
65           70           75           80
Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Asn Met Gly Ile Ser Ala
          85           90           95
Asp Thr Cys Ile Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp His Leu Val Ala Ile.
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Phe Arg Val Leu
          130          135          140
Gln Ile Gly Leu Ala Phe Ala Ile Lys Ser Ile Leu Leu Val Leu Pro
145          150          155          160
Pro Phe Thr Leu Lys Arg Leu Arg Tyr Cys Asn Lys His Leu Leu Ser
          165          170          175
His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
          180          185          190
Asn Arg Val Asn Phe Tyr Tyr Gly Leu Phe Val Ala Leu Cys Met Met

```

```

      195      200      205
Ser Asp Ser Val Phe Ile Ala Ile Ser Tyr Met L u Phe Ile Leu Lys
210      215      220
Thr Val Leu Gly Ile Ala Ser His Gly Glu Cys Leu Glu Ala Leu Asp
225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Leu Val Phe Tyr Val Pro Ile
      245      250      255
Ile Thr Leu Ala Thr Met Arg Arg Phe Ala Lys His Lys Ser Pro Leu
      260      265      270
Ala Met Ile Leu Ile Ala Asp Ala Phe Leu Leu Val Pro Pro Leu Met
      275      280      285
Asn Pro Ile Val Tyr Cys Val Lys Thr Arg Gln Ile Arg Val Lys Val
      290      295      300
Leu Glu Lys Leu Ala Leu Lys Pro Lys Xaa Trp Gly
305      310      315

```

&lt;210&gt; 1403

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g320 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1403

```

Met Met Ala Ser Glu Arg Asn Gln Ser Ser Thr Pro Thr Phe Ile Leu
1      5      10      15
Leu Gly Phe Ser Glu Tyr Pro Glu Ile Gln Val Pro Leu Phe Leu Val
      20      25      30
Phe Leu Phe Val Tyr Thr Val Thr Val Val Gly Asn Leu Gly Met Ile
      35      40      45
Ile Ile Ile Arg Leu Asn Ser Lys Leu His Thr Ile Met Cys Phe Phe
      50      55      60
Leu Ser His Leu Ser Leu Thr Asp Phe Cys Phe Ser Thr Val Val Thr
      65      70      75      80
Pro Lys Leu Leu Glu Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe
      85      90      95
Ser Gly Cys Ile Met Gln Phe Cys Phe Ala Cys Ile Phe Gly Val Thr
      100      105      110
Glu Thr Phe Met Leu Ala Ala Met Ala Tyr Asp Arg Phe Val Ala Val
      115      120      125
Cys Lys Pro Leu Leu Tyr Thr Thr Ile Met Ser Gln Lys Leu Cys Ala
      130      135      140
Leu Leu Val Ala Gly Ser Tyr Thr Trp Gly Ile Val Cys Ser Leu Ile
      145      150      155      160
Leu Thr Tyr Phe Leu Leu Asp Leu Ser Phe Cys Glu Ser Thr Phe Ile
      165      170      175
Asn Asn Phe Ile Cys Asp His Ser Val Ile Val Ser Ala Ser Tyr Ser
      180      185      190
Asp Pro Tyr Ile Ser Gln Arg Leu Cys Phe Ile Ile Ala Ile Phe Asn
      195      200      205
Glu Val Ser Ser Leu Ile Ile Ile Leu Thr Ser Tyr Met Leu Ile Phe
      210      215      220
Thr Thr Ile Met Lys Met Arg Ser Ala Ser Gly Arg Gln Lys Thr Phe
      225      230      235      240
Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
      245      250      255
Ile Leu Phe Leu Tyr Cys Val Pro Asn Pro Lys Thr Ser Ser Leu Ile
      260      265      270
Val Thr Val Ala Ser Val Phe Tyr Thr Val Ala Ile Pro Met Leu Asn
      275      280      285

```

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Asn Met Phe Glu  
 290 295 300  
 Lys Leu Val Val Thr Lys Leu Ile Tyr His  
 305 310

<210> 1404

<211> 322

<212> PRT

<213> Unknown (H38g321 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1404

His Thr Glu Pro Arg Asn His Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
 20 25 30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser  
 35 40 45  
 Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Asn Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr  
 65 70 75 80  
 Val Ala Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys  
 100 105 110  
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala  
 115 120 125  
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Ser Ser Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu  
 165 170 175  
 Ile Ser His Phe Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys  
 180 185 190  
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly  
 245 250 255  
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg  
 260 265 270  
 Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290 295 300  
 Arg Arg Leu Leu Ser Arg Thr Val Glu Phe His Asp Leu Phe His Ser  
 305 310 315 320  
 Phe Ser

<210> 1405  
 <211> 330  
 <212> PRT  
 <213> Unknown (H38g322 protein)

<220>  
 <223> Synthetic construct

<400> 1405

```

Met Ser Val Leu Asn Asn Thr Ile Ala Glu Pro Leu Ile Phe Leu Leu
 1           5           10           15
Met Gly Ile Pro Gly Leu Lys Ala Thr Gln Tyr Trp Ile Ser Ile Pro
          20           25           30
Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser Met Ile Leu
          35           40           45
Phe Val Val Leu Cys Glu Arg Ser Leu His Lys Pro Met Tyr Tyr Phe
          50           55           60
Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser Leu Cys Thr Leu
65           70           75           80
Ser Thr Thr Leu Gly Val Phe Trp Phe Glu Ala Arg Glu Ile Asn Leu
          85           90           95
Asn Ala Cys Ile Ala Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
          100          105          110
Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Arg Ile Ala
          130          135          140
Lys Ile Gly Met Ser Met Leu Ile Arg Asn Val Ala Val Met Leu Pro
145          150          155          160
Val Met Leu Phe Val Lys Arg Leu Ser Phe Cys Ser Ser Met Val Leu
          165          170          175
Ser His Ser Tyr Cys Tyr His Val Asp Leu Ile Gln Leu Ser Cys Thr
          180          185          190
Asp Asn Arg Ile Asn Ser Ile Leu Gly Leu Phe Ala Leu Leu Ser Thr
          195          200          205
Thr Gly Phe Asp Cys Pro Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ile
          210          215          220
Arg Ser Val Leu Ser Ile Ala Ser Ser Glu Glu Arg Arg Lys Ala Phe
225          230          235          240
Asn Thr Cys Thr Ser His Ile Ser Ala Val Ser Ile Phe Tyr Leu Pro
          245          250          255
Leu Ile Ser Leu Ser Leu Val His Arg Tyr Gly His Ser Ala Pro Pro
          260          265          270
Phe Val His Ile Ile Met Ala Asn Val Phe Leu Leu Ile Pro Pro Val
          275          280          285
Leu Asn Pro Ile Ile Tyr Ser Val Lys Ile Lys Gln Ile Gln Lys Ala
          290          295          300
Ile Ile Lys Val Leu Ile Gln Lys His Ser Lys Ser Asn His Gln Leu
305          310          315          320
Phe Leu Ile Arg Asp Lys Ala Ile Tyr Glu
          325          330

```

<210> 1406  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g323 protein)

<220>  
 <223> Synthetic construct

<400> 1406

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu  
 1 5 10 15  
 Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val  
 20 25 30  
 Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile  
 35 40 45  
 Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr  
 65 70 75 80  
 Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr  
 85 90 95  
 Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr  
 100 105 110  
 Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala  
 130 135 140  
 Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val  
 145 150 155 160  
 Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile  
 165 170 175  
 Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser  
 180 185 190  
 Asp Ile Leu Ile Pro His Leu Leu Leu Phe Ser Phe Ala Thr Phe Asn  
 195 200 205  
 Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe  
 210 215 220  
 Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe  
 225 230 235 240  
 Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr  
 245 250 255  
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr  
 260 265 270  
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn  
 275 280 285  
 Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp  
 290 295 300  
 Lys Leu Ile His Thr Gln Val Pro Phe His  
 305 310

&lt;210&gt; 1407

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g324 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1407

Met Val Leu Ala Ser Gly Asn Ser Ser Ser His Pro Val Ser Phe Ile  
 1 5 10 15  
 Leu Leu Gly Ile Pro Gly Leu Glu Ser Phe Gln Leu Trp Ile Ala Phe  
 20 25 30  
 Pro Phe Cys Ala Thr Tyr Ala Val Ala Val Val Gly Asn Ile Thr Leu  
 35 40 45  
 Leu His Val Ile Arg Ile Asp His Thr Leu His Glu Pro Met Tyr Leu  
 50 55 60  
 Phe Leu Ala Met Leu Ala Ile Thr Asp Leu Val Leu Ser Ser Ser Thr  
 65 70 75 80  
 Gln Pro Lys Met Leu Ala Ile Phe Trp Phe His Ala His Glu Ile Gln

```

      85      90      95
Tyr His Ala Cys Leu Ile Gln Val Phe Phe Ile His Ala Phe Ser Ser
      100      105      110
Val Glu Ser Gly Val Leu Met Ala Met Ala Leu Asp Cys Tyr Val Ala
      115      120      125
Thr Cys Phe Pro Leu Arg His Ser Ser Ile Leu Thr Pro Ser Val Val
      130      135      140
Ile Lys Leu Gly Thr Ile Val Met Leu Arg Gly Leu Leu Trp Val Ser
      145      150      155
Pro Phe Cys Phe Met Val Ser Arg Met Pro Phe Cys Gln His Gln Ala
      165      170      175
Ile Pro Gln Ser Tyr Cys Glu His Met Ala Val Leu Lys Leu Val Cys
      180      185      190
Ala Asp Thr Ser Ile Ser Arg Gly Tyr Gly Leu Phe Val Ala Phe Ser
      195      200      205
Val Ala Gly Phe Asp Met Ile Val Ile Gly Met Ser Tyr Val Met Ile
      210      215      220
Leu Arg Ala Val Leu Gln Leu Pro Ser Gly Glu Ala Arg Leu Lys Ala
      225      230      235
Phe Ser Thr Arg Ala Ser His Ile Cys Val Ile Leu Ala Leu Tyr Ile
      245      250      255
Pro Ala Leu Phe Ser Phe Leu Thr Tyr Arg Phe Gly His Asp Val Pro
      260      265      270
Arg Val Val His Ile Leu Phe Ala Asn Leu Tyr Leu Leu Ile Pro Pro
      275      280      285
Met Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gly Asp
      290      295      300
Arg Val Ile Gln Gly Cys Cys Gly Asn Ile
      305      310

```

&lt;210&gt; 1408

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g325 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(287)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1408

```

Tyr Ile Leu Leu Asp Ile Tyr Ile Cys Leu Asn Asn Thr His Val Xaa
  1           5           10           15
Leu Cys Val Glu Ser Gln Arg Gln Phe Lys Ile Ser Phe Tyr Phe Ser
      20           25           30
Phe Phe Leu Leu Ala Ile Thr Xaa Phe Xaa Xaa Xaa Ile Leu Ile Ile
      35           40           45
Met Lys Thr Xaa Gln Tyr Phe Leu Lys His Lys His Leu Lys Lys Lys
      50           55           60
Phe Ser Xaa Cys Leu Val Tyr Ile Leu Thr Tyr Ile Leu Ser Leu Xaa
      65           70           75           80
Ser Lys Phe Phe Ala Leu Cys Xaa Ile Phe Ala Asp Lys Ala Phe Gln
      85           90           95
Glu Gln Val Ser Gly Asn Xaa Xaa Ser Arg Ser Xaa Glu Ser Pro Val
      100          105          110
His Tyr Thr Leu Thr Met Ser Gln Lys Phe Cys Ser Ile His Pro Ala
      115          120          125
Gly Cys Tyr Asp Gln Gly Ile Xaa Ser Ile Pro Gly His Ser Phe Ser
      130          135          140

```



```

His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn
145          150          155          160
Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala
          165          170          175
Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu
          180          185          190
Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa
          195          200          205
Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His
          210          215          220
Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln
225          230          235          240
Ala Thr Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met
          245          250          255
Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser
          260          265          270
Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln
          275          280          285

```

&lt;210&gt; 1409

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g326 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1409

```

Ser His Thr Glu Pro Xaa Asn Leu Thr Ser Val Ser Glu Phe Leu Leu
1      5      10      15
Gln Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu
20     25     30
Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile
35     40     45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
50     55     60
Leu Ser Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65     70     75     80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Xaa
85     90     95
Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile
100    105    110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile
115    120    125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
130    135    140
Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Asp Ser Gln Leu
145    150    155    160
His Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile
165    170    175
Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser
180    185    190
Asp Gly Ile Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Leu Phe
195    200    205
Ser Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val
210    215    220
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe

```

```

225          230          235          240
Ser Ile Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr
          245          250          255
Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Gly Asn
          260          265          270
Gly Val Val Ala Ser Val Met Tyr Ala Val Gly Thr Pro Met Leu Asn
          275          280          285
Ser Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp
          290          295          300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Leu
305          310          315          320
Phe Leu Cys

```

```

<210> 1410
<211> 317
<212> PRT
<213> Unknown (H38g327 protein)

```

```

<220>
<223> Synthetic construct

```

```

<400> 1410
Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1          5          10          15
Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
          20          25          30
Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile
          35          40          45
Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe
          50          55          60
Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val
65          70          75          80
Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile
          85          90          95
Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly
          100          105          110
Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
          115          120          125
Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr
          130          135          140
Cys Ile Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro
145          150          155          160
Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn
          165          170          175
Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser
          180          185          190
Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu
          195          200          205
Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn
          210          215          220
Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys
225          230          235          240
Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr
          245          250          255
Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile
          260          265          270
Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met
          275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
290          295          300

```

Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln  
 305 310 315

<210> 1411  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g328 protein)

<220>  
 <223> Synthetic construct

<400> 1411  
 Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160  
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val  
 195 200 205  
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr  
 210 215 220  
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu  
 225 230 235 240  
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Lys Ile Ser  
 305 310

<210> 1412  
 <211> 223  
 <212> PRT  
 <213> Unknown (H38g329 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(223)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1412

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
1      5      10      15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
20      25      30
Leu Val Leu Phe Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
35      40      45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
50      55      60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
65      70      75      80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
85      90      95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
100     105     110
Val Ser Ser Ile Leu Arg Val Ser Ser Arg Gly Lys Tyr Lys Ala
115     120     125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
130     135     140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145     150     155     160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
165     170     175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
180     185     190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
195     200     205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
210     215     220

```

&lt;210&gt; 1413

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g330 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1413

```

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu Ala Val
1      5      10      15
Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu Ser Asn
20      25      30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met
35      40      45
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys
50      55      60
Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp Met
65      70      75      80
Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
85      90      95
Leu His Tyr Pro Val Ile Met Asn Pro His Leu Gly Val Phe Leu Val
100     105     110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
115     120     125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
130     135     140

```

```

Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val
145          150          155          160
Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Met Phe Gly Phe Leu
          165          170          175
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ala Asn Asn Val Pro Ser Ile
          180          185          190
Leu Arg Ile Ser Ser Ser Asp Arg Lys Ser Lys Ala Phe Ser Thr Cys
          195          200          205
Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
          210          215          220
Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val
225          230          235          240
Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
          245          250          255
Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu Arg
          260          265          270
Ser Arg Thr Val Glu Ser His Asp
          275          280

```

&lt;210&gt; 1414

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g331 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1414

```

Met Glu Thr Gln Asn Leu Thr Val Val Thr Glu Phe Ile Leu Leu Gly
1          5          10          15
Leu Thr Gln Ser Gln Asp Ala Gln Leu Leu Val Phe Val Leu Val Leu
          20          25          30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
          35          40          45
Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
          50          55          60
Asn Leu Ala Leu Leu Asp Ala Ser Tyr Ser Phe Ile Val Val Pro Arg
65          70          75          80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Ser
          85          90          95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Ala Gly Glu Met
          100          105          110
Phe Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Ser Thr Ile Met Asn Pro Arg Ala Cys Tyr Ala Leu
          130          135          140
Ser Leu Val Leu Trp Leu Gly Gly Phe Ile His Ser Ile Val Gln Val
145          150          155          160
Ala Leu Ile Leu His Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
          165          170          175
Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asn Thr
          180          185          190
Phe Val Val Glu Leu Leu Met Val Ser Asn Ser Gly Leu Leu Ser Leu
          195          200          205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
          210          215          220
Ile Arg Glu His Ser Ser Glu Gly Lys Ser Lys Ala Ile Ser Thr Cys
225          230          235          240
Thr Thr His Ile Ile Ile Phe Leu Met Phe Gly Pro Ala Ile Phe
          245          250          255
Ile Tyr Thr Cys Pro Phe Gln Ala Phe Pro Ala Asp Lys Val Val Ser

```

260 265 270  
 Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Arg Lys Leu Leu Ser Gln  
 290 295 300  
 His Met Phe Cys  
 305

<210> 1415  
 <211> 154  
 <212> PRT  
 <213> Unknown (H38g332 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(154)  
 <223> Xaa = Any Amino Acid

<400> 1415  
 Gly Met Arg Lys Glu Gln Ala Val Cys Gly Ser His Arg Met Ile Glu  
 1 5 10 15  
 Met Met Cys Gly Pro Xaa Val Arg Leu Pro Gly Ser Asn Ala Gly Ser  
 20 25 30  
 Leu Leu Phe Thr His Leu Ile Leu Ala Cys Gly Ser Leu Leu Ile  
 35 40 45  
 Pro Phe His Leu Gly Leu Val Ala Ser His Thr Ser Ile Phe Leu Thr  
 50 55 60  
 Val Leu His Met Lys Ser Pro Xaa Ser Arg Asn Lys Ala Leu Ala Asn  
 65 70 75 80  
 Cys Ser Ser His Leu Ser Val Gly Leu Tyr Leu Gly Thr Val Cys Leu  
 85 90 95  
 Ile Tyr Val Thr Gln Gly Phe Ser His Ile Pro Glu Gln Lys Gln Ala  
 100 105 110  
 Val Ser Val Phe Cys Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile  
 115 120 125  
 Tyr Ile Leu Arg Asn Lys Asp Val Val Arg Ala Leu Gln Lys Val Leu  
 130 135 140  
 Gly Thr His Gln Val Ser Lys Gln Asn Thr  
 145 150

<210> 1416  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g333 protein)

<220>  
 <223> Synthetic construct

<400> 1416  
 Met Ser Phe Phe Val Asp Leu Arg Pro Met Asn Arg Ser Ala Thr  
 1 5 10 15  
 His Ile Val Thr Glu Phe Ile Leu Leu Gly Phe Pro Gly Cys Trp Lys  
 20 25 30  
 Ile Gln Ile Phe Leu Phe Ser Leu Phe Leu Val Ile Tyr Val Leu Thr  
 35 40 45  
 Leu Leu Gly Asn Gly Ala Ile Ile Tyr Ala Val Arg Cys Asn Pro Leu  
 50 55 60  
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu  
 65 70 75 80

```
<210> 1417
<211> 315
<212> PRT
<213> Unknown (H38g334 protein)
```

<220>  
<223> Synthetic construct

<400> 1417																	
Met	Ala	Asn	Ile	Thr	Arg	Met	Ala	Asn	His	Thr	Gly	Lys	Leu	Asp	Phe		
1				5					10					15			
Ile	Leu	Met	Gly	Leu	Phe	Arg	Arg	Ser	Lys	His	Pro	Ala	Leu	Leu	Ser		
			20					25					30				
Val	Val	Ile	Phe	Val	Val	Phe	Leu	Lys	Ala	Leu	Ser	Gly	Asn	Ala	Val		
		35					40					45					
Leu	Ile	Leu	Leu	Ile	His	Cys	Asp	Ala	His	Leu	His	Ser	Pro	Met	Tyr		
	50					55					60						
Phe	Phe	Ile	Ser	Gln	Leu	Ser	Leu	Met	Asp	Met	Ala	Tyr	Ile	Ser	Val		
65				70						75					80		
Thr	Val	Pro	Lys	Met	Leu	Leu	Asp	Gln	Val	Met	Gly	Val	Asn	Lys	Val		
				85				90						95			
Ser	Ala	Pro	Glu	Cys	Gly	Met	Gln	Met	Phe	Leu	Tyr	Leu	Thr	Leu	Ala		
		100						105					110				
Gly	Ser	Glu	Phe	Phe	Leu	Leu	Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	Val		
		115					120					125					
Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr	Pro	Val	Leu	Met	Asn	His	Arg	Val		
	130					135					140						
Cys	Leu	Phe	Leu	Ala	Ser	Gly	Cys	Trp	Phe	Leu	Gly	Ser	Val	Asp	Gly		

```

145          150          155          160
Phe Met Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Arg Ser Trp
          165          170          175
Glu Ile His His Phe Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser
          180          185          190
Cys Ser Asp Thr Ser Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val
          195          200          205
Leu Met Leu Leu Ile Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu
          210          215          220
Ile Leu Leu Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys
225          230          235          240
Ala Phe Ala Thr Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr
          245          250          255
Gly Ala Ala Val Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro
          260          265          270
Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val
          275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala
290          295          300
Leu Lys Lys Met Leu Thr Val Arg Phe Val Leu
305          310          315

```

&lt;210&gt; 1418

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g335 protein)

&lt;220&gt; .

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(253)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1418

```

Ser His Leu Ser Val Ile Asp Thr Leu Tyr Ile Ser Thr Ile Val Pro
1          5          10          15
Lys Met Leu Val Asp Tyr Leu Met Gly Glu Gly Thr Ile Ser Phe Ile
          20          25          30
Ala Cys Thr Ala Gln Cys Phe Leu Tyr Met Gly Phe Met Gly Ala Glu
          35          40          45
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
Asn Pro Leu Arg Tyr Pro Val Leu Ile Ser Trp Arg Val Cys Trp Met
65          70          75          80
Ile Leu Ala Ser Ser Trp Phe Gly Gly Ala Leu Asp Ser Phe Leu Leu
          85          90          95
Thr Pro Ile Thr Met Ser Leu Pro Phe Cys Ala Ser His Gln Ile Asn
          100          105          110
His Phe Phe Cys Glu Ala Pro Thr Met Leu Arg Leu Ala Cys Gly Asp
          115          120          125
Lys Thr Thr Tyr Glu Thr Val Met Tyr Val Cys Cys Val Ala Met Leu
          130          135          140
Leu Ile Pro Phe Ser Val Val Thr Ala Ser Tyr Thr Arg Ile Leu Ile
145          150          155          160
Thr Val His Gln Met Thr Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala
          165          170          175
Thr Cys Ser Ser His Met Met Val Val Thr Leu Phe Tyr Gly Ala Ala
          180          185          190
Leu Tyr Thr Tyr Thr Leu Pro Gln Ser Tyr His Thr Pro Ile Lys Asp
          195          200          205

```



Lys Val Phe Ser Ala Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro  
 210 215 220  
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Met Gly Ala Leu Lys Arg  
 225 230 235 240  
 Val Val Ala Arg Cys Xaa Gly Thr Cys Gly Val Met Arg  
 245 250

<210> 1419  
 <211> 285  
 <212> PRT  
 <213> Unknown (H38g336 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(285)  
 <223> Xaa = Any Amino Acid

<400> 1419  
 Val Phe Ser Arg Thr Arg Val Arg Leu Asn Cys Lys Arg Ile Phe Trp  
 1 5 10 15  
 Leu Thr Pro Val Phe Phe Leu Ser Pro Ser Cys Pro Ser Pro Ile Ala  
 20 25 30  
 Val Ser Lys Ser Ala Val Ser Phe Val Ser Gln Ser Arg Arg Ile Arg  
 35 40 45  
 Phe Leu Gly Cys Asp Ile Gln Thr Tyr Val Phe Leu Ala Pro Gly Gly  
 50 55 60  
 Thr Glu Ala Leu Leu Phe Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala  
 65 70 75 80  
 Ile Cys His Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys  
 85 90 95  
 Cys Leu Met Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe  
 100 105 110  
 Ile His Thr Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu  
 115 120 125  
 Ile Asn His Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys  
 130 135 140  
 Gln Asp Thr Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile  
 145 150 155 160  
 Ile Leu Leu Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val  
 165 170 175  
 Leu Ile Val Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala  
 180 185 190  
 Val Ser Thr Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala  
 195 200 205  
 Thr Thr Leu Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser  
 210 215 220  
 Arg Asp Lys Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu  
 225 230 235 240  
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val  
 245 250 255  
 Arg Arg Leu Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr Asp Phe Arg  
 260 265 270  
 Ser Leu Tyr Xaa Leu Ser Ile Asn Asn Ile Lys Ser Cys  
 275 280 285

<210> 1420  
 <211> 271  
 <212> PRT  
 <213> Unknown (H38g337 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(271)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1420

```

Arg Arg Asp Ile Phe Tyr Phe Ala Phe Ile Cys Ser Tyr Ser Xaa Leu
 1           5           10           15
Thr Leu Arg Ser Phe Val Tyr Leu Phe Ile Arg Pro Ser Ile His Pro
 20           25           30
Ser Ile His Ser Ala Ile Leu Leu Phe Asn Ser Asp Leu Leu Asn Ser
 35           40           45
Leu Leu Cys Ser Ser Ile Phe Asp Met Pro His Asp Val Gln Gln Xaa
 50           55           60
Leu Leu Leu Lys Ser Xaa Phe Leu Val Ser His Cys Phe Ser Leu Val
 65           70           75           80
Leu Tyr Leu Leu Leu Leu Xaa Leu Arg Thr Glu Lys Ser Ile Glu Lys
 85           90           95
Ile Leu Leu Pro Gly Tyr Gly Thr Leu Leu Ser Met Ala Ile Ser Tyr
100           105           110
Cys Leu Cys Val Phe Gly Leu Ser Asn Pro Ala Ala Cys Val Tyr Ala
115           120           125
Gln Xaa Cys Ser Trp Asn Lys Met Val Trp Phe Leu Phe Gln Glu Val
130           135           140
Leu Pro Ser Leu Phe Xaa Leu Arg Ile Gly Leu Pro Arg Cys Ile Thr
145           150           155           160
Ser Leu Thr Leu Tyr Ser Cys Asp Phe Phe Leu Met Ile Gly Gln Ile
165           170           175
Cys Thr Lys Lys Ser Lys Ile Ile Tyr Tyr Ile Met Pro Phe Leu Leu
180           185           190
Leu Phe Met Pro Asp Xaa Ile Phe Leu Val Leu Gln Cys Pro Leu Leu
195           200           205
Ile Ser Ile Asn Lys Xaa Pro Phe Pro Asn Leu Leu Lys Ser Pro Cys
210           215           220
Gly Ile Gly His Leu Ser Val Asp Ser Ile Ser Ser Pro Ser Phe Phe
225           230           235           240
Cys Leu Pro Val Cys Pro Ser Ile Tyr Pro Ser Thr Xaa Leu Phe Val
245           250           255
Arg Ser Thr Met Ile Xaa Xaa Ile Pro Thr Tyr Cys Asp Pro Ile
260           265           270

```

&lt;210&gt; 1421

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g338 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1421

```

Met Ser Leu Ala Glu Gly Asn Gln Ser Ser Gly Ala Val Phe Thr Leu
 1           5           10           15
Leu Gly Phe Ser Glu Tyr Ala Asp Leu Gln Val Pro Leu Phe Leu Val
 20           25           30

```

```

Phe Leu Thr Ile Tyr Thr Ile Thr Val Leu Gly Asn Leu Gly Met Ile
    35                40                45
Met Ile Ile Arg Ile Asn Pro Lys Leu His Thr Arg Met Tyr Phe Phe
    50                55                60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Val Thr
    65                70                75                80
Pro Lys Leu Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
    85                90                95
Thr Gly Cys Ile Met Gln Phe Phe Leu Ala Cys Ile Cys Ala Val Ala
    100               105               110
Glu Thr Phe Met Leu Ala Val Met Ala Tyr Asp Xaa Tyr Val Ala Val
    115               120               125
Cys Asn Pro Leu Leu Tyr Thr Val Val Arg Ser Gln Lys Leu Cys Ala
    130               135               140
Ser Leu Val Ala Gly Pro Tyr Thr Trp Gly Ile Ile Ser Ser Leu Thr
    145               150               155               160
Leu Thr Tyr Phe Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Ile Ile
    165               170               175
Asn Asn Phe Val Cys Glu His Ser Val Ile Ile Ser Val Ser Cys Ser
    180               185               190
Asp Pro Tyr Ile Ser Gln Met Leu Cys Phe Val Ile Ala Ile Phe Asn
    195               200               205
Glu Val Ser Ser Leu Gly Val Ile Leu Thr Thr Tyr Ile Phe Ile Phe
    210               215               220
Ile Ala Val Ile Lys Met Pro Ser Ala Val Gly His Gln Lys Ala Phe
    225               230               235               240
Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
    245               250               255
Val Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Trp Leu Ile
    260               265               270
Val Lys Val Gly Ser Val Phe Tyr Thr Val Ile Ile Pro Thr Leu Asn
    275               280               285
Pro Leu Thr Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Met Phe Glu
    290               295               300
Ser Xaa Xaa Ile Thr Gln
    305                310

```

&lt;210&gt; 1422

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g339 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(217)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1422

```

Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met Phe Leu Thr Val Met
    1                5                10                15
Ala Tyr Asp Cys Phe Ile Ala Ile Cys His Pro Leu His Tyr Pro Val
    20               25               30
Ile Val Asn Pro His Leu Cys Val Phe Phe Ile Leu Val Ser Phe Phe
    35               40               45
Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Phe
    50               55               60
Thr Ile Ile Lys Asn Val Glu Val Ser Asn Phe Val Cys Asp Pro Ser
    65               70               75               80
Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe

```

```

      85              90              95
Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile
      100              105              110
Leu Trp Ser Tyr Tyr Lys Ile Val Pro Tyr Ile Leu Arg Ile Ser Ser
      115              120              125
Ser Asp Gly Lys Tyr Lys Ala Phe Ala Thr Cys Gly Ser His Leu Ala
      130              135              140
Val Ala Cys Xaa Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser
      145              150              155
Ala Val Ser Pro Pro Arg Asn Gly Val Val Ala Ser Val Met Tyr
      165              170              175
Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn
      180              185              190
Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Arg Pro Arg Thr Val Glu
      195              200              205
Ser His Asp Leu Phe His Pro Phe Ser
      210              215

```

&lt;210&gt; 1423

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g340 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1423

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
  1              5              10              15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
      20              25              30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Thr Ala Leu
      35              40              45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ser
      50              55              60
His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
      65              70              75              80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85              90              95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Gly Val Thr Glu Val
      100              105              110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115              120              125
Pro Leu Leu Tyr Met Val Thr Met Ser Gln Lys Leu Arg Val Glu Leu
      130              135              140
Thr Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Ser
      145              150              155              160
Ser Leu Ala Leu Arg Ile Leu Phe Tyr Arg Ser Asn Val Ile Asn His
      165              170              175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Ser Leu Ala Cys Ser Asp Val
      180              185              190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195              200              205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
      210              215              220
Ile Leu Lys Ile His Ser Ala Glu Ser Arg His Lys Ala Phe Ser Thr
      225              230              235              240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Ser His Gly Thr Ile Leu
      245              250              255
Tyr Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Val Asp Lys
      260              265              270

```

Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
                   275                                  280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Asn Lys Ala Leu Arg Lys Val  
                   290                                  295                  300  
 Met Gly Ser Lys Ile His Ser  
 305                                  310

<210> 1424

<211> 321

<212> PRT

<213> Unknown (H38g341 protein)

<220>

<223> Synthetic construct

<400> 1424

Met Phe Leu Thr Glu Arg Asn Thr Thr Ser Glu Ala Thr Phe Thr Leu  
   1                  5                                  10                  15  
 Leu Gly Phe Ser Asp Tyr Leu Glu Leu Gln Ile Pro Leu Phe Phe Val  
                   20                                  25                  30  
 Phe Leu Ala Val Tyr Gly Phe Ser Val Val Gly Asn Leu Gly Met Ile  
                   35                                  40                  45  
 Val Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe  
                   50                                  55                  60  
 Leu Asn His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala  
   65                                  70                  75                  80  
 Pro Met Met Leu Val Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe  
                   85                                  90                  95  
 Ser Gly Cys Leu Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr  
                   100                                  105                  110  
 Glu Leu Ile Leu Phe Ala Val Met Ala Tyr Asp His Phe Val Ala Ile  
                   115                                  120                  125  
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Ile Ser Gln Lys Leu Cys Ala  
                   130                                  135                  140  
 Met Leu Val Val Val Leu Tyr Ala Trp Gly Val Ala Cys Ser Leu Thr  
   145                                  150                  155                  160  
 Leu Ala Cys Ser Ala Leu Lys Leu Ser Phe His Gly Phe Asn Thr Ile  
                   165                                  170                  175  
 Asn His Phe Phe Cys Glu Leu Ser Ser Leu Ile Ser Leu Ser Tyr Pro  
                   180                                  185                  190  
 Asp Ser Tyr Leu Ser Gln Leu Leu Leu Phe Thr Val Ala Thr Phe Asn  
                   195                                  200                  205  
 Glu Ile Ser Thr Leu Leu Ile Ile Leu Thr Ser Tyr Ala Phe Ile Ile  
                   210                                  215                  220  
 Val Thr Thr Leu Lys Met Pro Ser Ala Ser Gly His Arg Lys Val Phe  
   225                                  230                  235                  240  
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr  
                   245                                  250                  255  
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr  
                   260                                  265                  270  
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Leu Leu Asn  
                   275                                  280                  285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ile Arg  
                   290                                  295                  300  
 Lys Ile Ile Asn Thr Lys Tyr Phe His Ile Lys His Arg His Trp Tyr  
   305                                  310                  315                  320  
 Pro

<210> 1425

<211> 101

<212> PRT  
 <213> Unknown (H38g342 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(101)  
 <223> Xaa = Any Amino Acid

<400> 1425  
 Cys Cys Pro Leu His His His Tyr Leu Pro Arg Gln Ser Leu Asp Gln  
 1 5 10 15  
 Leu Thr Tyr Leu Ile Ala Leu Ile Phe Asn Phe Leu Phe Val Phe Gly  
 20 25 30  
 Leu Gln Ser Ser Phe Ile Phe Leu Lys Ala Xaa Gln Cys Phe Pro Lys  
 35 40 45  
 Asp Ile His Tyr Ile Phe Val Lys Ala Arg Arg Ala Ser Gly Tyr Leu  
 50 55 60  
 Thr Tyr His Ile Ala Gly Asn Arg Ser Xaa Thr Val Phe Phe Leu Val  
 65 70 75 80  
 Cys Asn Cys His Tyr Tyr Gly Asp Asp Ile Gly Xaa Val Xaa Ile Phe  
 85 90 95  
 Tyr Val Asn Ile Leu  
 100

<210> 1426  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g343 protein)

<220>  
 <223> Synthetic construct

<400> 1426  
 Met Pro Val Gly Lys Leu Val Phe Asn Gln Ser Glu Pro Thr Glu Phe  
 1 5 10 15  
 Val Phe Arg Ala Phe Thr Thr Ala Thr Glu Phe Gln Val Leu Leu Phe  
 20 25 30  
 Leu Leu Phe Leu Leu Leu Tyr Leu Met Ile Leu Cys Gly Asn Thr Ala  
 35 40 45  
 Ile Ile Trp Val Val Cys Thr His Ser Thr Leu Arg Thr Pro Met Tyr  
 50 55 60  
 Phe Phe Leu Ser Asn Leu Ser Phe Leu Glu Leu Cys Tyr Thr Thr Val  
 65 70 75 80  
 Val Val Pro Leu Met Leu Ser Asn Ile Leu Gly Ala Gln Lys Pro Ile  
 85 90 95  
 Ser Leu Ala Gly Cys Gly Ala Gln Met Phe Phe Phe Val Thr Leu Gly  
 100 105 110  
 Ser Thr Asp Cys Phe Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu His Tyr Thr Leu Ile Met Thr Arg Glu Leu  
 130 135 140  
 Cys Thr Gln Met Leu Gly Gly Ala Leu Gly Leu Ala Leu Phe Pro Ser  
 145 150 155 160  
 Leu Gln Leu Thr Ala Leu Ile Phe Thr Leu Pro Phe Cys Gly His His  
 165 170 175  
 Gln Glu Ile Asn His Phe Leu Cys Asp Val Pro Pro Val Leu Arg Leu  
 180 185 190  
 Ala Cys Ala Asp Ile Arg Val His Gln Ala Val Leu Tyr Val Val Ser  
 195 200 205

```

Ile Leu Val Leu Thr Ile Pro Phe Leu Leu Ile Cys Val Ser Tyr Val
 210                215                220
Phe Ile Thr Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg Arg
225                230                235                240
Arg Ala Phe Ser Thr Cys Ser Phe His Leu Thr Val Val Leu Leu Gln
                245                250                255
Tyr Gly Cys Cys Ser Leu Val Tyr Leu Arg Pro Arg Ser Ser Thr Ser
                260                265                270
Glu Asp Glu Asp Ser Gln Ile Ala Leu Val Tyr Thr Phe Val Thr Pro
                275                280                285
Leu Leu Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly
                290                295                300
Ala Leu Arg Ser Ala Ile Ile Arg Lys Ala Ala Ser Asp Ala Asn
305                310                315

```

<210> 1427  
 <211> 208  
 <212> PRT  
 <213> Unknown (H38g344 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(208)  
 <223> Xaa = Any Amino Acid

```

<400> 1427
Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
 1                5                10                15
Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
                20                25                30
Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
                35                40                45
Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
                50                55                60
Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
65                70                75                80
Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
                85                90                95
Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
                100                105                110
Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
                115                120                125
Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
                130                135                140
Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
145                150                155                160
Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
                165                170                175
Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr
                180                185                190
Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile
195                200                205

```

<210> 1428  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g345 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1428

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Pro Gly Leu Ser
 20           25           30
Leu Ser Met Tyr Leu Leu Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35           40           45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50           55           60
Ser Asn Pro Ser Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro
 65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser
 85           90           95
Cys Leu Thr Gln Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp
 100          105          110
Met Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115          120          125
Ser Pro His Tyr Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe
 130          135          140
Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser
 145          150          155          160
Trp Thr Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn
 165          170          175
Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180          185          190
Val Ile Asp Ser Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe
 195          200          205
Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser
 210          215          220
Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr
 225          230          235          240
Cys Arg Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245          250          255
Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Gly Asp Gly Val
 260          265          270
Val Val Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Cys Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290          295          300
Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu
 305          310          315          320
Cys

```

<210> 1429

<211> 310

<212> PRT

<213> Unknown (H38g346 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid



&lt;400&gt; 1429

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr  
 1 5 10 15  
 Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu  
 20 25 30  
 Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn  
 35 40 45  
 Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu  
 50 55 60  
 Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr  
 65 70 75 80  
 Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser  
 85 90 95  
 Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met  
 100 105 110  
 Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr  
 115 120 125  
 Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val  
 130 135 140  
 Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala  
 145 150 155 160  
 Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn  
 165 170 175  
 Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn  
 180 185 190  
 Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Leu Thr Ala Phe Met  
 195 200 205  
 Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile  
 210 215 220  
 Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr  
 225 230 235 240  
 Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile  
 245 250 255  
 Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg  
 260 265 270  
 Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu  
 275 280 285  
 Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala  
 290 295 300  
 Ile Gly Asn Phe Trp Val  
 305 310

&lt;210&gt; 1430

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g347 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1430

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Arg  
 1 5 10 15  
 Gly Thr Ser Glu Asp Pro Glu Trp Gln Leu Val Leu Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu

```

      35              40              45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala
 65              70              75              80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85              90              95
Gly Cys Leu Thr Gln Met Ser Pro Phe Ala Ile Phe Gly Val Met Glu
      100              105              110
Glu Asn Thr Leu Leu Ser Val Met Ala Ser Asp Arg Phe Val Ala Ile
      115              120              125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130              135              140
Phe Leu Val Leu Leu Ser Phe Phe Phe Phe Cys Cys Leu Leu Asp Ala
 145              150              155              160
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
      165              170              175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
      180              185              190
Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala
      195              200              205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ser Leu Phe Ser Tyr Tyr Lys
      210              215              220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Xaa
 225              230              235              240
Ala Phe Ser Ser Cys Trp Ser His Leu Ser Val Val Cys Xaa Phe Tyr
      245              250              255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Xaa Asp Val Ser Ser Ser Pro
      260              265              270
Arg Lys Val Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
      275              280              285
Leu Asn Pro Phe Val Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val
      290              295              300
Leu Arg Trp Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu Ile
 305              310              315              320
Cys Ser Ile Pro Phe Val Val Xaa Val Lys Lys Gly Ser Lys Val Lys
      325              330              335

```

&lt;210&gt; 1431

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g348 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1431

```

Met Lys Thr Phe Ser Ser Phe Leu Gln Ile Gly Arg Asn Met His Gln
 1              5              10              15
Gly Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Phe Phe Lys
      20              25              30
Gln Asp Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Gly Met Tyr
      35              40              45
Leu Val Thr Val Ile Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu
      50              55              60
Asp Thr Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser
 65              70              75              80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
      85              90              95
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
      100              105              110

```

Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu  
           115                  120                  125  
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn  
           130                  135                  140  
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile  
   145                  150                  155                  160  
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu  
                   165                  170                  175  
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys  
                   180                  185                  190  
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn  
           195                  200                  205  
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe  
           210                  215                  220  
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg  
   225                  230                  235                  240  
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser  
                   245                  250                  255  
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr  
                   260                  265                  270  
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala  
                   275                  280                  285  
 Val Leu Phe Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr Ser  
           290                  295                  300  
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg  
   305                  310                  315                  320  
 Lys Ile Ser Ser Leu  
                   325

&lt;210&gt; 1432

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g349 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1432

Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser  
   1                  5                  10                  15  
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg  
           20                  25                  30  
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala  
           35                  40                  45  
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu  
           50                  55                  60  
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro  
   65                  70                  75                  80  
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu  
                   85                  90                  95  
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly  
           100                  105                  110  
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser  
           115                  120                  125  
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile  
           130                  135                  140  
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr  
   145                  150                  155                  160  
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro  
                   165                  170                  175  
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile

180					185					190					
Phe	His	Gly	Val	Ile	Leu	Leu	Leu	Tyr	Cys	Val	Pro	Asn	Ser	Lys	Ser
195					200					205					
Ser	Trp	Leu	Leu	Val	Lys	Val	Ala	Thr	Val	Leu	Phe	Thr	Val	Ile	Ile
210					215					220					
Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys
225					230					235					
Gly	Thr	Val	Arg	Lys	Leu	Ile	Asn	Ser	Gln	Ser	Pro	Phe	His	Ser	Lys
245					250					255					

**<210> 1433**

**<211> 318**

<212> PRT

<213> Unknown (H38g350 protein)

**<220>**

**<223> Synthetic construct**

## <221> VARIANT

<222> (1) ... (318)

<223> Xaa = Any Amino Acid

<400> 1433

Met 1	Ala	Glu	Ser	Gly 5	Thr	Thr	Val	Thr	Glu 10	Phe	Phe	Leu	Arg	Gly 15	Phe
Arg	Leu	Lys	Ala 20	Glu	Leu	Gln	Ile	Gly 25	Leu	Phe	Phe	Val	Phe 30	Leu	Val
Ile	Phe	Leu 35	Ile	Thr	Met	Gly	Gly 40	Asn	Leu	Gly	Met	Ile 45	Val	Leu	Met
Leu	Ile 50	Gln	Thr	Asp	Pro	Arg 55	Leu	Gln	Thr	Pro	Met 60	Tyr	Phe	Phe	Leu
Ser 65	His	Leu	Ser	Phe 70	Leu	Asp	Ile	Cys	Tyr	Ser 75	Ser	Val	Ile	Gly 80	Pro
Gln	Leu	Leu	Glu	Thr 85	Leu	Ala	Thr	Asp	Lys 90	Met	Ile	Ile	Thr	Tyr 95	Glu
Arg	Cys	Ala 100	Ser	Gln	Phe	Phe	Phe	Phe 105	Thr	Leu	Cys	Ala 110	Ser	Ile	Glu
Cys	Phe 115	Leu	Leu	Ala	Val	Met	Ala 120	Tyr	Asp	Arg	Tyr	Val 125	Ala	Val	Cys
Asn	Pro 130	Leu	Leu	Tyr	Ala	Ile 135	Val	Met	Thr	Pro	Lys 140	Thr	Arg	Leu	Ala
Leu 145	Leu	Ala	Gly	Ala 150	Tyr	Ser	Gly	Ala	Ile	Val 155	Asn	Ser	Val	Ile 160	Cys
Thr	Gly	Cys	Thr	Phe 165	Ser	Ile	Ser	Phe	Ser 170	Lys	Ser	Asn	His 175	Val	Asp
Phe	Phe	Phe 180	Cys	Asp	Leu	Pro	Pro	Leu 185	Leu	Lys	Leu	Ala 190	Cys	Ser	Glu
Thr	Arg 195	Pro	Arg	Glu	Trp	Val 200	Ile	Tyr	Leu	Ser	Ala 205	Phe	Leu	Val	Ile
Thr 210	Thr	Ser	Ile	Ser	Val	Ile 215	Leu	Thr	Ser	Tyr	Leu 220	Phe	Ile	Ile	Gln
Ser 225	Val	Leu	Lys	Ile	Arg 230	Thr	Ala	Gly	Gly	Arg 235	Ala	Lys	Thr	Phe	Ser
Thr	Cys	Ala	Ser	His 245	Met	Thr	Ala	Leu	Thr 250	Leu	Phe	Phe	Gly 255	Thr	Leu
Ile	Phe	Ile 260	Tyr	Leu	Lys	Gly	Asn	Met 265	Gly	Glu	Ser	Leu 270	Glu	Glu	Asp
Lys	Ile 275	Val	Ser	Ile	Phe	Tyr	Thr 280	Val	Val	Ile	Pro 285	Met	Leu	Asn	Pro
Met	Ile 290	Tyr	Ser	Leu	Arg	Asn 295	Lys	Asp	Met	Lys	Glu 300	Ala	Leu	Lys	Lys

Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu  
 305 310 315

<210> 1434

<211> 313

<212> PRT

<213> Unknown (H38g351 protein)

<220>

<223> Synthetic construct

<400> 1434

Met Leu Leu Thr Asp Arg Asn Thr Ser Gly Thr Thr Phe Thr Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asp Tyr Pro Glu Leu Gln Val Pro Leu Phe Leu Val Phe  
 20 25 30  
 Leu Ala Ile Tyr Asn Val Thr Val Leu Gly Asn Ile Gly Leu Ile Val  
 35 40 45  
 Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Gln Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala Pro  
 65 70 75 80  
 Lys Met Leu Val Asn Leu Val Val Lys Asp Arg Thr Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Val Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr Glu  
 100 105 110  
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Thr Val Asp Met Ser Gln Lys Leu Cys Val Leu  
 130 135 140  
 Leu Val Val Gly Ser Tyr Ala Trp Gly Val Ser Cys Ser Leu Glu Leu  
 145 150 155 160  
 Thr Cys Ser Ala Leu Lys Leu Cys Phe His Gly Phe Asn Thr Ile Asn  
 165 170 175  
 His Phe Phe Cys Glu Phe Ser Ser Leu Leu Ser Leu Ser Cys Ser Asp  
 180 185 190  
 Thr Tyr Ile Asn Gln Trp Leu Leu Phe Phe Leu Ala Thr Phe Asn Glu  
 195 200 205  
 Ile Ser Thr Leu Leu Ile Val Leu Thr Ser Tyr Ala Phe Ile Val Val  
 210 215 220  
 Thr Ile Leu Lys Met Arg Ser Val Ser Gly Arg Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile  
 245 250 255  
 Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr Val  
 260 265 270  
 Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Thr Val Thr Glu  
 290 295 300  
 Ile Leu Asp Thr Lys Val Phe Ser Tyr  
 305 310

<210> 1435

<211> 312

<212> PRT

<213> Unknown (H38g352 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1435

```

Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala
 1           5           10           15
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Phe Leu
           20           25           30
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu
           35           40           45
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
           50           55           60
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln
           65           70           75           80
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg
           85           90           95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys
           100          105          110
Tyr Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Thr Ala Val Cys Gln
           115          120          125
Pro Leu Leu Tyr Val Thr Ile Ile Thr Glu Lys Asp Arg Leu Gly Leu
           130          135          140
Val Thr Gly Ala Tyr Val Ala Gly Phe Phe Ser Ala Phe Val Arg Thr
           145          150          155          160
Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn Asn Glu Ile Asn Phe
           165          170          175
Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Gly Asp Ser
           180          185          190
Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala Leu Phe Val Met Pro
           195          200          205
Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
           210          215          220
Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
           225          230          235          240
Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
           245          250          255
Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
           260          265          270
Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
           275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
           290          295          300
Leu Ser Lys Ser Lys Pro Ala Arg
           305          310

```

&lt;210&gt; 1436

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g353 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1436

```

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Ser
 1           5           10           15
Ile Ser Thr Leu Val Thr Met Leu Ser Ile Phe Trp Phe Asn Val Arg
           20           25           30
Glu Ile Ser Phe Asn Ala Cys Leu Ser His Met Phe Phe Ile Lys Phe
           35           40           45
Phe Thr Val Met Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg
           50           55           60
Phe Val Ala Val Ser Asn Pro Leu Arg Tyr Ala Met Ile Leu Thr Asp
           65           70           75           80

```

```

Ser Arg Ile Ala Gln Ile Gly Val Ala Ser Val Ile Arg Gly Leu Leu
      85                      90                      95
Met Leu Thr Pro Met Val Ala Leu Leu Ile Arg Leu Ser Tyr Cys His
      100                    105                    110
Ser Gln Val Leu His His Ser Tyr Cys Tyr His Pro Asp Val Met Lys
      115                    120                    125
Leu Ser Cys Thr Asp Thr Arg Ile Asn Ser Ala Val Gly Leu Thr Ala
      130                    135                    140
Met Phe Ser Thr Val Gly Val Asp Leu Leu Leu Ile Leu Leu Ser Tyr
      145                    150                    155                    160
Val Leu Ile Ile Arg Thr Val Leu Ser Val Ala Ser Pro Glu Glu Arg
      165                    170                    175
Lys Glu Thr Phe Ser Thr Cys Val Ser His Ile Val Ala Phe Ala Ile
      180                    185                    190
Tyr Tyr Ile Pro Leu Ile Ser Leu Ser Ile Val His Arg Phe Gly Lys
      195                    200                    205
Gln Ala Pro Ala Tyr Val His Thr Met Ile Ala Asn Thr Tyr Leu Leu
      210                    215                    220
Ile Ser Pro Leu Met Asn Pro Val Ile Tyr Ser Val Lys Thr Lys Gln
      225                    230                    235                    240
Ile Arg Arg Ala Val Ile Lys Ile Leu His Ser Lys Glu Thr
      245                    250

```

&lt;210&gt; 1437

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g354 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1437

```

Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly
  1                      5                      10                      15
Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu
      20                    25                    30
Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu
      35                    40                    45
Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50                    55                    60
His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys
      65                    70                    75                    80
Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly
      85                    90                    95
Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys
      100                    105                    110
Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn
      115                    120                    125
Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu
      130                    135                    140
Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met
      145                    150                    155                    160
Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His
      165                    170                    175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Leu Ser
      180                    185

```

&lt;210&gt; 1438

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g355 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1438

```

Leu Asn Phe Ile Ile Phe Phe Arg Xaa Thr Ser Tyr Ile Glu Pro Met
 1           5           10           15
Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val Phe
      20           25           30
Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu Ser
      35           40           45
Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu Ile
      50           55           60
Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser His
      65           70           75           80
Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln Ile
      85           90           95
Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys Arg
      100          105          110
Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys Tyr
      115          120          125
Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn Pro
      130          135          140
Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe Leu
      145          150          155          160
Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr Thr
      165          170          175
Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe Phe
      180          185          190
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met Thr
      195          200          205
Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu Ala
      210          215          220
Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala Ile
      225          230          235          240
Leu Arg Val Lys Ser Ala Gly Gly Xaa Ala Lys Thr Phe Ser Thr Cys
      245          250          255
Thr Ser His Leu Thr Thr Val Val Leu Phe Phe Gly Thr Leu Ala Phe
      260          265          270
Met Tyr Gln Arg Ser Asn Ser Ala Lys Ser Ser Glu Glu Asp Lys Ile
      275          280          285
Val Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu Ile
      290          295          300
Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Gly Lys Leu Val
      305          310          315          320
Gly Lys Phe Gln Phe Pro
      325

```

&lt;210&gt; 1439

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g356 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT



&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1439

```

Met L u Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1          5          10          15
Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
      20          25          30
Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
      35          40          45
Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
      50          55          60
Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
      65          70          75          80
Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
      85          90          95
Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
      100          105          110
Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
      115          120          125
Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
      130          135          140
Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
      145          150          155          160
Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
      165          170          175
Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
      180          185          190
Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
      195          200          205
Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
      210          215          220
Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
      225          230          235          240
Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
      245          250          255
Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg
      260          265          270
His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
      275          280          285
Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
      290          295          300
Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
      305          310          315          320
Xaa Asn Tyr Lys Ile Leu Xaa Gly
      325

```

&lt;210&gt; 1440

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g357 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1440

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
      20          25          30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu

```

```

      35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
  50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
  65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130      135      140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
      145      150      155      160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165      170      175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180      185      190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195      200      205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
      210      215      220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245      250      255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260      265      270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
      290      295      300
Met Gly Ser Lys Ile His Ser
      305      310

```

&lt;210&gt; 1441

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g358 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(209)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1441

```

Cys His Pro Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
  1      5      10      15
Gly Leu Ala Leu Ser Ser Arg Phe Phe Phe Leu Ser Val Leu Asp
      20      25      30
Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp
      35      40      45
Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu
      50      55      60
Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala
      65      70      75      80
Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr
      85      90      95

```

Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln Tyr  
                   100                  105                  110  
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe  
                   115                  120                  125  
 Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser Ser  
                   130                  135                  140  
 Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Pro  
                   145                  150                  155                  160  
 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys Ser  
                   165                  170                  175  
 Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu Leu  
                   180                  185                  190  
 Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys Val  
                   195                  200                  205  
 Lys

&lt;210&gt; 1442

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g359 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1442

Ile Xaa Leu Lys Leu Ile Phe Gly Asn Pro Arg Xaa Xaa Xaa Ile Phe  
   1                  5                  10                  15  
 Arg Cys Val Tyr Asp Tyr Leu Trp Asp Cys Gln Pro Leu Leu Tyr Asp  
                   20                  25                  30  
 Thr Ile Thr Thr Leu Lys Met Ser Gly Arg Ser Trp Xaa Leu His Ile  
                   35                  40                  45  
 Val Glu Gly Leu Thr Asn Val Ile Gln Cys Ile His Phe Thr Cys Ser  
                   50                  55                  60  
 Leu Ser Phe Cys Gly Thr Ser Ser Ile Gly Phe Thr Leu Cys Asp Leu  
                   65                  70                  75                  80  
 Pro Leu Leu Leu Thr Leu Asn Cys Gly Asp Ser Phe Leu Gln Gln Leu  
                   85                  90                  95  
 Leu Ile Phe His Phe Ala Leu Tyr Met Ile Leu Thr Arg Leu Val Leu  
                   100                  105                  110  
 Ile Leu Phe Ser Asp Leu Phe Ile Ser Lys Ala Ile Xaa Thr Pro Ala  
                   115                  120                  125  
 Asn Gln Val Ser Arg Gln Arg Phe Leu Asn Leu Phe Leu Pro Leu Pro  
                   130                  135                  140  
 His Ala Glu Leu Gln Phe Gly Xaa Leu Leu Arg Leu Gln Leu Xaa Ser  
                   145                  150                  155                  160  
 Met Cys Ala Ala Val Gly Lys Ser Leu Thr Gly Glu Arg Ala Val Thr  
                   165                  170                  175  
 Met Phe Xaa Thr Glu Xaa Thr Pro Gly Xaa Pro Phe Gln Phe Tyr Ser  
                   180                  185                  190  
 Leu Arg Asn Lys Lys Ala Lys Glu Ala Leu Arg Lys Gly Leu Asn Lys  
                   195                  200                  205  
 Ala Lys Leu Phe  
                   210

&lt;210&gt; 1443

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g360 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1443

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 1           5           10           15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      20           25           30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35           40           45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50           55           60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65           70           75           80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
      85           90           95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
      100           105           110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
      115           120           125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
      130           135           140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
      145           150           155           160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
      165           170           175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
      180           185           190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
      195           200           205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
      210           215           220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
      225           230           235           240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
      245           250           255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
      260           265           270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
      275           280           285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
      290           295           300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln
      305           310           315

```

&lt;210&gt; 1444

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g361 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1444

```

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1           5           10           15
Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
      20           25           30

```

Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met  
 35 40 45  
 Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys  
 50 55 60  
 Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala  
 65 70 75 80  
 Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro  
 85 90 95  
 Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly  
 100 105 110  
 Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe  
 115 120 125  
 Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser  
 130 135 140  
 Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg  
 145 150 155 160  
 Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val  
 165 170 175  
 Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val  
 180 185 190  
 Leu Glu Leu Ser Ser Arg Arg Ala Ala Leu Lys Ala Phe Asn Thr Cys  
 195 200 205  
 Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly  
 210 215 220  
 Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val  
 225 230 235 240  
 Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu  
 245 250 255  
 Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met  
 260 265 270  
 Phe Ser Gln Gly Gly Lys  
 275

&lt;210&gt; 1445

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g362 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1445

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15  
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
 20 25 30  
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu  
 35 40 45  
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
 50 55 60  
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met

```

145          150          155          160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
          165          170          175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
          180          185          190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
          195          200          205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
          210          215          220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
          245          250          255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
          260          265          270
Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
          275          280          285
Pro Ala Thr Leu Asn Pro Ile Tyr Gly Met Arg Thr Lys Gln Leu
          290          295          300
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
305          310          315

```

&lt;210&gt; 1446

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g363 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1446

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
1          5          10          15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
          20          25          30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
          35          40          45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
          85          90          95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
          100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
          130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Thr Lys Leu Ala Cys Ile Asp Thr
          180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
          195          200          205
Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
          210          215          220
Val Arg Asn Arg Ser Ser Val Ser Met Val Lys Ala His Ser Thr Leu
225          230          235          240

```

Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Ser Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg  
 290 295 300  
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe  
 305 310 315 320  
 Leu Glu

<210> 1447

<211> 322

<212> PRT

<213> Unknown (H38g364 protein)

<220>

<223> Synthetic construct

<400> 1447

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15  
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
 20 25 30  
 Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile  
 35 40 45  
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
 50 55 60  
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile  
 145 150 155 160  
 Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn  
 165 170 175  
 Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala  
 180 185 190  
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
 195 200 205  
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
 210 215 220  
 Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys  
 225 230 235 240  
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
 245 250 255  
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val  
 260 265 270  
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
 275 280 285  
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln L u  
 290 295 300  
 Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser

305  
Asn Leu

310

315

320

<210> 1448  
<211> 314  
<212> PRT  
<213> Unknown (H38g365 protein)

<220>  
<223> Synthetic construct

<400> 1448  
Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
1 5 10 15  
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser  
20 25 30  
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
35 40 45  
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser  
50 55 60  
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met  
65 70 75 80  
Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys  
85 90 95  
Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val  
100 105 110  
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro  
115 120 125  
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val  
130 135 140  
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu  
145 150 155 160  
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser  
165 170 175  
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile  
180 185 190  
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu  
195 200 205  
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile  
210 215 220  
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys  
225 230 235 240  
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe  
245 250 255  
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser  
260 265 270  
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr  
275 280 285  
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile  
290 295 300  
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro  
305 310

<210> 1449  
<211> 317  
<212> PRT  
<213> Unknown (H38g366 protein)

<220>  
<223> Synthetic construct



&lt;400&gt; 1449

```

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
1      5      10
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
20      25      30
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
35      40      45
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
50      55      60
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
65      70      75      80
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
85      90      95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
100     105     110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115     120     125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
130     135     140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
145     150     155     160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
165     170     175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
180     185     190
Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu
195     200     205
Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile
210     215     220
Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr
225     230     235     240
Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val
245     250     255
Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro
260     265     270
Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro
275     280     285
Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu
290     295     300
Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg
305     310     315

```

&lt;210&gt; 1450

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g367 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(101)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1450

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
1      5      10      15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
20      25      30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr

```

```

          35          40          45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
  50          55          60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
65          70          75          80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
          85          90          95
Cys Cys Leu Ala Glu
          100

```

<210> 1451  
 <211> 169  
 <212> PRT  
 <213> Unknown (H38g368 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(169)  
 <223> Xaa = Any Amino Acid

```

<400> 1451
Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe
  1          5          10          15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
          20          25          30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
          35          40          45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
          50          55          60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
65          70          75          80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
          85          90          95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
          100          105          110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
          115          120          125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
          130          135          140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
145          150          155          160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
          165

```

<210> 1452  
 <211> 279  
 <212> PRT  
 <213> Unknown (H38g369 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(279)  
 <223> Xaa = Any Amino Acid

```

<400> 1452
Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
  1          5          10          15

```

Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys  
                   20                  25                  30  
 Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser  
                   35                  40                  45  
 Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met  
                   50                  55                  60  
 Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu  
                   65                  70                  75                  80  
 Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp  
                   85                  90  
 Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile  
                   100                  105                  110  
 Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe  
                   115                  120                  125  
 Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val  
                   130                  135                  140  
 Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala  
                   145                  150                  155                  160  
 His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa  
                   165                  170                  175  
 Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys  
                   180                  185                  190  
 Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu  
                   195                  200                  205  
 Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu  
                   210                  215                  220  
 Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr  
                   225                  230                  235                  240  
 Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe  
                   245                  250                  255  
 Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu  
                   260                  265                  270  
 Ser Ile Ile Leu Thr Leu Val  
                   275

&lt;210&gt; 1453

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g370 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(154)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1453

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile  
                   1                  5                  10                  15  
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe  
                   20                  25                  30  
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg  
                   35                  40                  45  
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys  
                   50                  55                  60  
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile  
                   65                  70                  75                  80  
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu  
                   85                  90                  95  
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe

<210> 1454  
<211> 186  
<212> PRT  
<213> Unknown (H38g371 protein)

```
<221> VARIANT
<222> (1)...(186)
<223> Xaa = Any Amino Acid
```

<210> 1455  
<211> 142  
<212> PRT  
<213> Unknown (H38g372 protein)

```
<221> VARIANT
<222> (1)...(142)
<223> Xaa = Any Amino Acid
```

742

```

Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys
      20      25      30
Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile
      35      40      45
Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys
      50      55      60
Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe
65      70      75      80
Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu
      85      90      95
Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met
      100     105     110
Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr
      115     120     125
Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe
      130     135     140

```

&lt;210&gt; 1456

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g373 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(82)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1456

```

Asn Val Phe Arg Xaa Phe Leu Asp Phe Cys Arg Asp Ser Asp Ile His
  1      5      10
Arg Ala Tyr Leu Cys Ile Leu Ser Ser Xaa Leu Arg Phe Ser Val Leu
      20      25      30
Gly Ile Phe Xaa Gly Arg Ala Met Asn Ile Leu Ile Gly Leu Thr Lys
      35      40      45
Val Leu Lys Cys Pro Ile Leu Cys Val Val Phe Asn His Thr Cys Ile
      50      55      60
Leu Ile Thr Thr Leu Ala Val Ile Ala Tyr Arg Phe Arg Gln Ser Gly
65      70      75      80
Tyr Ser

```

&lt;210&gt; 1457

&lt;211&gt; 207

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g374 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(207)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1457

```

Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe
  1      5      10      15
Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys
      20      25      30
Asn Met Arg Leu Pro Ser Asp Phe Phe Leu Ser Gln Ala Ile Tyr Tyr

```

<210> 1458  
<211> 313  
<212> PRT  
<213> Unknown (H38g375 protein)

<220>  
<223> Synthetic construct

Met 1	Arg	Asn	Leu	Ser 5	Gly	Gly	His	Val	Glu 10	Glu	Phe	Val	Leu	Val 15	Gly
Phe	Pro	Thr	Thr 20	Pro	Pro	Leu	Gln	Leu 25	Leu	Leu	Phe	Val	Leu 30	Phe	Phe
Ala	Ile	Tyr 35	Leu	Leu	Thr	Leu	Leu 40	Glu	Asn	Ala	Leu	Ile 45	Val	Phe	Thr
Ile	Trp 50	Leu	Ala	Pro	Ser	Leu 55	His	Arg	Pro	Met	Tyr 60	Phe	Phe	Leu	Gly
His 65	Leu	Ser	Phe	Leu	Glu 70	Leu	Trp	Tyr	Ile	Asn 75	Val	Thr	Ile	Pro	Arg
Leu	Leu	Ala	Ala 85	Phe	Leu	Thr	Gln	Asp 90	Gly	Arg	Val	Ser	Tyr 95	Val	Gly
Cys	Met	Thr	Gln 100	Leu	Tyr	Phe	Phe 105	Ile	Ala	Leu	Ala	Cys	Thr 110	Glu	Cys
Val	Leu 115	Leu	Ala	Val	Met	Ala	Tyr 120	Asp	Arg	Tyr	Leu	Ala 125	Ile	Cys	Gly
Pro	Leu 130	Leu	Tyr	Pro	Ser	Leu 135	Met	Pro	Ser	Ser	Leu 140	Ala	Thr	Arg	Leu
Ala 145	Ala	Ala	Ser	Trp	Gly 150	Ser	Gly	Phe	Phe	Ser	Ser	Met 155	Met	Lys	Leu
Leu	Phe	Ile	Ser 165	Gln	Leu	Ser	Tyr	Cys 170	Gly	Pro	Asn	Ile 175	Ile	Asn	His
Phe	Phe	Cys 180	Asp	Ile	Ser	Pro	Leu 185	Leu	Asn	Leu	Thr	Cys 190	Ser	Asp	Lys
Glu	Gln 195	Ala	Glu	Leu	Val	Asp	Phe 200	Leu	Leu	Ala	Leu	Val 205	Met	Ile	Leu
Leu	Pro 210	Leu	Leu	Ala	Val	Val 215	Ser	Ser	Tyr	Thr	Ala 220	Ile	Ile	Ala	Ala
Ile 225	Leu	Arg	Ile	Pro	Thr 230	Ser	Arg	Gly	Arg	His 235	Lys	Ala	Phe	Ser	Thr

<210> 1459  
<211> 322  
<212> PRT  
<213> Unknown (H38g376 protein)

```
<221> VARIANT
<222> (1)...(322)
<223> Xaa = Any Amino Acid
```

745

290 295 300  
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Leu His Pro  
 305 310 315 320  
 Phe Ser

<210> 1460  
 <211> 186  
 <212> PRT  
 <213> Unknown (H38g377 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(186)  
 <223> Xaa = Any Amino Acid

<400> 1460  
 Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu  
 1 5 10 15  
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser  
 20 25 30  
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn  
 35 40 45  
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val  
 50 55 60  
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr  
 65 70 75 80  
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp  
 85 90 95  
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly  
 100 105 110  
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His  
 115 120 125  
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr  
 130 135 140  
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg  
 145 150 155 160  
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr  
 165 170 175  
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu  
 180 185

<210> 1461  
 <211> 336  
 <212> PRT  
 <213> Unknown (H38g378 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(336)  
 <223> Xaa = Any Amino Acid

<400> 1461  
 Ser Arg Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Gly Ser Ser Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe  
 20 25 30



```

Leu Ser Thr Cys Leu Val Met Ala Leu Gly Asn Leu Leu Ile Ile Leu
  35                      40                      45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50                      55                      60
Ser Asn Leu Ser Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro
  65                      70                      75                      80
Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
                      85                      90                      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
                      100                      105                      110
Asp Asn Ile Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys
                      115                      120                      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
                      130                      135                      140
Phe Leu Leu Leu Leu Ser Phe Phe Ser Ser Leu Ser Leu Leu Asp Ala
  145                      150                      155                      160
Gln Leu Tyr Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
                      165                      170                      175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
                      180                      185                      190
Cys Cys Asp Thr Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala
                      195                      200                      205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys
                      210                      215                      220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
  225                      230                      235                      240
Ala Phe Ser Thr Tyr Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr
                      245                      250                      255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro
                      260                      265                      270
Arg Lys Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
                      275                      280                      285
Met Asn Pro Phe Ile Tyr Ser Pro Arg Asn Arg Asp Met Lys Ser Val
                      290                      295                      300
Leu Arg Arg Pro His Gly Ser Thr Phe Xaa Ser Gln Tyr Leu Leu Ile
  305                      310                      315                      320
Cys Ser Ile Pro Phe Ala Val Trp Val Glu Lys Gly Cys Met Met Lys
                      325                      330                      335

```

&lt;210&gt; 1462

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g379 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1462

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1                      5                      10                      15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
                      20                      25                      30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
                      35                      40                      45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
  50                      55                      60
Phe Leu Pro Lys Leu Gln Pro Phe Ser S r Cys His Val Ser Glu Leu

```

65					70					75				80	
Cys	Thr	Cys	Leu	Asp	Thr	Phe	Thr	Lys	Ser	Tyr	Ile	Thr	Xaa	Ile	Arg
				85					90					95	
Gly	Leu	Lys	Gly	Phe	Asn	His	Leu	Cys	Phe	Leu	Leu	His	Tyr	Cys	His
			100					105					110		
Cys	Ala	Arg	Ala	Gln	Val	Ser	Xaa	Asn	Ala	Pro	Trp	Ser	Leu	Ala	Gln
		115					120					125			
Arg	Cys	Gln	Pro	Asn	Met	Leu	Ile	Arg	Xaa	Leu	Phe	Cys	Leu	Lys	Leu
		130					135					140			
Val	Val	His	Asp	Arg	Leu	Xaa	His	Val	Leu	Ser	Leu	Leu			
145					150					155					

&lt;210&gt; 1463

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g380 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1463

Met	Lys	Ile	Asn	Gln	Thr	Ile	Leu	Lys	Glu	Phe	Ile	Leu	Val	Gly	Phe
1				5				10					15		
Ser	Val	Tyr	Pro	His	Val	Gln	Thr	Phe	Leu	Phe	Val	Val	Phe	Phe	Cys
			20					25					30		
Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Gly	Asn	Leu	Thr	Ile	Met	Gly	Leu	Thr
		35					40					45			
Xaa	Val	Asp	Arg	Ser	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Ala
	50					55					60				
Leu	Ser	Phe	Ser	Glu	Thr	Cys	Tyr	Thr	Leu	Thr	Ile	Val	Pro	Lys	Met
65					70					75				80	
Leu	Glu	Asp	Leu	Leu	Ala	Lys	Asp	Arg	Ser	Ile	Ser	Val	Thr	Gly	Cys
				85				90						95	
Ser	Leu	Gln	Met	Cys	Phe	Phe	Leu	Gly	Leu	Gly	Gly	Thr	Asn	Cys	Ile
			100					105					110		
Ile	Leu	Thr	Leu	Met	Gly	Tyr	Asp	Arg	Phe	Leu	Ala	Ile	Cys	Asn	Pro
		115					120					125			
Leu	Arg	Tyr	Pro	Leu	Leu	Met	Thr	Asn	Ile	Val	Cys	Gly	Gln	Leu	Val
		130					135					140			
Ala	Ser	Ala	Cys	Thr	Ala	Gly	Phe	Phe	Ile	Ser	Leu	Thr	Glu	Thr	Ala
145					150					155				160	
Leu	Ile	Phe	Arg	Asp	Ser	Phe	Cys	Arg	Pro	Asn	Leu	Val	Lys	His	Phe
			165					170						175	
Phe	Cys	His	Met	Leu	Ala	Val	Ile	Arg	Leu	Ser	Cys	Ile	Asp	Ser	Asn
			180					185					190		
His	Thr	Glu	Phe	Ile	Ile	Thr	Leu	Ile	Ser	Val	Ser	Gly	Leu	Leu	Gly
		195					200					205			
Thr	Leu	Leu	Leu	Ile	Ile	Leu	Thr	Asp	Val	Phe	Ile	Ile	Ser	Thr	Val
		210					215					220			
Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Lys	Gln	Lys	Ala	Phe	Thr	Thr	Cys
225					230					235				240	
Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	His	Phe	Gly	Phe	Ala	Ser	Ile
				245					250					255	
Val	Tyr	Leu	Lys	Pro	Glu	Ala	Ser	Gly	Asp	Asp	Thr	Leu	Ile	Ala	Val
		260						265					270		
Pro	Tyr	Thr	Val	Ile	Thr	Pro	Phe	Leu	Ser	Pro	Ile	Ile	Phe	Ser	Leu
		275					280						285		

Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr  
 290 295 300  
 Val Ala Leu Lys Lys Ile Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu  
 305 310 315 320  
 Gly Leu Asn Val Pro  
 325

<210> 1464  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g381 protein)

<220>  
 <223> Synthetic construct

<400> 1464  
 Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu  
 20 25 30  
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg  
 65 70 75 80  
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly  
 85 90 95  
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys  
 100 105 110  
 Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala  
 115 120 125  
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu  
 130 135 140  
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr  
 145 150 155 160  
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His  
 165 170 175  
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu  
 195 200 205  
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser  
 245 250 255  
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln  
 260 265 270  
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile  
 275 280 285  
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala  
 290 295 300  
 Phe Arg Gly Arg Leu Leu Gly Lys Gly  
 305 310

<210> 1465  
 <211> 289  
 <212> PRT  
 <213> Unknown (H38g382 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(289)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1465

```

Leu Leu Phe Phe Ile Leu Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
          20           25           30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
          35           40           45
Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
          50           55           60
Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
65          70          75          80
Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
          85          90          95
Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
          100          105          110
Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
          115          120          125
Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
          130          135          140
Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
145          150          155          160
Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
          165          170          175
Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
          180          185          190
Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
          195          200          205
Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
          210          215          220
Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
225          230          235          240
Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
          245          250          255
Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
          260          265          270
Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
          275          280          285
His

```

&lt;210&gt; 1466

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g383 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1466

```

Met Glu Ser Pro Asn Arg Thr Thr Ile Gln Glu Phe Ile Phe Ser Ala
 1           5           10           15
Phe Pro Tyr Ser Trp Val Lys Ser Val Val Cys Phe Val Pro Leu Leu
          20           25           30

```

Phe Ile Tyr Ala Phe Ile Val Val Gly Asn Leu Val Ile Ile Thr Val  
 35 40 45  
 Val Gln Leu Asn Thr His Leu His Thr Pro Met Tyr Thr Phe Ile Ser  
 50 55 60  
 Ala Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ser Ser Leu Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys  
 85 90 95  
 Leu Leu Gln Met Tyr Phe Phe His Ser Thr Gly Ile Cys Glu Val Cys  
 100 105 110  
 Leu Leu Thr Val Met Ala Phe Asp His Tyr Leu Ala Ile Cys Ser Pro  
 115 120 125  
 Leu His Tyr Pro Ser Ile Met Thr Pro Lys Leu Cys Thr Gln Leu Thr  
 130 135 140  
 Leu Ser Cys Trp Val Cys Gly Phe Ile Thr Pro Leu Pro Glu Ile Ala  
 145 150 155 160  
 Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn His Leu Glu His Ile  
 165 170 175  
 Phe Cys Asp Phe Leu Pro Val Leu Arg Leu Ala Cys Thr Asp Thr Arg  
 180 185 190  
 Ala Ile Val Met Ile Gln Val Val Asp Val Ile His Ala Val Glu Ile  
 195 200 205  
 Ile Thr Ala Val Met Leu Ile Phe Met Ser Tyr Asp Gly Ile Val Ala  
 210 215 220  
 Val Ile Leu Arg Ile His Ser Ala Gly Gly Arg Arg Thr Ala Phe Ser  
 225 230 235 240  
 Thr Cys Val Ser His Phe Ile Val Phe Ser Leu Phe Phe Gly Ser Val  
 245 250 255  
 Thr Leu Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Leu Phe Trp Asp  
 260 265 270  
 Ile Ala Ile Ala Leu Ala Phe Ala Val Leu Ser Pro Phe Phe Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Ile Lys Lys  
 290 295 300  
 His Ile Gly Gln Ala Lys Ile Phe Phe Ser Val Arg Pro Gly  
 305 310 315

&lt;210&gt; 1467

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g384 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1467

Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn Glu Val Ile Ile  
 1 5 10 15  
 Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe Leu Cys Ile Leu  
 20 25 30  
 Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys Val Pro Ser Thr  
 35 40 45  
 Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val  
 50 55 60  
 Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr Phe Asn Pro Leu  
 65 70 75 80  
 Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr Val Leu Tyr Thr  
 85 90 95  
 Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 100 105 110  
 Tyr Leu Lys Gly Ala Leu Lys Lys Val Val Gly Arg Val Val Phe Ser

115 120 125

Val

<210> 1468  
 <211> 162  
 <212> PRT  
 <213> Unknown (H38g385 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(162)  
 <223> Xaa = Any Amino Acid

<400> 1468

Leu	Leu	Ile	Ile	Pro	Ala	Ile	Ala	Thr	Asp	Thr	Arg	Leu	Ser	Val	Leu
1				5					10					15	
Val	Arg	Phe	Phe	Leu	Ala	Asn	Leu	Ala	Phe	Val	Val	Thr	Cys	Phe	Thr
		20						25					30		
Ser	Thr	Thr	Ile	Pro	Lys	Met	Leu	Ala	Cys	Lys	Glu	Ile	Pro	Cys	Val
		35					40					45			
Met	Ser	Gly	Cys	Lys	Gly	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Thr	Gln	Met
	50				55						60				
Leu	Phe	Phe	Ile	Trp	Leu	Gly	Ile	His	Ser	Phe	Leu	Leu	Thr	Ala	Met
65				70					75					80	
Ala	Asn	Glu	His	Cys	Val	Ala	Ile	Cys	His	Ser	Leu	Asn	Ser	Ile	Arg
			85					90					95		
Ser	Val	Thr	Pro	Xaa	Leu	Cys	Gly	Leu	Leu	Val	Val	Ala	Ser	Trp	Thr
		100					105					110			
Phe	Ala	Phe	Arg	Asn	Ala	Leu	Thr	His	Pro	Val	Leu	Leu	Thr	Arg	Leu
	115					120					125				
Ser	Leu	Cys	Thr	Tyr	Glu	Trp	Val	Ser	His	Val	Phe	Cys	Asn	Leu	Ser
	130				135					140					
Gln	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ala	Thr	Leu	Asn	Asn	Val	Thr
145				150					155					160	
Val	Gln														

<210> 1469  
 <211> 327  
 <212> PRT  
 <213> Unknown (H38g386 protein)

<220>  
 <223> Synthetic construct

<400> 1469

Met	Leu	Thr	Pro	Asn	Asn	Ala	Cys	Ser	Val	Pro	Thr	Ser	Phe	Arg	Leu
1				5					10					15	
Thr	Gly	Ile	Pro	Gly	Leu	Glu	Ser	Leu	His	Ile	Trp	Leu	Ser	Ile	Pro
		20						25					30		
Phe	Gly	Ser	Met	Tyr	Leu	Val	Ala	Val	Leu	Gly	Asn	Ile	Thr	Ile	Leu
	35					40					45				
Ala	Val	Val	Arg	Met	Glu	Tyr	Ser	Leu	His	Gln	Pro	Met	Tyr	Phe	Phe
	50				55					60					
Leu	Cys	Met	Leu	Ala	Val	Ile	Asp	Leu	Val	Leu	Ser	Thr	Ser	Thr	Met
65				70					75					80	
Pro	Lys	Leu	Leu	Ala	Ile	Phe	Trp	Phe	Gly	Ala	His	Asn	Ile	Gly	Val
			85					90						95	

Asn Ala Cys Leu Ala Gln Met Phe Phe Ile His Cys Phe Ala Thr Val  
                   100                  105                  110  
 Glu S r Gly Ile Phe Leu Ala Met Ala Phe Asp His Tyr Val Ala Ile  
                   115                  120                  125  
 Cys Asp Pro Leu His His Thr Leu Leu Leu Thr His Ala Val Val Gly  
                   130                  135                  140  
 Arg Leu Gly Leu Ala Ala Leu Leu Arg Gly Val Ile Tyr Ile Gly Pro  
 145                  150                  155                  160  
 Leu Pro Leu Val Ile Cys Leu Arg Leu Pro Leu Tyr His Thr Gln Ile  
                   165                  170                  175  
 Ile Ala His Ser Tyr Cys Glu His Met Ala Val Val Thr Leu Ala Cys  
                   180                  185                  190  
 Gly Asp Asp Thr Arg Val Asn Asn Leu Tyr Gly Met Gly Ile Gly Phe  
                   195                  200                  205  
 Leu Val Leu Ile Leu Asp Ser Leu Ala Ile Thr Ala Ser Tyr Val Met  
                   210                  215                  220  
 Ile Phe Arg Ala Val Met Gly Leu Ala Thr Ser Glu Ala Arg Leu Lys  
 225                  230                  235                  240  
 Thr Leu Gly Thr Cys Gly Ser His Ile Cys Ala Ile Leu Val Phe Tyr  
                   245                  250                  255  
 Ile Pro Ile Ala Val Ser Ser Leu Thr His Arg Phe Gly His Arg Val  
                   260                  265                  270  
 Pro Pro His Ile His Ile His Ile His Ile His Ile His Ile  
                   275                  280                  285  
 Leu Leu Ala Asn Ile Tyr Leu Leu Ile Pro Pro Ile Leu Asn Pro Ile  
                   290                  295                  300  
 Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu Ala Leu Leu His Ile  
 305                  310                  315                  320  
 Lys Ala Arg Thr Gln Thr Arg  
                   325

&lt;210&gt; 1470

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g387 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1470

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys  
   1                  5                  10                  15  
 Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser  
                   20                  25                  30  
 Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His  
                   35                  40                  45  
 Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser  
                   50                  55                  60  
 Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe  
 65                  70                  75                  80  
 Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn  
                   85                  90                  95  
 His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu  
                   100                  105                  110  
 Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu  
                   115                  120                  125  
 Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu

```

      130              135              140
Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val
145              150              155              160
Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile
      165              170              175
Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr
      180              185              190
Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn
      195              200              205
Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala
      210              215              220
Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ile Leu Arg Ile
225              230              235              240
Pro Ser Pro Thr Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His
      245              250              255
Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile
      260              265              270
Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met
      275              280              285
Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met
      290              295              300
Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser
305              310              315              320
His Ser Ser

```

&lt;210&gt; 1471

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g388 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1471

```

Leu His Phe Cys Gly Ile Asp Val Thr Ser Tyr Gln Ala Xaa Gln Ile
1      5      10      15
Leu Ala Xaa Gln Pro Tyr Asp Thr Thr Xaa Cys Gly Gln Arg Ile Val
      20      25      30
Gly Ile Met Ala Val Ala Trp Gly Ile Gly Phe Leu His Ser Leu Ser
      35      40      45
Gln Leu Ala Phe Ala Val His Leu Pro Phe Cys Gly Pro Asn Glu Phe
      50      55      60
Asp Ser Phe Tyr Cys Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr
65      70      75      80
Asp Thr Tyr Arg Leu Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu
      85      90      95
Thr Val Cys Ser Phe Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu
      100      105      110
Met Thr Ile Gln His Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser
      115      120      125
Thr Leu Thr Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Cys
      130      135      140
Val Phe Ile Tyr Ala Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe
145      150      155      160
Leu Ala Val Phe Tyr Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile
      165      170      175

```



Tyr Thr Leu Arg Asn Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg  
                   180                  185                  190  
 Lys Trp Asp Ala His Ser Ser Val Lys Phe  
                   195                  200

<210> 1472

<211> 311

<212> PRT

<213> Unknown (H38g389 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1472

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
 1                  5                  10                  15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
                   20                  25                  30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
                   35                  40                  45  
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
                   50                  55                  60  
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
 65                  70                  75                  80  
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
                   85                  90                  95  
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
                   100                  105                  110  
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
                   115                  120                  125  
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
                   130                  135                  140  
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
 145                  150                  155                  160  
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
                   165                  170                  175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
                   180                  185                  190  
 Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu  
                   195                  200                  205  
 Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser  
                   210                  215                  220  
 Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr  
 225                  230                  235                  240  
 Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile  
                   245                  250                  255  
 Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His  
                   260                  265                  270  
 His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro  
                   275                  280                  285  
 Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu  
                   290                  295                  300  
 Ser Tyr Ile Gln Arg Ala Arg  
 305                  310

<210> 1473

<211> 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g390 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1473

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1          5          10          15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
 20          25          30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Ile Phe
 35          40          45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
 65          70          75          80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85          90          95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
305          310          315

```

&lt;210&gt; 1474

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g391 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1474

```

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
          20           25           30
Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Ile Phe
          35           40           45
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
          65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
          145          150          155          160
Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
          165          170          175
His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
          180          185          190
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
          210          215          220
Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His Xaa Thr Pro Glu Ser
          305          310          315          320
Gly Ala Cys Cys Ala Pro
          325

```

&lt;210&gt; 1475

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g392 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1475

```

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1           5           10           15
Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
          20           25           30
Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
          35           40           45
Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50           55           60
Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys

```

```

65          70          75          80
Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
      85          90          95
Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
      100          105          110
Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
      115          120          125
Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
      130          135          140
Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
      145          150          155
Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
      165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180          185          190
Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
      195          200          205
Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
      210          215          220
Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
      225          230          235
Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
      245          250          255
Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
      260          265          270
Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
      290          295          300
Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
305          310

```

&lt;210&gt; 1476

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g393 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1476

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
1          5          10          15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20          25          30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35          40          45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50          55          60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
      65          70          75          80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85          90          95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100          105          110
Pro Arg Lys Asp Val
      115

```

&lt;210&gt; 1477

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g394 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1477

```

Met Pro Ser Gln Asn Tyr Ser Ile Ile Ser Glu Phe Asn Leu Phe Gly
1          5          10          15
Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
20          25          30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
35          40          45
Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
50          55          60
Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
65          70          75          80
Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
85          90          95
Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
100         105         110
Ser Phe Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
115         120         125
His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
130         135         140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
145         150         155         160
Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
165         170         175
His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
180         185         190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
195         200         205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
210         215         220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
225         230         235         240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
245         250         255
Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
260         265         270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
275         280         285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
290         295         300
Lys Asn Phe Tyr Arg Lys Phe Cys Pro Pro Ser Ser
305         310         315

```

&lt;210&gt; 1478

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g395 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1478

```

Met Cys Ser Phe Phe Leu Cys Gln Thr Gly Lys Gln Ala Lys Ile Ser
1          5          10          15
Met Gly Glu Glu Asn Gln Thr Phe Val Ser Lys Phe Ile Phe Leu Gly
20          25          30
Leu Ser Gln Asp Leu Gln Thr Gln Ile Leu Leu Phe Ile Leu Phe Leu

```

```

      35      40      45
Ile Ile Tyr Leu Leu Thr Val Leu Gly Asn Gln Leu Ile Ile Ile Leu
  50      55      60
Ile Phe Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
  65      70      75      80
Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Thr Ser Ile Val Pro Gln
      85      90      95
Val Leu Val His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Tyr Gly
      100      105      110
Cys Met Thr Gln Ile Ile Val Phe Leu Leu Val Gly Cys Thr Glu Cys
      115      120      125
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys
      130      135      140
Pro Leu Tyr Tyr Ser Thr Ile Met Thr Gln Arg Val Cys Leu Trp Leu
      145      150      155      160
Ser Phe Arg Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr
      165      170      175
Ser Phe Thr Phe His Leu Pro Tyr Trp Gly Gln Asn Ile Ile Asn His
      180      185      190
Tyr Phe Cys Glu Pro Pro Ala Leu Lys Leu Ala Ser Ile Asp Thr
      195      200      205
Tyr Ser Thr Glu Met Ala Ile Phe Ser Met Gly Val Val Ile Leu Leu
      210      215      220
Ala Pro Val Ser Leu Ile Leu Gly Ser Tyr Trp Asn Ile Ile Ser Thr
      225      230      235      240
Val Ile Gln Met Gln Ser Gly Glu Gly Arg Leu Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Gly Ile
      260      265      270
Phe Thr Tyr Met Arg Pro Asn Ser Lys Thr Thr Lys Glu Leu Asp Lys
      275      280      285
Met Ile Ser Val Phe Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Ile
      290      295      300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Arg Lys Leu
      305      310      315      320
Val Gly Arg Lys Cys Phe Ser His Arg Gln
      325      330

```

&lt;210&gt; 1479

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g396 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(227)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1479

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
  1      5      10      15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
      20      25      30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
      35      40      45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
      50      55      60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
      65      70      75      80

```

Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe  
                             85                            90                            95  
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser  
                             100                            105                            110  
 Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Gly Gly  
                             115                            120                            125  
 Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys  
                             130                            135                            140  
 Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser  
 145                            150                            155                            160  
 Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala  
                             165                            170                            175  
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile  
                             180                            185                            190  
 Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr  
                             195                            200                            205  
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser  
                             210                            215                            220  
 Lys Val Lys  
 225

<210> 1480

<211> 332

<212> PRT

<213> Unknown (H38g397 protein)

<220>

<223> Synthetic construct

<400> 1480

Met Lys Ile Phe Asn Thr Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe  
 1                            5                            10                            15  
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Val  
                             20                            25                            30  
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser  
                             35                            40                            45  
 Ile Asn Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr  
                             50                            55                            60  
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser  
 65                            70                            75                            80  
 Thr Val Pro Asn Val Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile  
                             85                            90                            95  
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly  
                             100                            105                            110  
 Ser Thr Glu Cys Phe Phe Leu Gly Ala Met Ala Phe Asp Leu Tyr Leu  
                             115                            120                            125  
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu  
                             130                            135                            140  
 Cys Asn Ile Leu Val Gly Ser Cys Trp Val Leu Gly Phe Leu Trp Phe  
 145                            150                            155                            160  
 Leu Ile Pro Ile Ser Val Ile Ser Gln Met Thr Cys Gly Ser Arg Ile  
                             165                            170                            175  
 Ile Asp His Phe Pro Cys Asp Pro Gly Pro Leu Leu Ala Leu Thr Cys  
                             180                            185                            190  
 Ala Arg Ala Pro Leu Leu Glu Leu Thr Ser Ser Thr Leu Ser Ser Leu  
                             195                            200                            205  
 Leu Leu Phe Ile Pro Phe Leu Phe Ile Val Gly Cys Tyr Ala Leu Val  
                             210                            215                            220  
 Leu Arg Ala Val Leu Arg Val Pro Ser Ala Ser Gly Arg Arg Lys Ala  
 225                            230                            235                            240  
 Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly

```

                245                250                255
Ser Met Met Ile Thr Tyr Val Ser Pro Thr Ser Gly His Glu Phe Gly
                260                265                270
Met Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu Ile
                275                280                285
Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys His Ala Met
                290                295                300
Arg Asn Tyr Thr Val Met Phe Tyr Leu Ser Arg Ile His Arg Ala Thr
305                310                315                320
Arg Asp Val Lys Asp Val Phe Tyr Leu Phe Asn Phe
                325                330

```

<210> 1481  
 <211> 269  
 <212> PRT  
 <213> Unknown (H38g398 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(269)  
 <223> Xaa = Any Amino Acid

```

<400> 1481
Phe Ser Ser Ile Tyr Ala Trp Tyr Ile Ser Asp Leu Tyr Leu Asn Tyr
 1                5                10                15
Leu Ser Asn His Leu Ser Ile Phe Lys Leu Val Asp Trp Ile Ile Asn
                20                25                30
Cys Tyr Leu Tyr Tyr Phe Tyr Ser Leu Leu Thr Leu Phe Xaa Gln Phe
 35                40                45
Ile Tyr Thr Cys Glu Met Asn Gln Phe Lys Xaa Xaa Gln Asn Arg Asn
 50                55                60
Asn Leu Thr Thr Phe Xaa Gly Tyr Phe Tyr Ser Gly Ile Cys Gly Arg
 65                70                75                80
Arg Asn Cys Thr Met Xaa Leu Ile Thr Ile Phe Ile Leu Lys Tyr Cys
                85                90                95
Xaa His Gly Phe Ile Thr Ile His Ser Val Met Asp Ser Gly Gln His
                100                105                110
Leu Ala Ile Cys His Pro Leu His Tyr Leu Ile Leu Met Thr Asp Glu
                115                120                125
Asn Arg Asp Arg Met Phe Met Gly Pro Leu Thr Ala Phe Pro Tyr Thr
                130                135                140
Asp Ala Thr Ser Gln Asn Met His Tyr Val Asn Phe Leu Ile Ile Ile
 145                150                155                160
Leu Ser Ile Leu Tyr Ile Pro Gly Pro Tyr Thr Leu Ile Leu Arg Ala
                165                170                175
Met Leu Gln Leu Leu Ser Ala Ala Ser His Gln Asn Ala Phe Ser Ile
                180                185                190
Arg Gly Ser His Leu Ile Val Val Ser Leu Phe Cys Glu Thr Ile Met
 195                200                205
Met Met Cys Val Asn Leu Ile Ser Asp His Leu Val Xaa Met Lys Met
 210                215                220
Thr Asn His Asn Ile Ile Met Ile Ser Ser Ile Lys Thr Leu Val Leu
 225                230                235                240
Asn Phe Val Asn Tyr Thr Leu Leu Asn Met Asn Leu Lys Leu Tyr Leu
                245                250                255
Gln Phe Phe Phe Tyr Gly Met Ser Ile Ser Gln Ser Ser
                260                265

```

<210> 1482



<211> 311  
 <212> PRT  
 <213> Unknown (H38g399 protein)

<220>  
 <223> Synthetic construct

<400> 1482

```

Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
 1           5           10           15
Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe
           20           25           30
Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
           35           40           45
Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
           50           55           60
Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
65           70           75           80
Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
           85           90           95
Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
           100          105          110
Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu
           115          120          125
Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
           130          135          140
Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe
145           150          155          160
Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg
           165          170          175
Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr
           180          185          190
Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro
           195          200          205
Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu
           210          215          220
Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys
225           230          235          240
Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr
           245          250          255
Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala
           260          265          270
Gly Lys Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu
           275          280          285
Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala
           290          295          300
Leu Lys Lys Phe Trp Gly Thr
305           310

```

<210> 1483  
 <211> 326  
 <212> PRT  
 <213> Unknown (H38g400 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(326)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1483

```

Thr Ala Leu Glu Phe Thr Asn Asn Ser Glu Thr Ser Thr Met Thr Glu
 1          5          10          15
Phe Val Leu Leu Gly Phe Pro Gly Cys Gln Glu Met Gln Ser Phe Leu
      20          25          30
Phe Ser Leu Phe Phe Val Ile Tyr Val Phe Thr Ile Ile Gly Asn Gly
      35          40          45
Thr Ile Val Cys Ala Val Arg Leu Asp Lys Arg Leu His Thr Pro Met
      50          55          60
Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu Glu Ile Arg Xaa Val Thr
      65          70          75          80
Ser Thr Val Pro Asn Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr
      85          90          95
Ile Ser Phe Val Gly Cys Phe Leu Gln Phe Tyr Phe Phe Thr Ser Leu
      100          105          110
Gly Thr Ile Glu Ala Tyr Phe Leu Cys Ile Met Ala Tyr Asp Arg Tyr
      115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Ile Met Thr Pro Gln
      130          135          140
Leu Cys Tyr Ile Leu Met Ser Phe Cys Trp Val Phe Gly Phe Leu Ser
      145          150          155          160
Tyr Ser Val Ser Thr Val Gln Leu Ser Gln Leu Pro Phe Cys Gly Pro
      165          170          175
Asn Ile Ile Asn His Phe Leu Cys Asp Met Asp Pro Leu Met Ala Leu
      180          185          190
Ser Cys Ala Ser Ala Pro Ile Thr Glu Ile Ile Phe Tyr Ile Leu Ser
      195          200          205
Ser Leu Ile Ile Ile Leu Thr Leu Leu Tyr Ile Cys Gly Ser Tyr Met
      210          215          220
Leu Leu Leu Ile Ala Val Leu Lys Val Pro Ser Ala Ala Gly Gln Gln
      225          230          235          240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe
      245          250          255
Phe Gly Ala Leu Leu Ala Met Tyr Val Ser Pro Thr Thr Asp Asn Pro
      260          265          270
Ala Ala Ile Xaa Lys Ile Ile Thr Leu Phe Tyr Ser Val Val Thr Pro
      275          280          285
Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Ala
      290          295          300
Ala Leu Lys Lys Val Leu Arg Ile Glu Xaa Glu Xaa Ser His Leu His
      305          310          315          320
Glu Thr Lys Gln Thr Ile
      325

```

&lt;210&gt; 1484

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g401 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1484

```

Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
 1          5          10          15
Phe Pro Gln Leu Gln Asp Gly Ser Leu Leu Tyr Phe Phe Pro Leu Leu
      20          25          30
Phe Ile Tyr Thr Phe Ile Ile Ile Asp Asn Leu Leu Ile Phe Ser Ala
      35          40          45
Val Arg Leu Asp Thr His Leu His Asn Pro Met Tyr Asn Phe Ile Ser
      50          55          60

```

```

Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
65          70          75          80
Met Leu Ser Asn Leu Ile Ser Glu Lys Lys Ala Ile Ser Met Thr Gly
          85          90          95
Cys Ile Leu Gln Met Tyr Phe Phe His Ser Leu Glu Asn Ser Glu Gly
          100          105          110
Ile Leu Leu Thr Thr Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Gln Met Ile Met Thr Pro Arg Leu Cys Ala Gln Leu
          130          135          140
Ser Ala Gly Ser Cys Leu Phe Gly Phe Leu Ile Leu Leu Pro Glu Ile
145          150          155          160
Val Met Ile Ser Thr Leu Pro Phe Cys Gly Pro Asn Gln Ile His Gln
          165          170          175
Ile Phe Cys Asp Leu Val Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
          180          185          190
Ser Met Ile Leu Ile Glu Asp Val Ile His Ala Val Thr Ile Ile Ile
          195          200          205
Thr Phe Leu Ile Ile Ala Leu Ser Tyr Val Arg Ile Val Thr Val Ile
          210          215          220
Leu Arg Ile Pro Ser Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
225          230          235          240
Ala Gly His Leu Met Val Phe Leu Ile Phe Phe Gly Ser Val Ser Leu
          245          250          255
Met Tyr Leu Arg Phe Ser Asp Thr Tyr Pro Pro Val Leu Asp Thr Ala
          260          265          270
Ile Ala Leu Met Phe Thr Val Leu Ala Pro Phe Phe Asn Pro Ile Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Asn Asn Ala Ile Lys Lys Leu Phe
          290          295          300
Cys Leu Gln Lys Val Leu Asn Lys Pro Gly Gly
305          310          315

```

&lt;210&gt; 1485

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g402 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1485

```

Met His Phe Val Thr Glu Phe Val Leu Leu Gly Phe His Gly Gln Arg
1          5          10          15
Glu Met Gln Ser Cys Phe Phe Ser Phe Ile Leu Val Leu Tyr Leu Leu
          20          25          30
Thr Leu Leu Gly Asn Gly Ala Ile Val Cys Ala Val Lys Leu Asp Arg
          35          40          45
Arg Leu His Thr Pro Met Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu
          50          55          60
Glu Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn Ile
65          70          75          80
Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe
          85          90          95
Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser Val
          100          105          110
Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro
          115          120          125
Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys Trp
          130          135          140
Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser Gln

```

```

145          150          155          160
L u Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp Pro
          165          170          175
Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu Leu
          180          185          190
Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu Ser
          195          200          205
Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile Pro
          210          215          220
Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
225          230          235          240
Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val Ser
          245          250          255
Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu Val
          260          265          270
Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          275          280          285
Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Leu Thr Val
          290          295          300
Ser Gln Asn
305

```

&lt;210&gt; 1486

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g403 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1486

```

Met Tyr Asn Phe Ile Ser Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr
1          5          10          15
Thr Ala Thr Ile Pro Lys Met Leu Ser Ile Leu Ile Ser Arg Gln Arg
          20          25          30
Thr Ile Ser Met Val Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser
          35          40          45
Leu Gly Asn Ser Glu Gly Ile Leu Leu Thr Thr Met Ala Ile Asp Arg
          50          55          60
Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Thr Pro
65          70          75          80
Gly Leu Cys Val Gln Leu Ser Val Gly Ser Cys Ile Phe Gly Phe Leu
          85          90          95
Val Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly
          100          105          110
Pro Asn Gln Ile His Gln Ile Phe Cys Asp Phe Glu Pro Val Leu Arg
          115          120          125
Leu Ala Cys Thr Asp Thr Ser Met Ile Leu Ile Glu Asp Val Ile His
          130          135          140
Ala Val Ala Ile Val Phe Ser Val Leu Ile Ile Ala Leu Ser Tyr Ile
145          150          155          160
Arg Ile Ile Thr Val Ile Leu Arg Ile Pro Ser Val Glu Gly Arg Gln
          165          170          175
Lys Ala Phe Ser Thr Cys Ala Ala His Leu Ser Val Phe Leu Met Phe
          180          185          190
Tyr Gly Ser Val Ser Leu Met Tyr Leu Arg Phe Ser Ala Thr Phe Pro
          195          200          205
Pro Ile Leu Asp Thr Ala Val Ala Leu Met Phe Ala Val Leu Ala Pro
210          215          220
Phe Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Ile
225          230          235          240

```

Ala Ile Lys Lys Leu Phe Cys Pro Gln Lys Met Val Asn Leu Ser Val  
                   245                  250                  255

<210> 1487

<211> 320

<212> PRT

<213> Unknown (H38g404 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1487

Ser Leu Gly Ser Met Asn Asn Ser Gln Ile Ser Thr Val Thr Gln Phe  
 1                  5                  10                  15  
 Val Leu Leu Gly Phe Pro Gly Pro Trp Lys Ile Gln Ile Ile Phe Phe  
                   20                  25                  30  
 Ser Met Ile Leu Leu Val Tyr Ile Phe Thr Leu Thr Gly Asn Met Ala  
                   35                  40                  45  
 Ile Ile Cys Ala Val Arg Trp Asp His Arg Leu His Thr Pro Met Tyr  
                   50                  55                  60  
 Val Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Cys  
 65                  70                  75                  80  
 Thr Val Pro Asn Met Leu Val Asn Phe Phe Ser Lys Thr Lys Thr Ile  
                   85                  90                  95  
 Ser Phe Ser Gly Cys Phe Thr Gln Phe His Phe Phe Phe Ser Leu Gly  
                   100                  105                  110  
 Thr Thr Glu Cys Phe Phe Leu Cys Val Met Ala Tyr Asp Arg Tyr Leu  
                   115                  120                  125  
 Ala Ile Cys His Pro Leu His Tyr Pro Ser Ile Met Thr Gly Gln Leu  
                   130                  135                  140  
 Cys Gly Ile Leu Val Ser Leu Cys Trp Leu Ile Gly Phe Leu Gly His  
 145                  150                  155                  160  
 Ser Ile Ser Ile Phe Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn  
                   165                  170                  175  
 Ile Ile Asp His Phe Leu Cys Asp Val Asp Pro Leu Met Ala Leu Ser  
                   180                  185                  190  
 Ser Ala Pro Thr His Ile Ile Gly His Val Phe His Ser Val Ser Ser  
                   195                  200                  205  
 Leu Phe Ile Asn Leu Thr Met Val Tyr Ile Leu Gly Ser Tyr Thr Leu  
                   210                  215                  220  
 Val Leu Arg Thr Val Leu Xaa Val Pro Ser Ser Ala Gly Trp Gln Lys  
 225                  230                  235                  240  
 Ala Ile Ser Thr Cys Gly Ser His Leu Val Val Val Ser Leu Phe Tyr  
                   245                  250                  255  
 Gly Ala Ile Met Leu Met Tyr Val Ser Pro Thr Pro Gly Asn Ser Val  
                   260                  265                  270  
 Ala Met His Lys Leu Ile Thr Leu Ile Tyr Ser Val Val Thr Pro Val  
                   275                  280                  285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Tyr Ala  
                   290                  295                  300  
 Leu His His Val Phe Cys Gly Met Arg Ile Ile Gln Arg Ser Xaa Ile  
 305                  310                  315                  320

<210> 1488

<211> 319

<212> PRT

<213> Unknown (H38g405 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1488

```

Met Asp Pro Glu Asn Gln Thr Met Val Thr Glu Phe Tyr Phe Ser Asp
 1           5           10           15
Phe Pro Gln Ser Lys Asn Gly Ser Leu Phe Phe Ile Pro Met Leu
           20           25           30
Phe Ile Tyr Ile Phe Ile Leu Val Gly Asn Phe Met Ile Phe Phe Ala
           35           40           45
Val Gln Pro Asp Pro His Leu His Asn Pro Met Tyr Ser Phe Ile Ser
           50           55           60
Val Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Val Thr Ile Pro Lys
           65           70           75           80
Met Leu Ser Asn Leu Leu Ser Glu Gln Lys Thr Ile Ser Phe Ile Gly
           85           90           95
Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly Val Thr Glu Ala
           100          105          110
Leu Val Leu Thr Val Met Ala Ile Asp Arg Cys Val Ala Ile Cys Asn
           115          120          125
Pro Leu Arg Tyr Ala Ile Thr Met Ser Pro Xaa Leu Cys Ile Gln Leu
           130          135          140
Ser Thr Gly Ser Cys Ile Phe Gly Phe Leu Met Leu Leu Pro Glu Ile
           145          150          155          160
Val Cys Ile Ser Thr Leu Pro Phe Cys Gly Ala Asn Gln Ile His Gln
           165          170          175
Leu Phe Cys Asp Phe Glu Pro Val Leu Gln Leu Ala Cys Thr Asp Thr
           180          185          190
Tyr Ile Ile Leu Val Glu Asp Val Ile Arg Ala Ile Ser Ile Leu Thr
           195          200          205
Ser Val Ser Val Ile Thr Leu Phe Tyr Leu Arg Ile Ile Thr Val Ile
           210          215          220
Leu Arg Ile Pro Ser Gly Glu Ser Arg Gln Lys Ala Phe Phe Thr Cys
           225          230          235          240
Ala Ala His Ile Ala Ile Phe Leu Leu Phe Phe Gly Ser Val Ser Leu
           245          250          255
Met Tyr Leu Arg Phe Ser Val Thr Phe Pro Pro Leu Leu Asp Lys Ala
           260          265          270
Ile Ala Leu Met Phe Ala Val Leu Ala Leu Leu Phe Asn Pro Val Ile
           275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Thr Lys Lys Ile Leu
           290          295          300
Cys Ser Gln Lys Met Phe Asn Ala Ser Gly Ser Xaa Trp Ser Ser
           305          310          315

```

&lt;210&gt; 1489

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g406 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1489

```

Met Thr Gln Leu Thr Ala Ser Gly Asn Gln Thr Met Val Thr Glu Phe
 1           5           10           15

```

Leu Phe Ser Met Phe Pro His Ala His Arg Gly Gly Leu Leu Phe Phe  
                   20                  25                  30  
 Ile Pro Leu Leu Leu Ile Tyr Gly Phe Ile Leu Thr Gly Asn Leu Ile  
                   35                  40                  45  
 Met Phe Ile Val Ile Gln Val Gly Met Ala Leu His Thr Pro Leu Tyr  
                   50                  55                  60  
 Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Cys Tyr Thr Thr Thr  
 65                  70                  75                  80  
 Thr Ile Pro Lys Met Leu Ser Cys Leu Ile Ser Glu Gln Lys Ser Ile  
                   85                  90                  95  
 Ser Val Ala Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly  
                   100                  105                  110  
 Ile Thr Glu Ser Cys Val Leu Thr Ala Met Ala Ile Asp Arg Tyr Ile  
                   115                  120                  125  
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Ile Pro Lys Leu  
                   130                  135                  140  
 Cys Ile Gln Leu Thr Val Gly Ser Cys Phe Cys Gly Phe Leu Leu Val  
 145                  150                  155                  160  
 Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn  
                   165                  170                  175  
 Gln Ile His Gln Ile Phe Cys Asp Phe Thr Pro Val Leu Ser Leu Ala  
                   180                  185                  190  
 Cys Thr Asp Thr Phe Leu Val Val Ile Val Asp Ala Ile His Ala Ala  
                   195                  200                  205  
 Glu Ile Val Ala Ser Phe Leu Val Ile Ala Leu Ser Tyr Ile Arg Ile  
                   210                  215                  220  
 Ile Ile Val Ile Leu Gly Met His Ser Ala Glu Gly His His Lys Ala  
 225                  230                  235                  240  
 Phe Ser Thr Cys Ala Ala His Leu Ala Val Phe Leu Leu Phe Phe Gly  
                   245                  250                  255  
 Ser Val Ala Val Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe  
                   260                  265                  270  
 Trp Asp Thr Ala Ile Ala Val Thr Phe Val Ile Leu Ala Pro Phe Phe  
                   275                  280                  285  
 Asn Pro Ile Ile Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile  
                   290                  295                  300  
 Gly Arg Leu Phe His Tyr Gln Lys Arg Ala Gly Trp Ala  
 305                  310                  315

&lt;210&gt; 1490

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g407 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1490

Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu Asp  
 1                  5                  10                  15  
 Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu  
                   20                  25                  30  
 Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp  
                   35                  40                  45  
 Phe Leu Ser Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile Gln  
                   50                  55                  60  
 Ser Phe Phe Phe Ser Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu Ala  
 65                  70                  75                  80  
 Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His Tyr  
                   85                  90                  95  
 Pro Ile Arg Met Ser Lys Arg Met Cys Val Leu Met Ile Thr Gly Ser

```

      100              105              110
Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val Leu
      115              120              125
His Ile Pro Tyr Cys Gln Ser Arg Ala Ile Asn His Phe Phe Cys Asp
      130              135              140
Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp Val Tyr Glu
      145              150              155              160
Gly Thr Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile
      165              170              175
Ala Ile Ser Cys Ser Tyr Gly Arg Val Leu Leu Ala Val Tyr His Met
      180              185              190
Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys Ser Thr His
      195              200              205
Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr Thr Tyr Leu
      210              215              220
Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val
      225              230              235              240
Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu
      245              250              255
Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg Ile
      260              265              270
Cys Ser Val Lys Met
      275

```

&lt;210&gt; 1491

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g408 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(241)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1491

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1              5              10              15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
      20              25              30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35              40              45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
      50              55              60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
      65              70              75              80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85              90              95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100              105              110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115              120              125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130              135              140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
      145              150              155              160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165              170              175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180              185              190

```



Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu  
 195 200 205  
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser  
 210 215 220  
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val  
 225 230 235 240  
 Gly

<210> 1492

<211> 312

<212> PRT

<213> Unknown (H38g409 protein)

<220>

<223> Synthetic construct

<400> 1492

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly  
 1 5 10 15  
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu Leu  
 20 25 30  
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val  
 35 40 45  
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser  
 50 55 60  
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys  
 100 105 110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile  
 130 135 140  
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile  
 145 150 155 160  
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His  
 165 170 175  
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu  
 195 200 205  
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr  
 210 215 220  
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu  
 245 250 255  
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln  
 260 265 270  
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln  
 290 295 300  
 Leu Lys Arg Ile Gly Ile Leu Ala  
 305 310

<210> 1493

<211> 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g410 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1493

```

Glu Phe Leu Phe Tyr Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu
 1           5           10           15
Leu Gly Leu Phe Pro Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu
           20           25           30
Ile Phe Leu Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile
           35           40           45
Leu Leu Ile Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu
           50           55           60
Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val
65           70           75           80
Pro Lys Met Val Tyr Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe
           85           90           95
Thr Gly Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala
           100          105          110
Glu Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
           115          120          125
Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val
130          135          140
Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala
145          150          155          160
His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile
           165          170          175
Asn His Phe Phe Cys Glu Gly Ser Ser Glu Arg Tyr Leu Gly Cys Met
           180          185          190
Gln Ala Trp Arg Trp Ala Ala Val Glu Thr Ala Xaa Leu Val Lys Pro
           195          200          205
Trp Ala Gly Pro
           210

```

&lt;210&gt; 1494

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g411 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1494

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Cys Arg Ile Leu Phe Ala Thr Phe Phe Leu
           20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Val Val Ile Ile Thr Val
           35           40           45
Cys Val Asp Lys Cys Leu Gln Ser Pro Ile Tyr Phe Phe Leu Gly His
           50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Val Pro Phe Met
65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
           85           90           95

```

Cys Ala Ala Gln Leu Tyr Leu Tyr Leu Ser Leu Gly Thr Leu Glu Leu  
                   100                  105                  110  
 Ala Leu Met Gly Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn  
                   115                  120                  125  
 Pro Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Phe Ile Trp Val  
                   130                  135                  140  
 Ile Ile Val Ser Trp Val Leu Gly Phe Leu Ser Glu Ile Trp Pro Val  
 145                  150                  155                  160  
 Tyr Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Ser Val Leu Asp His  
                   165                  170                  175  
 Phe Tyr Cys Asp Arg Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr  
                   180                  185                  190  
 Leu Phe Arg Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile  
                   195                  200                  205  
 Gly Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr  
                   210                  215                  220  
 Asn Leu Lys Ile Pro Ser Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr  
 225                  230                  235                  240  
 Cys Ala Ser His Phe Thr Tyr Val Val Ile Gly Tyr Gly Ser Cys Leu  
                   245                  250                  255  
 Phe Leu Tyr Val Lys Pro Lys  
                   260

&lt;210&gt; 1495

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g412 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1495

Met Asp Gln Tyr Asn His Ser Ser Leu Ala Glu Phe Val Phe Leu Gly  
 1                  5                  10                  15  
 Phe Ala Ser Val Gly Tyr Val Arg Gly Trp Leu Phe Val Leu Leu Leu  
                   20                  25                  30  
 Leu Ala Tyr Leu Phe Thr Ile Cys Gly Asn Met Leu Ile Phe Ser Val  
                   35                  40                  45  
 Ile Arg Leu Asp Ala Ala Leu His Thr Pro Met Tyr His Phe Val Ser  
                   50                  55                  60  
 Val Leu Ser Phe Leu Glu Leu Trp Tyr Thr Ala Thr Thr Ile Pro Lys  
 65                  70                  75                  80  
 Met Leu Ser Asn Ile Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly  
                   85                  90                  95  
 Cys Leu Leu Gln Thr Tyr Phe Phe His Ser Leu Gly Ala Ser Glu Cys  
                   100                  105                  110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg  
                   115                  120                  125  
 Pro Leu His Tyr Pro Ile Ile Met Thr Thr Thr Leu Cys Ala Lys Met  
                   130                  135                  140  
 Ala Ala Ala Cys Trp Thr Cys Gly Phe Leu Cys Pro Ile Ser Glu Val  
 145                  150                  155                  160  
 Ile Leu Ala Ser Gln Leu Pro Phe Cys Ala Tyr Asn Glu Ile Gln His  
                   165                  170                  175  
 Ile Phe Cys Asp Phe Pro Pro Leu Leu Ser Leu Ala Cys Lys Asp Thr  
                   180                  185                  190  
 Ser Ala Asn Ile Leu Val Asp Phe Ala Ile Asn Ala Phe Ile Ile Leu  
                   195                  200                  205  
 Ile Thr Phe Phe Phe Ile Met Ile Ser Tyr Ala Arg Ile Ile Gly Ala  
                   210                  215                  220  
 Val Leu Lys Ile Lys Thr Ala Ser Gly Arg Lys Lys Ala Phe Ser Thr

225                      230                      235                      240  
 Cys Ala Ser His Leu Ala Val Val L u Ile Phe Phe Gly Ser Ile Ile  
                                  245                      250                      255  
 Phe Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Thr Leu Asp Arg  
                                  260                      265                      270  
 Thr Leu Ala Ile Val Tyr Ser Val Leu Thr Pro Met Val Asn Pro Ile  
                                  275                      280                      285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Ile Lys Ala Ile Lys Arg Thr  
                                  290                      295                      300  
 Ile Phe Gln Lys Gly Asp Lys Ala Ser Leu Ala His Leu  
 305                      310                      315

<210> 1496

<211> 315

<212> PRT

<213> Unknown (H38g413 protein)

<220>

<223> Synthetic construct

<400> 1496

Met Gln Gly Leu Asn His Thr Ser Val Ser Glu Phe Ile Leu Val Gly  
 1                      5                      10                      15  
 Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu  
                                  20                      25                      30  
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr  
                                  35                      40                      45  
 Val Trp Ser Glu Arg Ser Leu His Met Pro Met Tyr Leu Phe Leu Cys  
                                  50                      55                      60  
 Ala Leu Ser Ile Thr Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg  
 65                      70                      75                      80  
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala  
                                  85                      90                      95  
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser  
                                  100                      105                      110  
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His  
                                  115                      120                      125  
 Pro Leu Arg Tyr Asn Val Leu Met Ser Leu Arg Gly Cys Thr Cys Arg  
                                  130                      135                      140  
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr  
 145                      150                      155                      160  
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His  
                                  165                      170                      175  
 Phe Phe Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp  
                                  180                      185                      190  
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu  
                                  195                      200                      205  
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala  
                                  210                      215                      220  
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser  
 225                      230                      235                      240  
 Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Phe Ala  
                                  245                      250                      255  
 Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro Gln Ser Pro Glu Gly Asp  
                                  260                      265                      270  
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro  
                                  275                      280                      285  
 Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys  
                                  290                      295                      300  
 Thr Cys Phe Thr Lys Leu Phe Pro Gln Asn Cys  
 305                      310                      315

<210> 1497  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g414 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid

<400> 1497  
 His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser  
 20 25 30  
 Pro Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Val Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Pro Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Thr Val Asp Met Gln Ser His Ile Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Ser Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu  
 100 105 110  
 Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe  
 130 135 140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145 150 155 160  
 Ser Xaa Ile Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser His  
 165 170 175  
 Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Ser Ile Phe Met Tyr Phe Asn Ser Thr Met Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser  
 305 310 315

<210> 1498  
 <211> 157  
 <212> PRT  
 <213> Unknown (H38g415 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1498

Val	Ser	Pro	Leu	Trp	Glu	Cys	Val	Ser	Xaa	Gln	Arg	Ser	Pro	His	Phe
1				5					10					15	
Leu	Cys	Ser	Gly	Asp	Ser	Val	Phe	Cys	Leu	Val	His	Ser	Val	Gly	Cys
			20					25					30		
Cys	Thr	Leu	Leu	Leu	Ser	Gln	Ser	Leu	Arg	Leu	Leu	Ser	Val	Phe	Leu
		35				40						45			
Leu	Ser	Ser	Cys	Ala	Ala	Ser	Trp	Lys	Lys	Val	His	Ser	Met	Asn	Leu
		50				55					60				
Tyr	Thr	Pro	Phe	Cys	Leu	Ser	Lys	Trp	Xaa	Asn	His	Val	Asn	Asn	Ala
65					70					75				80	
Phe	Asn	Leu	Pro	Ser	Trp	Lys	Lys	Ser	Lys	Ser	Val	Val	Thr	Met	Phe
				85					90					95	
Xaa	Gly	Pro	Ala	Met	Ile	Thr	Tyr	Leu	Arg	Ser	Asp	Ser	Xaa	Tyr	Asn
			100					105					110		
Pro	Thr	Val	Gly	Lys	Gln	Leu	Val	Leu	Phe	Tyr	Ser	Ile	Val	Ser	Ala
		115				120						125			
Phe	Ile	Lys	Pro	Ile	Ile	Ser	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly
		130				135					140				
Ala	Ser	Trp	Lys	Val	Leu	Arg	Val	Lys	Gly	Thr	Ala	Gln			
145					150					155					

<210> 1499

<211> 287

<212> PRT

<213> Unknown (H38g416 protein)

<220>

<223> Synthetic construct

<400> 1499

Met	Glu	Asn	Tyr	Asn	Gln	Thr	Ser	Thr	Asp	Phe	Ile	Leu	Leu	Gly	Leu
1				5					10					15	
Phe	Pro	Pro	Ser	Arg	Ile	Asp	Leu	Phe	Phe	Phe	Ile	Leu	Phe	Val	Leu
			20					25					30		
Ile	Phe	Leu	Met	Ala	Leu	Ile	Gly	Asn	Leu	Ser	Met	Ile	Leu	Leu	Ile
		35				40						45			
Phe	Leu	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Ser	Gln
		50				55					60				
Leu	Ser	Leu	Ile	Asp	Leu	Asn	Tyr	Ile	Ser	Thr	Ile	Val	Pro	Lys	Met
65					70					75				80	
Ala	Ser	Asp	Phe	Leu	Tyr	Gly	Asn	Lys	Ser	Ile	Ser	Phe	Ile	Gly	Cys
			85					90						95	
Gly	Ile	Gln	Ser	Phe	Phe	Phe	Met	Thr	Phe	Ala	Gly	Ala	Glu	Ala	Leu
		100						105					110		
Leu	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro
		115				120						125			
Leu	His	Tyr	Pro	Ile	Arg	Met	Ser	Lys	Arg	Met	Tyr	Val	Leu	Met	Ile
		130				135					140				
Thr	Gly	Ser	Trp	Met	Ile	Gly	Ser	Ile	Asn	Ser	Cys	Ala	His	Thr	Val
145					150					155				160	
Tyr	Ala	Phe	Arg	Ile	Pro	Tyr	Cys	Lys	Ser	Arg	Ala	Ile	Asn	His	Phe
			165					170						175	
Phe	Cys	Asp	Val	Pro	Ala	Met	Leu	Thr	Leu	Ala	Cys	Thr	Asp	Thr	Trp
			180					185						190	

Val	Tyr	Glu	Tyr	Thr	Val	Phe	Leu	Ser	Ser	Thr	Ile	Phe	Leu	Val	Phe
	195						200					205			
Pro	Phe	Thr	Gly	Ile	Ala	Cys	Ser	Tyr	Gly	Trp	Val	Leu	Leu	Ala	Val
	210					215					220				
Tyr	Arg	Met	His	Ser	Ala	Glu	Gly	Arg	Lys	Lys	Ala	Tyr	Ser	Thr	Cys
225					230					235					240
Ser	Thr	His	Leu	Thr	Val	Val	Thr	Phe	Tyr	Tyr	Ala	Pro	Leu	Arg	Tyr
			245						250					255	
Thr	Tyr	Leu	Cys	Pro	Arg	Ser	Leu	Phe	Ile	Ser	Thr	Glu	Asp	Lys	Val
		260						265					270		
Gly	Gly	Gly	Gly	Tyr	Thr	Ile	Leu	Thr	Ser	Met	Leu	Asn	Pro	Ile	
	275						280					285			

&lt;210&gt; 1500

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g417 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1500

Met	Asp	Lys	Glu	Asn	Ser	Ser	Met	Val	Thr	Glu	Phe	Ile	Phe	Met	Gly
1				5					10					15	
Ile	Thr	Gln	Asp	Pro	Gln	Met	Glu	Ile	Ile	Phe	Phe	Val	Val	Phe	Leu
		20					25					30			
Ile	Val	Tyr	Leu	Val	Asn	Val	Val	Gly	Asn	Ile	Gly	Met	Ile	Ile	Leu
	35					40					45				
Ile	Thr	Thr	Asp	Thr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Cys
	50					55					60				
Asn	Leu	Ser	Phe	Val	Asp	Leu	Gly	Tyr	Ser	Ser	Ala	Ile	Ala	Pro	Arg
65					70					75				80	
Met	Leu	Ala	Asp	Phe	Leu	Thr	Asn	His	Lys	Val	Ile	Ser	Phe	Ser	Ser
			85						90					95	
Cys	Ala	Thr	Gln	Phe	Ala	Phe	Phe	Val	Gly	Phe	Val	Asp	Ala	Glu	Cys
		100						105					110		
Tyr	Val	Leu	Ala	Ala	Met	Ala	Tyr	Gly	Arg	Phe	Val	Ala	Ile	Cys	Arg
	115					120						125			
Pro	Leu	His	Tyr	Ser	Thr	Phe	Met	Ser	Lys	Gln	Val	Cys	Leu	Ala	Leu
	130					135					140				
Met	Leu	Gly	Ser	Tyr	Leu	Ala	Gly	Leu	Val	Ser	Leu	Val	Ala	His	Thr
145					150					155				160	
Thr	Leu	Thr	Phe	Ser	Leu	Ser	Tyr	Cys	Gly	Ser	Asn	Ile	Ile	Asn	His
			165					170						175	
Phe	Phe	Cys	Glu	Ile	Pro	Pro	Leu	Leu	Ala	Leu	Ser	Cys	Ser	Asp	Thr
		180						185					190		
Tyr	Ile	Ser	Glu	Ile	Leu	Leu	Phe	Ser	Leu	Cys	Gly	Phe	Ile	Glu	Phe
	195					200						205			
Ser	Thr	Ile	Leu	Ile	Ile	Phe	Ile	Ser	Tyr	Thr	Phe	Ile	Leu	Val	Ala
	210					215					220				
Ile	Ile	Arg	Met	Arg	Ser	Ala	Glu	Gly	Arg	Leu	Lys	Ala	Phe	Ser	Thr
225					230					235				240	
Cys	Gly	Ser	His	Leu	Thr	Gly	Ile	Thr	Leu	Phe	Tyr	Gly	Thr	Val	Met
			245						250					255	
Phe	Met	Tyr	Leu	Arg	Pro	Thr	Ser	Ser	Tyr	Ser	Leu	Asp	Gln	Asp	Lys
		260						265					270		
Trp	Ala	Ser	Val	Phe	Tyr	Thr	Val	Ile	Ile	Pro	Met	Leu	Asn	Pro	Leu
	275						280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Ala	Ala	Phe	Lys	Lys	Leu
	290					295					300				
Ile	Gly	Lys	Lys	Ser	Gln										

305

310

&lt;210&gt; 1501

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g418 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1501

```

Ser Thr Asp Pro Gln Asn Leu Ile Asp Val Ser Ile Phe Leu Leu Leu
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
           20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
           35           40           45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
           50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65           70           75           80
Lys Met Ile Val Asp Ile Arg Ser His Ser Arg Val Ile Ser Tyr Ala
           85           90           95
Gly Cys Leu Thr Gln Thr Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
           100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
           115          120          125
Cys His Pro Leu Tyr His Ser Ala Val Met Asn Pro Cys Phe Cys Gly
           130          135          140
Phe Leu Val Leu Leu Thr Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
           165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Pro Leu Pro His Leu Ala Cys
           180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
           195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
           210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
           245          250          255
Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
           260          265          270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
           275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu
           290          295          300
Arg Trp Leu His Gly Ser Ser Val Xaa Ser Gln His Leu Leu Ile Cys
305          310          315          320
Cys Ile Pro Phe Val Trp Val Lys Lys Gly Ser Arg Val Lys
           325          330          335

```

&lt;210&gt; 1502

&lt;211&gt; 303

&lt;212&gt; PRT



<213> Unknown (H38g419 protein)

<220>

<223> Synthetic construct

<400> 1502

```

Met Asp His Val Ser His Asn Trp Thr Gln Ser Phe Ile Leu Ala Gly
 1          5          10          15
Phe Thr Thr Thr Gly Thr Leu Gln Pro Leu Ala Phe Leu Gly Thr Leu
      20          25          30
Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Ile Leu Ile Ile Val Leu
      35          40          45
Val Gln Leu Asp Ser Gly Leu Phe Thr Pro Met Tyr Leu Phe Ile Ser
      50          55          60
Val Leu Ser Phe Val Glu Val Trp Tyr Val Ser Thr Thr Val Pro Met
      65          70          75          80
Leu Leu His Thr Leu Leu Gln Gly Cys Ser Pro Val Ser Ser Ala Val
      85          90          95
Cys Phe Ile Gln Thr Met Phe Phe His Ser Leu Gly Met Thr Glu Cys
      100          105          110
Tyr Leu Leu Gly Val Met Ala Leu Asp Ser Tyr Leu Ile Ile Cys His
      115          120          125
Pro Leu His Tyr His Ala Leu Met Ser Arg Gln Val Gln Leu Arg Leu
      130          135          140
Ala Gly Ala Ser Trp Val Ala Gly Phe Ser Ala Ala Leu Val Pro Ala
      145          150          155          160
Thr Leu Thr Ala Thr Leu Pro Phe Cys Leu Lys Glu Val Ala His Tyr
      165          170          175
Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala Cys Val Asp Thr Ser
      180          185          190
Trp His Ala Arg Ala His Gly Thr Val Ile Gly Val Ala Thr Gly Cys
      195          200          205
Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly Ile Leu Asn Ala Val
      210          215          220
Leu Lys Leu Pro Ser Ala Ala Ser Ser Ala Lys Ala Phe Ser Thr Cys
      225          230          235          240
Ser Ser His Val Thr Val Val Ala Leu Phe Tyr Ala Ser Ala Phe Thr
      245          250          255
Val Tyr Val Gly Ser Pro Gly Ser Arg Pro Glu Ser Thr Asp Lys Leu
      260          265          270
Val Ala Leu Val Tyr Ala Leu Ile Thr Pro Phe Leu Asn Pro Ile Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Arg Arg Val
      290          295          300

```

<210> 1503

<211> 336

<212> PRT

<213> Unknown (H38g420 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1503

```

Pro Thr Lys Arg Glu Asn His Thr Val Ile Arg Glu Phe Val Phe Gln
 1          5          10          15
Gly Phe Ser Ser Phe His Glu His Lys Leu Thr Leu Phe Val Val Phe

```

<210> 1504  
<211> 315  
<212> PRT  
<213> Unknown (H38g421 protein)

<220>  
<223> Synthetic construct

<400> 1504															
Met	Ser	Ile	Thr	Lys	Ala	Trp	Asn	Ser	Ser	Ser	Val	Thr	Met	Phe	Ile
1				5					10					15	
Leu	Leu	Gly	Phe	Thr	Asp	His	Pro	Glu	Leu	Gln	Ala	Leu	Leu	Phe	Val
			20					25					30		
Thr	Phe	Leu	Gly	Ile	Tyr	Leu	Thr	Thr	Leu	Ala	Trp	Asn	Leu	Ala	Leu
		35					40					45			
Ile	Phe	Leu	Ile	Arg	Gly	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe
	50					55					60				
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Ile	Cys	Tyr	Ser	Ser	Ala	Val
65					70					75				80	
Ala	Pro	Asn	Met	Leu	Thr	Asp	Phe	Phe	Trp	Glu	Gln	Lys	Thr	Ile	Ser
				85					90					95	

Phe Val Gly Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu  
                   100                  105                  110  
 Ser Glu Cys Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala  
                   115                  120                  125  
 Ile Ser Ser Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys  
                   130                  135                  140  
 Thr Arg Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu  
 145                  150                  155                  160  
 Ile Gln Ala Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile  
                   165                  170                  175  
 Ile Asn His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys  
                   180                  185                  190  
 Ser Asp Thr Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr  
                   195                  200                  205  
 Val Gly Gly Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile  
                   210                  215                  220  
 Val Ser Ala Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala  
 225                  230                  235                  240  
 Cys Asn Thr Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly  
                   245                  250                  255  
 Thr Ala Leu Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly  
                   260                  265                  270  
 Arg Asp Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu  
                   275                  280                  285  
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu  
                   290                  295                  300  
 Trp Lys Val Leu Glu Arg Lys Lys Val Phe Ser  
 305                  310                  315

&lt;210&gt; 1505

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g422 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1505

Met Pro Xaa Lys Met Glu Ser Ile Asn Thr Asn Phe Thr Val Thr Glu  
   1                  5                  10                  15  
 Phe Val Phe Leu Gly Leu Ser Ser Glu Pro Lys Ile Gln Leu Ile Leu  
                   20                  25                  30  
 Phe Ile Met Phe Leu Phe Tyr Leu Ser Thr Val Ala Gly Asn Val Ile  
                   35                  40                  45  
 Ile Ile Thr Ile Ile Xaa Met Glu Pro Leu Leu Gln Thr Pro Met Tyr  
                   50                  55                  60  
 Phe Phe Leu Thr Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Thr  
 65                  70                  75                  80  
 Asn Val Pro Gln Met Leu Ser Asn Met Ala Gly Lys Lys Asn Thr Ile  
                   85                  90                  95  
 Ser Phe Ser Ser Cys Ala Thr Gln Met Tyr Phe Ser Leu Ser Phe Gly  
                   100                  105                  110  
 Ser Asp Cys Val Leu Leu Gly Val Met Ala Tyr Asp Arg Tyr Val Ala  
                   115                  120                  125  
 Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn Thr Cys  
                   130                  135                  140  
 Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Ser Ser Met

```

145          150          155          160
Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro Asn Ile
          165          170          175
Leu Asn His Phe Phe Cys Glu Val Leu Ser Val Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser Ile Ile
          195          200          205
Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg Ile
          210          215          220
Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr Gln Ala
225          230          235          240
Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly
          245          250          255
Thr Ala Ile Phe Met Asp Met Arg Pro Gln Ser Arg Ser Ser Trp Ala
          260          265          270
Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Val Lys Gly Ala Arg
          290          295          300
Arg Arg Ala Ile Ala Lys Gln Arg Met Xaa Gln Leu Leu
305          310          315

```

<210> 1506  
 <211> 340  
 <212> PRT  
 <213> Unknown (H38g423 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(340)  
 <223> Xaa = Any Amino Acid

```

<400> 1506
Met Pro Lys Leu Asn Ser Thr Phe Val Thr Glu Phe Leu Phe Glu Gly
 1          5          10          15
Phe Ser Ser Phe Arg Arg Gln His Lys Leu Val Phe Phe Val Val Phe
          20          25          30
Leu Thr Leu Tyr Leu Leu Thr Leu Ser Gly Asn Val Ile Ile Met Thr
          35          40          45
Ile Ile Arg Leu Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Cys Met Leu Ser Ile Ser Glu Thr Cys Tyr Thr Val Ala Ile Ile Pro
65          70          75          80
His Met Leu Ser Gly Leu Leu Asn Pro His Gln Pro Ile Ala Thr Gln
          85          90          95
Ser Cys Ala Thr Gln Leu Phe Phe Tyr Leu Thr Phe Gly Ile Asn Asn
          100          105          110
Cys Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Arg Tyr Ser Val Ile Met Gly Lys Arg Ala Cys Ile Gln
          130          135          140
Leu Ala Ser Gly Ser Leu Gly Ile Gly Leu Gly Met Ala Ile Val Gln
145          150          155          160
Val Thr Ser Val Phe Gly Leu Pro Phe Cys Asp Ala Phe Val Ile Ser
          165          170          175
His Phe Phe Cys Asp Val Arg His Leu Leu Lys Leu Ala Cys Thr Asp
          180          185          190
Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val Cys Val Leu
          195          200          205

```

```

Val Leu Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser
210                215                220
Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Gln Lys Lys Ala Phe Ala
225                230                235                240
Thr Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala
                245                250                255
Ser Ile Ile Tyr Leu Lys Pro Lys Ser Gln Ser Ser Leu Gly Gln Asp
                260                265                270
Arg Leu Ile Ser Val Thr Tyr Thr Ile Thr Pro Leu Leu Asn Pro Val
                275                280                285
Val Tyr Ser Leu Lys Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala
                290                295                300
Val Gly Gln Lys Thr Leu Ser Pro Xaa Xaa Arg Glu Val Val Lys Ala
305                310                315                320
Phe Pro Phe Val Tyr Lys Tyr Val Leu Ile Phe Asn Ala Leu Ser Ile
                325                330                335
Met Pro Leu Cys
                340

```

&lt;210&gt; 1507

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g424 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1507

```

Met Asp Ile Gly Leu Ser Ile Ala Asn Ser Ser Gly Phe Gln Leu Ser
1          5          10          15
Glu Phe Ile Leu Ile Gly Phe Pro Gly Ile His Glu Trp Gln His Trp
20          25          30
Leu Ser Leu Pro Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile Ile Thr
35          40          45
Ile Gln His Glu Thr Met Leu His Glu Pro Met Tyr His Leu Leu Gly
50          55          60
Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met Pro Lys
65          70          75          80
Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu Pro Glu
85          90          95
Cys Phe Ala Gln Ile Tyr Ala Ile His Ser Phe Met Cys Met Glu Ser
100         105         110
Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Met Ala Ile Cys Tyr
115         120         125
Pro Leu Gln Tyr Thr Ser Ile Val Thr Glu Ala Phe Val Ile Lys Ala
130         135         140
Thr Leu Ser Val Val Leu Arg Asn Gly Leu Leu Thr Ile Pro Val Pro
145         150         155         160
Val Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile Asp Gln
165         170         175
Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp Thr
180         185         190
Thr Ile Asn Arg Phe Tyr Gln Leu Ala Leu Val Trp Val Val Val Gly
195         200         205
Ser Asp Met Gly Leu Val Phe Ala Ser Tyr Ser Leu Ile Ile His Ser
210         215         220
Val Leu Lys Leu Asn Ser Ala Lys Ala Thr Ser Lys Ala Leu Asn Thr

```

225		230		235		240									
Cys	Ser	Ser	His	Leu	Ile	Leu	Ile	Leu	Phe	Phe	Tyr	Thr	Ala	Ile	Ile
			245						250					255	
Val	Val	Ser	Val	Thr	Asn	Leu	Ala	Gly	Arg	Arg	Ala	Pro	Arg	Ile	Pro
			260						265					270	
Val	Leu	Leu	Asn	Val	Leu	His	Ile	Val	Ile	Pro	Ser	Ala	Leu	Asn	Pro
			275						280					285	
Ile	Val	Tyr	Ala	Leu	Arg	Thr	Xaa	Glu	Leu	Arg	Ala	Gly	Phe	Gln	Lys
		290					295				300				
Leu	Leu	Gly	Leu	Gly	Glu	Tyr	Val	Ser							
305					310										

&lt;210&gt; 1508

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g425 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1508

Met	Phe	Ser	Pro	Asn	His	Thr	Ile	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly
1			5						10					15	
Leu	Thr	Asp	Asp	Pro	Val	Leu	Glu	Lys	Ile	Leu	Phe	Gly	Val	Phe	Leu
			20					25					30		
Ala	Ile	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Cys	Met	Ile	Leu	Leu
			35				40					45			
Ile	Arg	Thr	Asn	Ser	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly
			50			55					60				
His	Leu	Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Val	Thr	Pro	Asn
					70					75					80
Met	Leu	His	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Thr	Ile	Ser	Tyr	Ala	Gly
				85					90					95	
Cys	Phe	Thr	Gln	Cys	Leu	Leu	Phe	Ile	Ala	Leu	Val	Ile	Thr	Glu	Phe
			100					105					110		
Tyr	Ile	Leu	Ala	Ser	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser
			115				120					125			
Pro	Leu	His	Tyr	Ser	Ser	Arg	Met	Ser	Lys	Asn	Ile	Cys	Val	Cys	Leu
			130			135					140				
Val	Thr	Ile	Pro	Tyr	Met	Tyr	Gly	Phe	Leu	Ser	Gly	Phe	Ser	Gln	Ser
					150					155					160
Leu	Leu	Thr	Phe	His	Leu	Ser	Phe	Cys	Gly	Ser	Leu	Glu	Ile	Asn	His
				165					170					175	
Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Met	Leu	Ala	Cys	Ser	Asp	Thr
			180					185					190		
Arg	Val	Lys	Lys	Met	Ala	Met	Phe	Val	Val	Ala	Gly	Phe	Asn	Leu	Ser
			195				200					205			
Ser	Ser	Leu	Phe	Ile	Ile	Leu	Leu	Ser	Tyr	Leu	Phe	Ile	Phe	Ala	Ala
			210			215					220				
Ile	Phe	Arg	Ile	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr
					230				235						240
Cys	Ala	Ser	His	Leu	Thr	Ile	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe
				245					250					255	
Cys	Met	Tyr	Val	Arg	Pro	Pro	Ser	Glu	Lys	Ser	Val	Glu	Glu	Ser	Lys
			260					265					270		
Ile	Thr	Ala	Val	Phe	Tyr	Thr	Phe	Leu	Ser	Pro	Met	Leu	Asn	Pro	Leu
			275					280					285		
Ile	Tyr	Ser	Leu	Arg	Asn	Thr	Asp	Val	Ile	Leu	Ala	Met	Gln	Gln	Met
			290			295					300				
Ile	Arg	Gly	Lys	Ser	Phe	His	Lys	Ile	Ala	Val					
305					310					315					

<210> 1509  
 <211> 257  
 <212> PRT  
 <213> Unknown (H38g426 protein)

<220>  
 <223> Synthetic construct

<400> 1509  
 Met Phe Leu Leu Leu Ala Ile Leu Ala Ala Thr Asp Leu Gly Leu Ala  
 1 5 10 15  
 Thr Ser Ile Ala Pro Gly Leu Leu Ala Val Leu Trp Leu Gly Pro Arg  
 20 25 30  
 Ser Val Pro Tyr Ala Val Cys Leu Val Gln Met Phe Phe Val His Ala  
 35 40 45  
 Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met Ala Cys Asp Arg  
 50 55 60  
 Ala Ala Ala Ile Gly Arg Pro Leu His Tyr Pro Val Leu Val Thr Lys  
 65 70 75 80  
 Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Lys Ala Val Ala  
 85 90 95  
 Ile Val Val Pro Phe Pro Leu Leu Val Ala Lys Phe Glu His Phe Gln  
 100 105 110  
 Ala Lys Thr Ile Gly His Thr Tyr Cys Ala His Met Ala Val Val Glu  
 115 120 125  
 Leu Val Val Gly Asn Thr Gln Ala Thr Asn Leu Tyr Gly Leu Ala Leu  
 130 135 140  
 Ser Leu Ala Ile Ser Gly Met Asp Ile Leu Gly Ile Thr Gly Ser Tyr  
 145 150 155 160  
 Gly Leu Ile Ala His Ala Val Leu Gln Leu Pro Thr Arg Glu Ala His  
 165 170 175  
 Ala Lys Ala Phe Gly Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala  
 180 185 190  
 Phe Tyr Ile Pro Gly Leu Phe Ser Tyr Leu Ala His Arg Phe Gly His  
 195 200 205  
 His Thr Val Pro Lys Pro Val His Ile Leu Leu Ser Asn Ile Tyr Leu  
 210 215 220  
 Leu Leu Pro Pro Ala Leu Asn Pro Leu Ile Tyr Gly Ala Arg Thr Lys  
 225 230 235 240  
 Gln Ile Arg Asp Arg Leu Leu Glu Thr Phe Thr Phe Arg Lys Ser Pro  
 245 250 255  
 Leu

<210> 1510  
 <211> 358  
 <212> PRT  
 <213> Unknown (H38g427 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(358)  
 <223> Xaa = Any Amino Acid

<400> 1510  
 Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro  
 1 5 10 15  
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala

```

      20      25      30
Thr Asn Ala Thr Pro Pro Met Leu Val Asn Phe Val Phe Ser Lys Arg
      35      40      45
Lys Thr Val Ser Phe Ile Gly Cys Phe Ile Gln Phe His Leu Phe Ile
      50      55      60
Ala Leu Val Ile Thr Asp Tyr His Met Leu Thr Val Met Val Tyr Asp
65      70      75      80
His Tyr Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Ser
      85      90      95
Arg Cys Val Cys Leu Cys Leu Thr Ala Ala Pro Tyr Ile Tyr Gly Ser
      100      105      110
Ala Asn Gly Leu Val Gln Val Ile Leu Met Leu Cys Leu Phe Phe Cys
      115      120      125
Glu Pro Asn Glu Ile Asn His Phe Phe Phe Phe Gly Glu Asn Ala Leu
      130      135      140
Tyr Ala His Leu Ile Pro Leu Xaa Ile Phe Glu Trp Thr Val Gly Glu
145      150      155      160
Glu Gly Arg Asn Asn Ile Asn Gly Glu Asn Thr Thr Gln Lys Val Tyr
      165      170      175
Thr Met Gly Glu Arg Asn Leu Leu Ile Gln Val Ser Ile Phe Leu Leu
      180      185      190
Trp His Ile Arg Ser Xaa Leu Phe Ser Gln Tyr Glu Ala Ser Pro Arg
      195      200      205
Ala Asp Ser Asp Val Lys Leu Glu Ile Asn His Phe Tyr Tyr Ala Glu
      210      215      220
Pro Pro Leu Leu Val Leu Ala Cys Leu Asp Thr Tyr Val Lys Glu Thr
225      230      235      240
Ala Met Phe Met Val Ala Gly Ser Asn Leu Ile Cys Pro Leu Thr Ile
      245      250      255
Ile Phe Ile Ser Tyr Thr Phe Ile Phe Thr Asp Ile Leu His Ile Cys
      260      265      270
Thr Ala Glu Gly Arg Tyr Asn Ala Phe Ser Thr Cys Gly Ser Leu Val
      275      280      285
Thr Ala Val Thr Val Phe Gln Gly Thr Leu Phe His Met Cys Leu Arg
      290      295      300
Pro Pro Ser Glu Ala Ser Val Glu Gln Gly Lys Ile Val Ala Ala Phe
305      310      315      320
Tyr Ile Phe Val Ser Pro Thr Leu Asn Pro Leu Ile Tyr Arg Leu Arg
      325      330      335
Asn Lys Asn Val Lys Arg Thr Ile Arg Glu Val Ile Gln Lys Lys Leu
      340      345      350
Phe Ala Lys Xaa Gly Arg
      355

```

&lt;210&gt; 1511

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g428 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1511

```

Met Phe Gly Ala Asn Leu Thr Thr Phe His Pro Thr Leu Phe Ile Leu
1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Ile Trp Leu Ser Ile Pro
      20      25      30

```



Phe Tyr Leu Met Tyr Ile Thr Ala Val Leu Gly Asn Gly Ala Leu Ile  
 35 40 45  
 Leu Val Val Leu Ser Glu His Thr Leu His Val Phe Leu Ser Met Leu  
 50 55 60  
 Ala Gly Thr Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys Ala Leu  
 65 70 75 80  
 Ala Ile Phe Trp Val His Ala Gly Glu Ile Ala Phe Asp Ala Cys Ile  
 85 90 95  
 Thr Gln Met Phe Ile His Val Ala Phe Val Ala Glu Ser Gly Ile  
 100 105 110  
 Leu Leu Ala Met Ala Phe Asp Ser Tyr Val Ala Ile Cys Thr Pro Leu  
 115 120 125  
 Arg Tyr Thr Thr Ile Leu Thr Ser Met Val Asn Gly Lys Met Thr Leu  
 130 135 140  
 Thr Ile Trp Gly Gln Ser Ile Gly Thr Ile Phe Pro Val Ile Phe Leu  
 145 150 155 160  
 Leu Lys Arg Leu Pro Tyr Cys Gln Thr Asn Ile Ile Pro His Ser Tyr  
 165 170 175  
 Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Thr Val  
 180 185 190  
 Asn Ile Trp Tyr Gly Phe Ser Val Pro Met Ala Ser Val Leu Val Asp  
 195 200 205  
 Val Ala Phe Ile Gly Phe Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe  
 210 215 220  
 Arg Leu Pro Ser Gln Glu Ser Gln His Lys Ala Leu Asn Thr Cys Gly  
 225 230 235 240  
 Ser His Ile Gly Val Val Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr  
 245 250 255  
 Phe Leu Thr His Arg Phe Gly Lys Asn Ile Pro His His Val His Ile  
 260 265 270  
 Leu Leu Ala Asn Leu Tyr Leu Leu Val Pro Pro Met Leu Asn Pro Ile  
 275 280 285  
 Ile Tyr Gly Glu Lys Thr Lys Gln Ile Arg Asp Ser Met Ala His Met  
 290 295 300  
 Leu Ser Val Val Gly Lys Ser Xaa Asp  
 305 310

&lt;210&gt; 1512

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g429 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1512

Met Lys Met Lys Ile Asp Pro Lys Cys Asn Gly Thr Glu Val Thr Glu  
 1 5 10 15  
 Phe Ile Leu Leu Gly Leu Thr Ser Gln Pro Glu Leu Gln Pro Met Leu  
 20 25 30  
 Phe Val Val Phe Leu Leu Ile Tyr Leu Ile Thr Leu Thr Gly Lys Phe  
 35 40 45  
 Gly Met Ile Phe Leu Ile Arg Phe Thr Pro Gln Leu Gln Thr His Met  
 50 55 60  
 Tyr Phe Phe Leu Thr His Leu Ala Cys Val Asp Ile Phe Tyr Ser Thr  
 65 70 75 80  
 Asn Val Ser Pro Gln Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr  
 85 90 95  
 Ile Ser Tyr Ala Gly Cys Leu Ala Gln Cys Phe Val Phe Val Thr Leu  
 100 105 110  
 Leu Leu Thr Glu Tyr Tyr Met Leu Gly Ala Met Ala Tyr Asp Cys Tyr

```

      115      120      125
Met Ala Ile Cys Asn Pro Leu His Tyr Ser Ser Lys Met Ser Arg Ala
  130      135      140
Val Cys Ile Cys Leu Val Thr Phe Pro Tyr Phe Trp Gly Ser Met Val
  145      150      155      160
Gly Thr Met Gln Val Ile Leu Thr Ser Arg Leu Ser Phe Phe Gly Pro
      165      170      175
Asn Thr Ile Asn His Phe Tyr Cys Thr Asp Pro Pro Leu Leu Met Leu
      180      185      190
Thr Ser Ser Asp Thr Tyr Ile Lys Gln Thr Ala Leu Phe Val Ser Ala
      195      200      205
Gly Ile Asn Leu Thr Val Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile
      210      215      220
Phe Ile Phe Ile Thr Ile Met Arg Ile Arg Ser Ser Glu Gly Gln Leu
  225      230      235      240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Ala Val Thr Met Phe
      245      250      255
Tyr Gly Ser Leu Phe Cys Met Tyr Leu Arg Pro Thr Asn Glu Leu Ser
      260      265      270
Val Glu Gln Gly Lys Met Gly Val Val Phe Cys Ile Phe Val Ser Pro
      275      280      285
Met Leu Asn Pro Phe Ile Tyr Arg Leu Arg Asn Lys Asp Val Lys Gln
      290      295      300
Ala Leu Lys Arg Val Phe Met Arg Asn Leu
  305      310

```

&lt;210&gt; 1513

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g430 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1513

```

Met Ser Leu Leu Phe Xaa Asp Xaa Asp Met Arg Asn Phe Thr Pro Leu
  1      5      10      15
Ser Gly Phe Ile Ile Leu Gly Phe Thr Asp His Pro Glu Leu Gln Cys
      20      25      30
Leu Leu Phe Val Leu Phe Leu Leu Ile Tyr Met Phe Thr Val Val Gly
      35      40      45
Asn Leu Gly Met Ile Leu Leu Ile Lys Ile Asp Ser His Leu His Thr
      50      55      60
Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Leu Val Asp Phe Cys Tyr
  65      70      75      80
Ser Ser Val Ile Ala Pro Asn Met Leu Ile Asn Phe Trp Val Glu Asn
      85      90      95
Pro Val Ile Ser Phe Asn Glu Cys Ala Thr Gln Phe Phe Phe Phe Gly
      100      105      110
Ser Phe Ala Gly Ile Glu Gly Phe Leu Leu Ala Val Met Ala Tyr Asp
      115      120      125
Cys Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Thr Val Leu Met Ser
      130      135      140
Pro His Leu Ser Ala Leu Leu Val Leu Ala Thr Tyr Leu Leu Gly Phe
  145      150      155      160
Val Asn Ala Ala Ile His Thr Gly Phe Thr Phe Gln Leu Ser Phe Cys
      165      170      175

```

His	Ser	Asn	Ile	Ile	Asn	Tyr	Phe	Phe	Cys	Asp	Ile	Pro	Pro	Leu	Leu
		180						185					190		
Lys	Leu	Cys	Ser	Asp	Thr	His	Ile	Asn	Glu	Val	Val	Ile	Phe	Ala	Phe
		195					200					205			
Ala	Ser	Phe	Asn	Glu	Leu	Ser	Cys	Leu	Leu	Leu	Ile	Leu	Val	Ser	Cys
		210				215					220				
Leu	Tyr	Ile	Leu	Ala	Ala	Ile	Leu	Lys	Ile	His	Ser	Ala	Glu	Gly	Arg
		225			230					235					240
His	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Ala	Val	Val	Thr	Ile
			245						250					255	
Phe	Phe	Gly	Thr	Ile	Leu	Phe	Met	Tyr	Leu	Leu	Arg	Pro	Ser	Ser	Ser
			260					265					270		
Tyr	Ser	Met	Asp	Gln	Asp	Lys	Val	Val	Ser	Val	Phe	Tyr	Thr	Val	Val
		275					280					285			
Ile	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val
		290				295					300				
Lys	Ala	Ser	Leu	Ser	Lys	Met	Phe	Lys	Thr	Val	Ser	Tyr	Ile	Ser	Thr
		305			310					315					320

&lt;210&gt; 1514

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g431 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1514

Met	Gly	Leu	Pro	Gly	Ile	His	Glu	Trp	Gln	His	Trp	Leu	Ser	Leu	Pro
1				5					10					15	
Leu	Thr	Leu	Leu	Tyr	Leu	Leu	Ala	Leu	Gly	Ala	Asn	Leu	Leu	Ile	Ile
			20					25					30		
Ile	Thr	Ile	Gln	His	Glu	Thr	Val	Leu	His	Glu	Pro	Met	Tyr	His	Leu
		35					40					45			
Leu	Gly	Ile	Leu	Ala	Val	Val	Asp	Ile	Gly	Leu	Ala	Thr	Thr	Ile	Met
	50				55					60					
Pro	Lys	Ile	Leu	Ala	Ile	Phe	Trp	Phe	Asp	Ala	Lys	Ala	Ile	Ser	Leu
	65				70				75						80
Pro	Met	Cys	Phe	Ala	Gln	Ile	Tyr	Ala	Ile	His	Cys	Phe	Phe	Cys	Ile
			85					90					95		
Glu	Ser	Gly	Ile	Phe	Leu	Cys	Met	Ala	Val	Asp	Arg	Tyr	Ile	Ala	Ile
			100					105					110		
Cys	Arg	Pro	Leu	Gln	Tyr	Pro	Ser	Ile	Val	Thr	Lys	Ala	Phe	Val	Phe
		115					120					125			
Lys	Ala	Thr	Gly	Phe	Ile	Met	Leu	Arg	Asn	Gly	Leu	Leu	Thr	Ile	Pro
		130				135					140				
Val	Pro	Ile	Leu	Ala	Ala	Gln	Arg	His	Tyr	Cys	Ser	Arg	Asn	Glu	Ile
				150						155				160	
Glu	His	Cys	Leu	Cys	Ser	Asn	Leu	Gly	Val	Ile	Ser	Leu	Ala	Cys	Asp
			165					170						175	
Asp	Ile	Thr	Val	Asn	Lys	Phe	Tyr	Gln	Leu	Met	Leu	Ala	Trp	Val	Leu
			180					185					190		
Val	Gly	Ser	Asp	Met	Ala	Leu	Val	Phe	Ser	Ser	Tyr	Ala	Val	Ile	Leu
		195				200						205			
His	Ser	Val	Leu	Arg	Leu	Asn	Ser	Ala	Glu	Ala	Met	Ser	Lys	Ala	Leu
		210				215					220				
Ser	Thr	Cys	Ser	Ser	His	Leu	Ile	Leu	Ile	Leu	Phe	His	Thr	Gly	Ile
				230						235					240
Ile	Val	Leu	Ser	Val	Thr	His	Leu	Ala	Glu	Lys	Lys	Ile	Pro	Leu	Ile
				245					250					255	
Pro	Val	Phe	Leu	Asn	Val	Leu	His	Asn	Val	Ile	Pro	Pro	Ala	Leu	Asn

Pro	Leu	Ala	260	Cys	Ala	Leu	Arg	Met	265	His	Lys	Leu	Arg	Leu	270	Gly	Phe	Gln
		275						280						285				
Arg	Leu	Leu	Gly	Leu	Gly	Gln	Asp	Val	Ser	Lys								
		290					295											

&lt;210&gt; 1515

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g432 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1515

Met	Met	Arg	Leu	Met	Lys	Glu	Val	Arg	Gly	Arg	Asn	Gln	Thr	Glu	Val
1				5					10					15	
Thr	Glu	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Asp	Asn	Pro	Asp	Leu	Gln	Gly
			20					25					30		
Val	Leu	Phe	Ala	Leu	Phe	Leu	Leu	Ile	Tyr	Met	Ala	Asn	Met	Val	Gly
		35				40					45				
Asn	Leu	Gly	Met	Ile	Val	Leu	Ile	Lys	Ile	Asp	Leu	Cys	Leu	His	Thr
	50				55					60					
Pro	Met	Tyr	Phe	Phe	Leu	Ser	Ser	Leu	Ser	Phe	Val	Asp	Ala	Ser	Tyr
65					70				75					80	
Ser	Ser	Ser	Val	Thr	Pro	Lys	Met	Leu	Val	Asn	Leu	Met	Ala	Glu	Asn
			85					90					95		
Lys	Ala	Ile	Ser	Phe	His	Gly	Cys	Ala	Ala	Gln	Phe	Tyr	Phe	Phe	Gly
			100					105					110		
Ser	Phe	Leu	Gly	Thr	Glu	Cys	Phe	Leu	Leu	Ala	Met	Met	Ala	Tyr	Asp
		115				120					125				
Arg	Tyr	Ala	Ala	Ile	Trp	Asn	Pro	Leu	Leu	Tyr	Pro	Val	Leu	Val	Ser
		130				135					140				
Gly	Arg	Ile	Cys	Phe	Leu	Leu	Ile	Ala	Thr	Ser	Phe	Leu	Ala	Gly	Cys
145					150					155				160	
Gly	Asn	Ala	Ala	Ile	His	Thr	Gly	Met	Thr	Phe	Arg	Leu	Ser	Phe	Cys
			165					170						175	
Gly	Ser	Asn	Arg	Ile	Asn	His	Phe	Tyr	Cys	Asp	Thr	Pro	Pro	Leu	Leu
		180						185					190		
Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Phe	Asn	Gly	Ile	Val	Ile	Met	Ala
		195				200						205			
Phe	Ser	Ser	Phe	Ile	Val	Ile	Ser	Cys	Val	Met	Ile	Val	Leu	Ile	Ser
		210				215						220			
Tyr	Leu	Cys	Ile	Phe	Ile	Ala	Val	Leu	Lys	Met	Pro	Ser	Leu	Glu	Gly
225					230					235				240	
Arg	His	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	Tyr	Leu	Met	Ala	Val	Thr
			245					250						255	
Ile	Phe	Phe	Gly	Thr	Ile	Leu	Phe	Met	Tyr	Leu	Arg	Pro	Thr	Ser	Ser
		260						265					270		
Tyr	Ser	Met	Glu	Gln	Asp	Lys	Val	Val	Ser	Val	Phe	Tyr	Thr	Val	Ile
		275				280						285			
Ile	Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Lys	Asn	Lys	Asp	Val
		290				295					300				
Lys	Lys	Ala	Leu	Lys	Lys	Ile	Leu	Trp	Lys	His	Ile	Leu			
305					310					315					

&lt;210&gt; 1516

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g433 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1516

```

Met Ser His Thr Asn Val Thr Ile Phe His Pro Ala Val Phe Val Leu
 1           5           10           15
Pro Gly Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro
      20           25           30
Leu Cys Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile
      35           40           45
Val Val Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe
      50           55           60
Leu Ser Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val
      65           70           75           80
Pro Lys Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe
      85           90           95
Asp Ala Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly
      100          105          110
Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
      115          120          125
Cys Ala Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly
      130          135          140
Arg Ile Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro
      145          150          155          160
Val Ile Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val
      165          170          175
Pro His Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala
      180          185          190
Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met
      195          200          205
Val Ile Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu
      210          215          220
Arg Ala Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu
      225          230          235          240
Ser Thr Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro
      245          250          255
Ser Phe Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln
      260          265          270
His Val His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met
      275          280          285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gly
      290          295          300
Val Ala His Arg Phe Phe Asp Ile Lys Thr Trp Cys Cys
      305          310          315

```

&lt;210&gt; 1517

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g434 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1517

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
      20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
      35           40           45
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Ala Gly Asn

```

50 55 60  
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile  
 65 70 75 80  
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys  
 85 90 95  
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr  
 100 105 110  
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro  
 115 120 125  
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val  
 130 135 140  
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys  
 145 150 155 160  
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe  
 165 170 175  
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly  
 180 185 190  
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys  
 195 200 205  
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val  
 210 215 220  
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr  
 245 250 255  
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile  
 260 265 270  
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu  
 290 295 300  
 Pro  
 305

&lt;210&gt; 1518

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g435 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1518

Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu  
 1 5 10 15  
 Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu  
 35 40 45  
 Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe  
 50 55 60  
 Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu  
 65 70 75 80  
 Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe  
 85 90 95  
 Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met  
 100 105 110  
 Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr  
 130 135 140

Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile  
 165 170 175  
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly  
 180 185 190  
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ser  
 195 200 205  
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu  
 210 215 220  
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe  
 225 230 235 240  
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro  
 245 250 255  
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro  
 260 265 270  
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met  
 275 280 285  
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Tyr  
 290 295 300  
 Val Leu Ser Leu Phe Gln Arg Lys Asn Met  
 305 310

&lt;210&gt; 1519

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g436 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1519

Met Leu Lys Lys Asn His Thr Ala Val Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Arg Ala Glu Leu Gln Ser Leu Leu Phe Val Val Phe Leu  
 20 25 30  
 Val Ile Tyr Leu Ile Thr Val Ile Gly Asn Val Ser Met Ile Leu Leu  
 35 40 45  
 Ile Arg Ser Asp Ser Thr Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Phe Val Asp Leu Cys Tyr Thr Thr Asn Val Thr Pro Gln  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Phe Ile Gln Phe His Phe Phe Ile Ala Leu Val Ile Thr Asp Tyr  
 100 105 110  
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys Val Cys Leu Cys Leu  
 130 135 140  
 Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn Gly Leu Ser Gln Thr  
 145 150 155 160  
 Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro Asn Asp Ile Asn His  
 165 170 175  
 Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala Gly Ser Asn Leu Ile  
 195 200 205  
 Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Thr Ala  
 210 215 220  
 Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg Lys Ala Phe Ser Thr

225		230		235		240
Cys Gly Ser His Val Thr Ala Val Thr Val Phe Tyr Gly Thr Leu Phe						
	245		250		255	
Cys Met Tyr Leu Arg Pro Pro Ser Glu Thr Ser Ile Gln Gln Gly Lys						
	260		265		270	
Ile Val Ala Val Phe Tyr Ile Phe Val Ser Pro Met Leu Asn Pro Leu						
	275		280		285	
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ser Ile Arg Lys Val						
	290		295		300	
Ile Gln Lys Lys Leu Phe Ala Lys						
305		310				

&lt;210&gt; 1520

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g437 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1520

Met Ser Ala Ser Asn Ile Thr Leu Thr His Pro Thr Ala Phe Leu Leu																			
1			5				10					15							
Val Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro																			
	20					25					30								
Phe Cys Leu Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu																			
	35					40					45								
Leu Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe																			
	50				55					60									
Leu Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu																			
65			70					75										80	
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe																			
	85						90											95	
Phe Ala Cys Leu Ala Gln Met Phe Phe Leu His Ser Phe Ser Ile Met																			
	100						105											110	
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile																			
	115					120												125	
Cys Lys Pro Leu His Tyr Thr Lys Val Leu Thr Gly Ser Leu Ile Thr																			
	130					135												140	
Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro																			
145			150					155										160	
Leu Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile																			
	165							170										175	
Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly																			
	180						185											190	
Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile																			
	195					200												205	
Val Val Leu Asp Leu Leu Leu Val Ile Leu Ser Tyr Ile Phe Ile Leu																			
	210					215												220	
Gln Ala Val Leu Leu Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe																			
225			230					235										240	
Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Thr																			
	245							250										255	
Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro																			
	260						265											270	
His Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met																			
	275					280												285	
Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser																			
	290					295												300	
Ile Leu Gly Val Phe Pro Arg Lys Asp Met																			
305						310													



<210> 1521  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g438 protein)

<220>  
 <223> Synthetic construct

<400> 1521  
 Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu  
 1 5 10 15  
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu  
 35 40 45  
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Ile Tyr Leu Phe Leu  
 50 55 60  
 Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu Pro  
 65 70 75 80  
 Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe Phe  
 85 90 95  
 Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met Glu  
 100 105 110  
 Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr Lys  
 130 135 140  
 Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro Leu  
 145 150 155 160  
 Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile Ala  
 165 170 175  
 Arg Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly Asn  
 180 185 190  
 Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile Gly  
 195 200 205  
 Val Leu Asp Leu Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln  
 210 215 220  
 Ala Val Leu Gln Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly  
 225 230 235 240  
 Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser  
 245 250 255  
 Val Ile Ser Ser Val Met His Arg Val Ala Arg Cys Ala Ala Pro His  
 260 265 270  
 Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val  
 290 295 300  
 Leu Gly Val Phe Pro Arg Lys Asp Val  
 305 310

<210> 1522  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g439 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1522

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1          5          10          15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
          20          25          30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
          35          40          45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
65          70          75          80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
          85          90          95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
          100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
          130          135          140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
145          150          155          160
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
          165          170          175
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
          180          185          190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
          195          200          205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu
          210          215          220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu
225          230          235          240
Gly Thr Cys Gly Ser His Leu Arg Val Ile Ser Met Phe Tyr Leu Pro
          245          250          255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Leu
          260          265          270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met
          275          280          285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys
          290          295          300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile
305          310          315

```

&lt;210&gt; 1523

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g440 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1523

```

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
          20          25          30
Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
          35          40          45
Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50          55          60

```

```

Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
65          70          75          80
Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
      85          90          95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
      100        105        110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
      115        120        125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
      130        135        140
Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
145          150          155          160
Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
      165        170        175
Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
      180        185        190
Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
      195        200        205
Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
      210        215        220
Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225          230          235          240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
      245        250        255
Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
      260        265        270
Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
      275        280        285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
      290        295        300
Val Ala Arg Val Phe Leu Ile Lys Lys
305          310

```

&lt;210&gt; 1524

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g441 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1524

```

Met Glu Lys Ser Asn Val Ser Ser Val Tyr Gly Phe Ile Leu Val Gly
1          5          10          15
Phe Ser Asp Arg Pro Lys Leu Glu Met Val Leu Phe Thr Val Asn Phe
      20          25          30
Ile Leu Tyr Ser Val Ala Val Leu Gly Asn Ser Thr Ile Ile Leu Val
      35          40          45
Cys Ile Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Ser Thr Ser Cys Ile Pro Gln
65          70          75          80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Cys Ala Gly
      85          90          95
Cys Val Val Gln Leu Phe Ser Phe Leu Ser Val Arg Gly Ile Glu Cys
      100        105        110
Ile Leu Leu Ala Val Met Ala Tyr Asp Ser Tyr Ala Ala Val Cys Lys

```

```

      115      120      125
Pro Leu Arg Tyr Leu Val Ile Met His Leu Gln Leu Cys Leu Gly Leu
  130      135      140
Met Ala Ala Ala Trp Gly Ser Gly Leu Val Asn Ala Val Val Met Ser
  145      150      155      160
Pro Leu Thr Met Thr Leu Ser Arg Ser Gly Arg Arg Arg Val Asn His
      165      170      175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Met Ala Cys Leu Asp Val
      180      185      190
Arg Ala Val Glu Met Leu Ala Phe Ala Phe Ala Val Leu Ile Val Leu
  195      200      205
Leu Pro Leu Thr Leu Ile Leu Val Ser Tyr Gly Tyr Ile Ala Ala Ala
  210      215      220
Val Leu Ser Ile Lys Ser Ala Ala Arg Gln Trp Lys Ala Phe His Thr
  225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
      245      250      255
Tyr Met Tyr Met Gln Pro Gly Asn Ser Ser Ser Gln Asp Gln Gly Lys
  260      265      270
Phe Leu Thr Leu Phe Tyr Asn Leu Val Thr Pro Met Leu Asn Leu Leu
  275      280      285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Lys Val
  290      295      300
Leu Gly Arg Gln Xaa Xaa Thr Gly Glu Ile Xaa Xaa Val Val Lys Ser
  305      310      315      320
Xaa Ala Lys Tyr Leu Phe Gln Tyr Thr Phe Ile Leu Cys
      325      330

```

&lt;210&gt; 1525

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g442 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1525

```

Gln Val Val His Thr Gly Phe Ser Pro Xaa Leu Tyr Val Phe Thr Leu
  1      5      10      15
Leu Gly Asn Gly Ser Ile Leu Gly Leu Ile Trp Leu Asp Ser Arg Leu
      20      25      30
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Ile Ile Asp Ile
      35      40      45
Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr Asn Leu Gly Leu
      50      55      60
Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr Met Gln Thr Phe
      65      70      75      80
Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile Leu Val Met Met
      85      90      95
Ser Tyr Asp Arg Tyr Met Ala Val Cys His Pro Leu Gln Tyr Ser Val
      100      105      110
Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val Thr Ser Trp Ala
      115      120      125
Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu Ile Leu Arg Leu
      130      135      140
Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe Cys Glu Ile Leu
  145      150      155      160

```

Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val  
 165 170 175  
 Ile Phe Ala Ser Ser Val Phe Ile Leu Val Gly Ala Leu Cys Leu Val  
 180 185 190  
 Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu Arg Asn Gln Ser  
 195 200 205  
 Gly Glu Gly Arg Arg Lys Gly Phe Ser Thr Cys Tyr Ser His Leu Cys  
 210 215 220  
 Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met Ala Pro  
 225 230 235 240  
 Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu Phe Tyr  
 245 250 255  
 Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn  
 260 265 270  
 Ala Glu Val Lys Gly Ala Leu Arg Ser Ala Leu Arg Lys Glu Arg Leu  
 275 280 285  
 Thr Xaa Asp Ile Ser Lys Gly Thr Met Gly Arg Glu Pro Cys Ser Leu  
 290 295 300  
 Gln Asn Ile Glu Val Gly Phe Phe Phe Cys Leu Leu Leu  
 305 310 315

&lt;210&gt; 1526

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g443 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(239)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1526

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val  
 1 5 10 15  
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr  
 20 25 30  
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr  
 35 40 45  
 Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Met Thr  
 50 55 60  
 Trp Ser Asp Asn Ser Phe Ile Phe Val Ile Met Tyr Thr Leu Ile Leu  
 65 70 75 80  
 Lys Phe Pro Ser Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His  
 85 90 95  
 Val Leu Leu Ala Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu  
 100 105 110  
 Glu Met Ser Val Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu  
 115 120 125  
 Ile Ser Asn Phe Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met  
 130 135 140  
 Asn Thr Ser Asn Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His  
 145 150 155 160  
 His His His Arg Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile  
 165 170 175  
 Ile Val Xaa Met Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln  
 180 185 190  
 Glu Arg Phe Phe Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys  
 195 200 205  
 Leu Leu Val Tyr Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg

<400> 1528  
Leu Ser Xaa Pro Thr Arg Ala Ala Gln Lys Gln Phe Ile Leu Leu Gly  
1 5 10 15

Phe Ser Gly Arg Pro Arg Leu Glu His Val Leu Phe Val Phe Val Leu  
 20 25 30  
 Ile Phe Tyr Leu Val Thr Leu Val Gly Asn Ile Ile Ile Ile Leu Ile  
 35 40 45  
 Ser His Leu Asp Pro Cys Leu His Met Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ser Ile Pro Gln  
 65 70 75 80  
 Leu Leu Phe Asn Leu Gly Ser Pro Gly Lys Thr Ile Ser His Thr Gly  
 85 90 95  
 Cys Ala Ile Gln Leu Phe Met Phe Leu Gly Leu Gly Gly Thr Glu Cys  
 100 105 110  
 Ile Leu Leu Ala Ala Val Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Ser Val Ile Met His Pro Gln Leu Cys Trp Lys Leu  
 130 135 140  
 Val Ser Val Ala Arg Gly Cys Trp Thr Pro Gln Phe Ser Ser Tyr Val  
 145 150 155 160  
 Ser Trp Thr Met Lys Leu Pro Arg Cys Gly Arg Cys Lys Leu Lys His  
 165 170 175  
 Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Ile Thr Cys Val Asp Thr  
 180 185 190  
 Val Ala Met Glu Ser Thr Val Phe Thr Leu Ser Val Val Ile Val Leu  
 195 200 205  
 Met Pro Leu Cys Leu Ile Leu Ile Ser Tyr Ser Tyr Ile Ala Leu Ala  
 210 215 220  
 Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Arg Lys Ala Phe Asn Met  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile  
 245 250 255  
 Tyr Met Tyr Met Gln Pro Xaa Asn Asn Ser Ser Gln Asp Gln Gly Lys  
 260 265 270  
 Phe Leu Thr Leu Phe Tyr Asn Leu Met Thr Pro Met Leu Asn Pro Val  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Arg Leu  
 290 295 300  
 Val Ser Arg Lys His Ser Asp Ser Asp Cys Ser Xaa Asp Cys Phe Phe  
 305 310 315 320

&lt;210&gt; 1529

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g446 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1529

Met Glu Asn Tyr Asn Gln Thr Ser Thr Ala Phe Ile Leu Leu Gly Leu  
 1 5 10 15  
 Ser Pro Pro Pro Lys Ile Gly His Phe Ile Phe Ile Leu Ile Asn Phe  
 20 25 30  
 Val Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile  
 35 40 45  
 Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
 50 55 60  
 Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65 70 75 80  
 Val Tyr Asp Phe Ser Cys His Gly Asn Lys Ser Ile Ser Phe Thr Gly  
 85 90 95  
 Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala

	100		105		110								
Leu	Leu	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile
	115		120									125	

&lt;210&gt; 1530

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g447 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1530

Met	Glu	Arg	Ala	Asn	Asp	Ser	Thr	Phe	Ser	Gly	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Asn	Arg	Pro	Gln	Leu	Glu	Thr	Ala	Leu	Phe	Val	Val	Ile	Leu
		20						25					30		
Ile	Ile	Tyr	Phe	Leu	Ser	Phe	Leu	Gly	Asn	Gly	Thr	Ile	Ile	Leu	Leu
		35					40					45			
Ser	Ile	Val	Asp	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
		50				55					60				
Asn	Leu	Ser	Phe	Met	Asp	Leu	Cys	Leu	Thr	Thr	Cys	Thr	Val	Pro	Gln
65					70					75				80	
Thr	Leu	Val	Asn	Phe	Lys	Gly	Lys	Asp	Lys	Thr	Ile	Thr	Tyr	Gly	Gly
			85						90					95	
Cys	Val	Thr	Gln	Leu	Phe	Ile	Ala	Leu	Gly	Leu	Gly	Gly	Ser	Glu	Cys
			100					105					110		
Val	Leu	Leu	Ser	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Arg
		115					120					125			
Pro	Leu	His	Tyr	Met	Val	Ser	Met	His	Pro	Gln	Leu	Cys	Leu	Gln	Leu
		130					135					140			
Val	Val	Thr	Thr	Trp	Leu	Thr	Gly	Phe	Gly	Asn	Ser	Val	Ile	Gln	Thr
145					150					155				160	
Ala	Leu	Thr	Met	Thr	Leu	Pro	Leu	Cys	Asp	Lys	Asn	Gln	Val	Asp	His
			165						170					175	
Phe	Phe	Cys	Glu	Val	Pro	Val	Met	Leu	Lys	Leu	Ser	Cys	Thr	Asn	Thr
		180						185					190		
Ser	Ile	Asn	Glu	Ala	Glu	Ile	Phe	Ala	Val	Ser	Val	Phe	Phe	Leu	Val
		195					200					205			
Val	Pro	Leu	Ser	Leu	Ile	Leu	Ala	Ser	Tyr	Gly	His	Ile	Thr	His	Ala
		210				215						220			
Val	Leu	Lys	Ile	Lys	Ser	Ala	Gln	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr
225					230					235				240	
Cys	Gly	Ser	His	Leu	Leu	Val	Val	Ile	Ile	Phe	Phe	Gly	Thr	Leu	Ile
			245						250					255	
Ser	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Gln	Asp	Val	Asn	Lys
		260						265					270		
Ser	Ile	Ala	Leu	Phe	Tyr	Thr	Leu	Val	Thr	Pro	Leu	Leu	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Thr	Lys	Lys	Thr
		290				295					300				
Ser	Gly	Glu	Asp	His	Arg	Cys	Met	Arg	Lys	Leu	Thr	Gln	Gly	Leu	Gln
305					310					315				320	
Phe	Gln	Thr	Phe	Val	His										
					325										

&lt;210&gt; 1531

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g448 protein)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1531

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1          5          10          15
Phe Pro Pro Ser Ile Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe
 20          25          30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
 35          40          45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50          55          60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
 65          70          75          80
Ala Ser Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys
 85          90          95
Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu
100          105          110
Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro
115          120          125
Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile
130          135          140
Thr Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val
145          150          155          160
Tyr Val Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe
165          170          175
Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
180          185          190
Val Tyr Glu Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu Val Phe
195          200          205
Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe Ala Val
210          215          220
Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys
225          230          235          240
Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr
245          250          255
Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val
260          265          270
Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile
275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser
290          295          300
Gln Arg Ile Cys Ser Val Lys Met
305          310

```

&lt;210&gt; 1532

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g449 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1532

```

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1          5          10          15
Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
 20          25          30
Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr
 35          40          45
Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu

```

```

      50      55      60
Ser Ile Leu Asp Ala Cys Tyr Ile Ser Val Thr Val Pro Thr Ser Cys
65      70      75      80
Val Asn Ser Leu Leu Asp Ser Thr Thr Ile Ser Lys Ala Gly Cys Val
      85      90      95
Ala Gln Val Phe Leu Val Val Phe Phe Val Tyr Val Glu Leu Leu Phe
      100      105      110
Leu Thr Ile Met Ala His Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115      120      125
His Tyr Pro Val Ile Val Asn Ser Arg Ile Cys Ile Gln Met Thr Leu
      130      135      140
Ala Ser Leu Leu Ser Gly Leu Val Tyr Ala Gly Met His Thr Gly Ser
145      150      155      160
Thr Phe Gln Leu Pro Phe Cys Arg Ser Asn Val Ile His Gln Phe Phe
      165      170      175
Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ser
      180      185      190
Asn Glu Val Met Ile Val Val Ser Ala Leu Gly Val Gly Gly Gly Cys
      195      200      205
Phe Ile Phe Ile Ile Arg Ser Tyr Ile His Ile Phe Ser Thr Val Leu
      210      215      220
Gly Phe Pro Arg Gly Ala Asp Arg Thr Lys Ala Phe Ser Thr Cys Ile
225      230      235      240
Pro His Ile Leu Val Ser Val Phe Leu Ser Ser Cys Ser Ser Val
      245      250      255
Tyr Leu Arg Pro Pro Ala Ile Pro Ala Ala Thr Gln Asp Leu Ile Leu
      260      265      270
Ser Gly Phe Tyr Ser Ile Met Pro Pro Leu Phe Asn Pro Ile Ile Tyr
      275      280      285
Ser Leu Arg Asn Lys Gln Ile Lys Val Ala Ile Lys Lys Ile Met Lys
      290      295      300
Arg Ile Phe Tyr Ser Glu Asn Val
305      310

```

&lt;210&gt; 1533

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g450 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1533

```

Arg Asn Ala Pro Leu Glu Lys Tyr Asn Gln Thr Ser Thr Asp Phe Ile
1      5      10      15
Leu Leu Gly Ile Phe Pro Pro Ser Arg Ile Gly Phe Leu Leu Phe Ile
      20      25      30
Leu Leu Val Leu Ile Leu Leu Leu Ala Leu Ile Gly Asn Gln Ser Val
      35      40      45
Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro Ile Tyr Phe
      50      55      60
Leu Leu Ser Arg Leu Tyr Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile
65      70      75      80
Val Pro Lys Met Phe Ser Asp Phe Leu Phe Gly Asn Lys Ser Ile Ser
      85      90      95
Phe Ile Gly Cys Gly Ile Gln Ser Phe Phe Phe Val Thr Leu Ala Gly
      100      105      110
Ala Glu Met Leu Pro Leu Thr Ser Met Ala Cys Asp His Tyr Val Ala
      115      120      125
Val Cys Phe Pro Leu His Tyr Pro Ile His Met Ser Lys Ile Val Cys
130      135      140

```

```

Leu Met Ile Ile Gly Ser Trp Ile Met Gly Ser Ile Asp Thr Cys Ala
145          150          155          160
His Ile Ser Tyr Met Pro His Ile Pro Val Cys Ser Ala Arg Ala Cys
          165          170          175
Asp Val Pro Ala Met Val Thr Leu Ala Phe Val Asp Thr Trp Val Tyr
          180          185          190
Glu Cys Thr Val Phe Leu Ser Thr Thr Leu Phe Leu Met Phe Thr Phe
          195          200          205
Ile Gly Ile Ala Cys Ser Tyr Gly Glu Val Leu Leu Thr Val Tyr His
          210          215          220
Ile Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr
225          230          235          240
His Leu Thr Val Val Ile Ile Tyr Tyr Ala Met Phe Ala Tyr Thr Tyr
          245          250          255
Leu Tyr Pro Arg Tyr Leu Gln Ser Pro Thr Glu Asp Lys Val Leu Ala
          260          265          270
Val Phe Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser
          275          280          285
Leu Arg Asn Arg Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg
          290          295          300
Ile Phe Pro Val Lys Met Lys
305          310

```

&lt;210&gt; 1534

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g451 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(192)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1534

```

Arg His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu
1          5          10          15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu
          20          25          30
Ser Leu Ser Leu Ser Leu Ser Leu Tyr Leu Val Met Val Leu Arg Asn
          35          40          45
Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro
          50          55          60
Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr
65          70          75          80
Ser Ala Thr Val Pro Lys Val Thr Val Asp Met Gln Ser His Ser Arg
          85          90          95
Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu
          100          105          110
Phe Ala Cys Ile Glu Cys Met Leu Leu Thr Val Met Ala Tyr Asp Gly
          115          120          125
Phe Val Ala Ile Cys Leu Pro Leu His Tyr Pro Val Ile Met Asn Pro
          130          135          140
His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu
145          150          155          160
Asp Ser Gln Leu His Gly Trp Ile Val Xaa Gln Phe Thr Ile Met Lys
          165          170          175
Asn Val Glu Ile Ser His Phe Val Ser Asp Pro Ser Gln Leu Leu Asn
          180          185          190

```

<210> 1535  
 <211> 317  
 <212> PRT  
 <213> Unknown (H38g452 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1535  
 Met Asp Arg Arg Asn Gln Thr Cys Ile Tyr Glu Phe Leu Leu Met Gly  
 1 5 10 15  
 Phe Ser Glu His Gln Glu Gln Ala Leu Leu Phe Gly Leu Phe Leu  
 20 25 30  
 Val Met Tyr Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Gly Ser Asp Leu His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys  
 65 70 75 80  
 Met Leu Asp His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu  
 85 90 95  
 Cys Leu Thr Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn  
 100 105 110  
 Asn Phe Leu Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser  
 115 120 125  
 His Pro Leu His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu  
 130 135 140  
 Leu Val Ala Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His  
 145 150 155 160  
 Thr Leu Leu Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro  
 165 170 175  
 His Phe Phe Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser  
 180 185 190  
 Thr Cys Val Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu  
 195 200 205  
 Ile Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu  
 210 215 220  
 Ala Ile Leu Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser  
 225 230 235 240  
 Ser Cys Thr Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala  
 245 250 255  
 Ile Gly Val Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp  
 260 265 270  
 Arg Val Phe Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Gly Lys  
 290 295 300  
 Leu Leu Gly Ile Lys Thr Ser Xaa His Pro Tyr Ser Arg  
 305 310 315

<210> 1536  
 <211> 252  
 <212> PRT  
 <213> Unknown (H38g453 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(252)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1536

```

His Leu Xaa Trp Cys Val Phe Arg Tyr Leu Gly Ile Val Val Glu Ile
 1           5           10           15
His Ile Val Phe Xaa Thr Phe Arg Cys Arg Ser Leu Val Ala Gly Tyr
      20           25           30
Val Leu Xaa Thr Phe Val Ala Ile His Leu Arg Arg Asn Ala Ala Phe
      35           40           45
Ser Ile Glu Phe Leu Cys Tyr Lys Xaa Arg Met Gln Asp Ile Asn Xaa
 50           55           60
Thr Lys Xaa Gly Lys Ile Leu Tyr Ser Leu Arg Glu Phe Lys Arg Leu
65           70           75           80
Leu Ala Thr Ser Leu Tyr Ser Ala Xaa Val Asn Arg Phe Leu Leu Asn
      85           90           95
Lys Leu Leu Pro Gly Leu Val Ser Lys Gln Ile Glu Thr Tyr Phe Arg
      100          105          110
Lys Glu Ile Tyr Ile Leu Ile Ser Thr Ile Arg Phe Ser Tyr Val Glu
      115          120          125
Thr Leu Glu Gly Glu Xaa Gly Val Asn Val Ser Ser Ile Ile Phe Leu
      130          135          140
Leu Ile Pro Phe Ser Met Ile Ser Ala Ser Ser Val Gln Ile Leu Xaa
      145          150          155          160
Gly Val Leu Xaa Met Lys Leu Ser Gln Ala Trp Lys Arg Ser Phe Ser
      165          170          175
Thr Trp Ser Ile Leu Met Ile Ala Val Val Thr Tyr Trp Asp Ser Phe
      180          185          190
Ile Phe Thr Tyr Val Tyr Glu Thr Xaa Ile Ile His Ile Ser Gly Gln
      195          200          205
Val Lys Phe Leu Glu Ile Phe Tyr Ala Phe Leu Ala Leu Thr Leu Asn
      210          215          220
Pro Val Val Tyr Ser Val Gly Thr Asp Ser Val Leu Val Ala Met Lys
      225          230          235          240
Asn Met Leu Xaa Ser Asn Ile Leu His Lys Lys Lys
      245          250

```

&lt;210&gt; 1537

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g454 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1537

```

Met Asp Gln Ile Asn His Thr Asn Val Lys Glu Phe Phe Phe Leu Glu
 1           5           10           15
Leu Thr Arg Ser Arg Glu Leu Glu Phe Phe Leu Phe Val Val Phe Phe
      20           25           30
Ala Val Tyr Val Ala Thr Val Leu Gly Asn Ala Leu Ile Val Val Thr
      35           40           45
Ile Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50           55           60
Asn Lys Ser Val Leu Asp Ile Val Phe Ser Ser Ile Thr Val Pro Lys
65           70           75           80
Phe Leu Val Asp Leu Leu Ser Asp Arg Lys Thr Ile Ser Tyr Asn Asp
      85           90           95
Cys Met Ala Gln Ile Phe Phe Phe His Phe Ala Gly Gly Ala Asp Ile

```

```

      100      105      110
Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Ala Lys
      115      120      125
Pro Leu His Tyr Val Thr Met M t Arg Lys Glu Val Trp Val Ala Leu
      130      135      140
Val Val Ala Ser Trp Val Ser Gly Gly Leu His Ser Ile Ile Gln Val
      145      150      155      160
Ile Leu Met Leu Pro Phe Pro Phe Cys Gly Pro Asn Thr Leu Asp Ala
      165      170      175
Phe Tyr Cys Tyr Val Leu Gln Val Val Lys Leu Ala Cys Thr Asp Thr
      180      185      190
Phe Ala Leu Glu Leu Phe Met Ile Ser Asn Asn Gly Leu Val Thr Leu
      195      200      205
Leu Trp Phe Leu Leu Leu Leu Gly Ser Tyr Thr Val Ile Leu Val Met
      210      215      220
Leu Arg Ser His Ser Gly Glu Gly Arg Asn Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ser His Met Leu Val Val Thr Leu His Phe Val Pro Cys Val Tyr
      245      250      255
Ile Tyr Cys Arg Pro Phe Met Thr Leu Pro Met Asp Thr Thr Ile Ser
      260      265      270
Ile Asn Asn Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser
      275      280      285
Leu Arg Asn Gln Glu Met Lys Ser Ala Met Gln Arg Leu Gln Arg Arg
      290      295      300
Leu Gly Pro Ser Glu Ser Arg Lys Trp
      305      310

```

&lt;210&gt; 1538

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g455 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1538

```

Met Glu Arg Ile Asn His Thr Ser Ser Val Ser Glu Phe Ile Leu Leu
  1      5      10      15
Gly Leu Ser Ser Arg Pro Glu Asp Gln Lys Thr Leu Phe Val Leu Phe
      20      25      30
Leu Ile Val Tyr Leu Val Thr Ile Thr Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Ile Arg Phe Asn Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Leu Thr Asp Ile Cys Phe Thr Thr Ser Val Val Pro
      65      70      75      80
Lys Met Leu Met Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Tyr Phe Leu Tyr Ala Leu Gly Asn Ser Asp
      100      105      110
Ser Cys Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
      115      120      125
Asp Pro Phe His Tyr Val Thr Thr Met Ser His His His Cys Val Leu
      130      135      140
Leu Val Ala Phe Ser Cys Ser Phe Pro His Leu His Ser Leu Leu His
      145      150      155      160
Thr Leu Leu Leu Asn Arg Leu Thr Phe Cys Asp Ser Asn Val Ile His
      165      170      175
His Phe Leu Cys Asp Leu Ser Pro Val Leu Lys Leu Ser Cys Ser Ser
      180      185      190

```

Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu Ala Pro Ile Val Leu  
 195 200 205  
 Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr Ile Arg Ile Leu Thr  
 210 215 220  
 Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys Arg Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile  
 245 250 255  
 Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr Ala Val Lys Asp His  
 260 265 270  
 Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln Gly Leu Arg Lys Leu  
 290 295 300  
 Met Ser Lys Arg Ser  
 305

<210> 1539

<211> 313

<212> PRT

<213> Unknown (H38g456 protein)

<220>

<223> Synthetic construct

<400> 1539

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser  
 1 5 10 15  
 Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile  
 20 25 30  
 Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr  
 35 40 45  
 Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu  
 50 55 60  
 Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile  
 65 70 75 80  
 Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala  
 85 90 95  
 Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile  
 100 105 110  
 Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu  
 115 120 125  
 Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser  
 130 135 140  
 Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly  
 145 150 155 160  
 Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe  
 165 170 175  
 Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met  
 180 185 190  
 Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys  
 195 200 205  
 Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu  
 210 215 220  
 Lys Ile Pro Thr Thr Lys Gly Gln Ser Lys Ala Phe Ser Thr Cys Phe  
 225 230 235 240  
 Pro His Leu Thr Val Phe Thr Val Phe Ile Ile Thr Ala Tyr Phe Val  
 245 250 255  
 Tyr Leu Lys Pro Pro Ser Asn Ser Pro Ser Val Ile Asp Arg Leu Leu  
 260 265 270  
 Ser Val Ile Tyr Thr Val Met Pro Pro Val Phe Asn Pro Val Thr Tyr

275                      280                      285  
 Ser Leu Arg Asn Asn Asp Met Lys Cys Ala Leu Ile Arg Leu Leu Gln  
 290                      295                      300  
 Lys Thr Tyr Gly Gln Glu Ala Tyr Phe  
 305                      310

<210> 1540

<211> 324

<212> PRT

<213> Unknown (H38g457 protein)

<220>

<223> Synthetic construct

<400> 1540

Met Ala Val Gly Arg Asn Asn Thr Ile Val Thr Lys Phe Ile Leu Leu  
 1                      5                      10                      15  
 Gly Leu Ser Asp His Pro Gln Met Lys Ile Phe Leu Phe Met Leu Phe  
 20                      25                      30  
 Leu Gly Leu Tyr Leu Leu Thr Leu Ala Trp Asn Leu Ser Leu Ile Ala  
 35                      40                      45  
 Leu Ile Lys Met Asp Ser His Leu His Met Pro Met Tyr Phe Phe Leu  
 50                      55                      60  
 Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Ser Thr Ala Pro  
 65                      70                      75                      80  
 Lys Met Leu Ser Asp Ile Ile Thr Glu Gln Lys Thr Ile Ser Phe Val  
 85                      90                      95  
 Gly Cys Ala Thr Gln Tyr Phe Val Phe Cys Gly Met Gly Leu Thr Glu  
 100                      105                      110  
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
 115                      120                      125  
 Asn Pro Leu Leu Tyr Thr Val Leu Ile Ser His Thr Leu Cys Leu Lys  
 130                      135                      140  
 Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Phe Ile Glu  
 145                      150                      155                      160  
 Thr Tyr Ser Val Tyr Gln His Asp Phe Cys Gly Pro Tyr Met Ile Asn  
 165                      170                      175  
 His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp  
 180                      185                      190  
 Thr Phe Thr Ser Glu Val Val Thr Phe Ile Val Ser Val Val Val Gly  
 195                      200                      205  
 Ile Val Ser Val Leu Val Val Leu Ile Ser Tyr Gly Tyr Ile Val Ala  
 210                      215                      220  
 Ala Val Val Lys Ile Ser Ser Ala Thr Gly Arg Thr Lys Ala Phe Ser  
 225                      230                      235                      240  
 Thr Cys Ala Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ser Gly  
 245                      250                      255  
 Phe Phe Met Tyr Met Arg Pro Ser Ser Ser Tyr Ser Leu Asn Arg Asp  
 260                      265                      270  
 Lys Val Val Ser Ile Phe Tyr Ala Leu Val Ile Pro Val Val Asn Pro  
 275                      280                      285  
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Asn Ala Met Arg Lys  
 290                      295                      300  
 Ala Met Glu Arg Asp Pro Gly Ile Ser His Gly Gly Pro Phe Ile Phe  
 305                      310                      315                      320  
 Met Thr Leu Gly

<210> 1541

<211> 314

<212> PRT



<213> Unknown (H38g458 protein)

<220>

<223> Synthetic construct

<400> 1541

```

Met Thr Asn Gln Thr Gln Met Met Glu Phe Leu Leu Val Arg Phe Thr
 1           5           10           15
Glu Asn Trp Val Leu Leu Arg Leu His Ala Leu Leu Phe Ser Leu Ile
          20           25           30
Tyr Leu Thr Ala Val Leu Met Asn Leu Val Ile Ile Leu Leu Met Ile
          35           40           45
Leu Asp His Arg Leu His Met Ala Met Tyr Phe Phe Leu Arg His Leu
          50           55           60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Ala Thr Val Pro Lys Ser Ile
65           70           75           80
Leu Asn Ser Val Ala Ser Thr Asp Ser Ile Ser Phe Leu Gly Cys Val
          85           90           95
Leu Gln Leu Phe Leu Val Val Leu Leu Ala Gly Ser Glu Ile Gly Ile
          100          105          110
Leu Thr Ala Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Cys Pro Leu
          115          120          125
His Cys Glu Ala Val Met Ser Arg Gly Leu Cys Val Gln Leu Met Ala
          130          135          140
Leu Ser Trp Leu Asn Arg Gly Ala Leu Gly Leu Leu Tyr Thr Ala Gly
145          150          155          160
Thr Phe Ser Leu Asn Phe Tyr Gly Ser Asp Glu Leu His Gln Phe Phe
          165          170          175
Cys Asp Val Pro Ala Leu Leu Lys Leu Thr Cys Ser Lys Glu His Ala
          180          185          190
Ile Ile Ser Val Ser Val Ala Ile Gly Val Cys Tyr Ala Phe Ser Cys
          195          200          205
Leu Val Cys Ile Val Val Ser Tyr Val Tyr Ile Phe Ser Ala Val Leu
          210          215          220
Arg Ile Ser Gln Arg Gln Arg Gln Ser Lys Ala Phe Ser Asn Cys Val
225          230          235          240
Pro His Leu Ile Val Val Thr Val Phe Leu Val Thr Gly Ala Val Ala
          245          250          255
Tyr Leu Lys Pro Gly Ser Asp Ala Pro Ser Ile Leu Asp Leu Leu Val
          260          265          270
Ser Val Phe Tyr Ser Val Ala Pro Pro Thr Leu Asn Pro Val Ile Tyr
          275          280          285
Cys Leu Lys Asn Lys Asp Ile Lys Ser Ala Leu Ser Lys Val Leu Trp
          290          295          300
Asn Val Arg Ser Ser Gly Val Met Lys Arg
305          310

```

<210> 1542

<211> 307

<212> PRT

<213> Unknown (H38g459 protein)

<220>

<223> Synthetic construct

<400> 1542

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1           5           10           15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
          20           25           30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr

```

```

      35      40      45
Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
 50      55      60
Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
65      70      75      80
Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
      85      90      95
Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
      100      105      110
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      115      120      125
Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
      130      135      140
Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
      145      150      155      160
Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
      165      170      175
Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
      180      185      190
Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
      195      200      205
Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
      210      215      220
Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
      225      230      235      240
His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
      245      250      255
Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
      260      265      270
Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
      275      280      285
Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
      290      295      300
Leu Lys His
305

```

&lt;210&gt; 1543

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g460 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1543

```

Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
 1      5      10      15
Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
      20      25      30
Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
      65      70      75      80
Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
      85      90      95
Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
      100      105      110
Cys Cys Leu Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
      115      120      125

```

```

Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
  130                      135                      140
Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
145                      150                      155                      160
Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln
                      165                      170                      175
His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn
                      180                      185                      190
Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
                      195                      200                      205
Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
                      210                      215                      220
Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
225                      230                      235                      240
Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
                      245                      250                      255
Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
                      260                      265                      270

```

&lt;210&gt; 1544

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g461 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1544

```

Tyr Ser Lys Glu Ile Ile Glu Xaa Cys Thr Ser Asn Asp Ile Ile Lys
  1                      5                      10                      15
Cys Gly Xaa His Asn Lys Ile Thr Phe Phe Leu Phe Ile Leu Leu Glu
                      20                      25                      30
Phe Thr Glu Asp Leu Gly Leu Gln Gln Val Leu Phe Phe Ile Phe Leu
                      35                      40                      45
Ile Ile Tyr Val Ile Ser Leu Ser Gly Asn Ile Ile Leu Asn Ser Leu
                      50                      55                      60
Ile Cys Ala Asp Ser Trp Pro Tyr Thr Pro Met Tyr Phe Phe Thr Gly
65                      70                      75                      80
Asn Arg Phe Leu Leu Asp Leu Trp Tyr Ser Ser Val His Ile Pro Asp
                      85                      90                      95
Ile Leu Leu Thr Cys Ile Ser Asp Asp Lys Thr Ile Ser Phe Pro Gly
                      100                      105                      110
Cys Leu Ala Gln Phe Phe Ser Ala Val Leu Ala Xaa Asn Glu Cys Tyr
                      115                      120                      125
Met Met Ala Ser Met Ala Tyr Asp Arg Tyr Met Ala Ile Ser Lys Pro
130                      135                      140
Leu Leu Tyr Ser Arg Ala Thr Phe Pro Glu Leu Cys Ala Ser Leu Val
145                      150                      155                      160
Glu Ala Ser His Leu Gly Gly Phe Val Asn Ser Thr Ile Ile Thr Ser
                      165                      170                      175
Glu Thr Pro Thr Leu Ser Phe Cys Gly Ser Asn Ile Ile Asp Asp Phe
                      180                      185                      190
Phe Cys Asp Leu Pro Pro Leu Val Lys Leu Val Cys Asp Val Lys Glu
195                      200                      205
Arg Tyr Gln Ala Val Leu His Phe Met Leu Ala Ser Asn Ile Thr Pro
210                      215                      220
Thr Ala Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Ala Ala Ile Ser

```

225                      230                      235                      240  
 Lys Ile Arg Ser Ile Lys Gly Arg Leu Gln Val Phe Ser Thr Cys Gly  
                                  245                      250                      255  
 Ser Pro Leu Thr Ala Leu Thr Leu Tyr Tyr Gly Ala Ile Phe Phe Ile  
                                  260                      265                      270  
 Tyr Ser Gln Pro Arg Thr Ser Tyr Ala Leu Lys Met Asp Lys Leu Gly  
                                  275                      280                      285  
 Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr  
                                  290                      295                      300  
 Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Lys Lys Met Leu Asp  
 305                      310                      315                      320  
 Arg Leu Gln Phe Leu Lys Glu Lys Tyr  
                                  325

<210> 1545  
 <211> 349  
 <212> PRT  
 <213> Unknown (H38g462 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(349)  
 <223> Xaa = Any Amino Acid

<400> 1545  
 Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly  
 1                      5                      10                      15  
 Leu Phe Ser Lys Pro Val Ser Pro Gly Phe Phe Ala Leu Ile Leu Leu  
                                  20                      25                      30  
 Val Phe Val Thr Ser Ile Ala Ser Asn Val Val Lys Ile Ile Leu Ile  
                                  35                      40                      45  
 His Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln  
 50                      55                      60  
 Leu Ser Leu Arg Asp Ile Leu Tyr Ile Ser Thr Ile Val Pro Lys Met  
 65                      70                      75                      80  
 Leu Val Asp Gln Val Met Ser Gln Arg Ala Ile Ser Phe Ala Gly Cys  
                                  85                      90                      95  
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Ala Gly Ala Glu Phe Phe  
                                  100                      105                      110  
 Leu Leu Gly Leu Met Ser Cys Asp Arg Tyr Val Ala Ile Cys Asn Pro  
                                  115                      120                      125  
 Leu His Tyr Pro Asp Leu Met Ser Arg Lys Ile Cys Trp Leu Ile Val  
 130                      135                      140  
 Ala Ala Ala Trp Leu Gly Gly Ser Ile Asn Gly Phe Leu Leu Thr Pro  
 145                      150                      155                      160  
 Val Thr Thr Gln Phe Pro Phe Cys Ala Ser Arg Glu Ile Asn His Phe  
                                  165                      170                      175  
 Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser  
                                  180                      185                      190  
 Ala Tyr Glu Thr Ala Met Tyr Val Cys Cys Ile Met Met Leu Leu Ile  
                                  195                      200                      205  
 Pro Phe Ser Val Ile Ser Gly Ser Tyr Thr Arg Ile Leu Ile Thr Val  
                                  210                      215                      220  
 Tyr Arg Met Ser Glu Ala Glu Gly Arg Arg Lys Ala Val Ala Thr Cys  
 225                      230                      235                      240  
 Ser Ser His Met Val Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr  
                                  245                      250                      255  
 Thr Tyr Val Leu Pro His Ser Tyr His Thr Pro Glu Gln Asp Lys Ala  
                                  260                      265                      270

Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Gln Lys Val Val  
 290 295 300  
 Gly Arg Cys Val Ser Ser Gly Lys Val Thr Thr Phe Lys Gln Ile Ala  
 305 310 315 320  
 Tyr Ala Ala Arg Asp Leu Lys Xaa Arg Ile Gln Asp Phe Ile Ile Ala  
 325 330 335  
 Leu Glu Phe Lys Tyr Ser Leu Pro Gly Asn Lys Xaa Pro  
 340 345

&lt;210&gt; 1546

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g463 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1546

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly  
 1 5 10 15  
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala  
 20 25 30  
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala  
 35 40 45  
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala  
 50 55 60  
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg  
 85 90 95  
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys  
 100 105 110  
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser  
 115 120 125  
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val  
 130 135 140  
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu Leu His Val  
 145 150 155 160  
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln  
 165 170 175  
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met  
 180 185 190  
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile  
 195 200 205  
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr  
 245 250 255  
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala  
 260 265 270  
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val  
 275 280 285  
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu

290 295 300  
 Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr  
 305 310 315

<210> 1547  
 <211> 280  
 <212> PRT  
 <213> Unknown (H38g464 protein)

<220>  
 <223> Synthetic construct

<400> 1547  
 Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu Ile  
 1 5 10 15  
 Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser His  
 20 25 30  
 Leu Ala Leu Thr Tyr Phe Ser Phe Ser Ser Val Thr Val Pro Lys Met  
 35 40 45  
 Leu Met Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys  
 50 55 60  
 Ile Ser Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe  
 65 70 75 80  
 Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro  
 85 90 95  
 Leu His Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val  
 100 105 110  
 Ala Val Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu  
 115 120 125  
 Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val  
 130 135 140  
 Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe  
 145 150 155 160  
 Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu  
 165 170 175  
 Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile  
 180 185 190  
 Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys  
 195 200 205  
 Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly  
 210 215 220  
 Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile  
 225 230 235 240  
 Val Ala Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile  
 245 250 255  
 Tyr Ser Ile Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe  
 260 265 270  
 Ser Arg Ala Thr Phe Phe Ser Trp  
 275 280

<210> 1548  
 <211> 303  
 <212> PRT  
 <213> Unknown (H38g465 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(303)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1548

```

Met Asn Ser Ser Ser Asp Xaa Arg Gln Pro Val Met Asp Gly Val Asn
 1          5          10          15
Asp Ser Ser Leu Gln Gly Phe Val Leu Met Gly Ile Ser Asp His Pro
 20          25          30
Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu Phe Ser Tyr Leu Leu
 35          40          45
Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu Ser Arg Leu Glu Ala
 50          55          60
Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Ser Leu
 65          70          75          80
Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln Met Leu Ile Asn Leu
 85          90          95
Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly Cys Ile Thr Gln Leu
100          105          110
Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys Ile Leu Leu Val Val
115          120          125
Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg Pro Leu Arg Tyr Thr
130          135          140
Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu Ala Val Ile Ala Cys
145          150          155          160
Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser Thr Phe Thr Leu Gln
165          170          175
Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly Phe Leu Cys Glu Val
180          185          190
Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr Ser Leu Asn Gln Ala
195          200          205
Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala Val Pro Leu Ser Ile
210          215          220
Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala Val Leu Lys Ile Arg
225          230          235          240
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Leu Ser His Leu
245          250          255
Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser Tyr Gly Tyr Leu Leu
260          265          270
Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys Phe Ile Ser Leu Phe
275          280          285
Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu Ile Tyr Thr Leu
290          295          300

```

&lt;210&gt; 1549

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g466 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(309)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1549

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1          5          10          15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20          25          30
Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35          40          45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn

```

```

      50              55              60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65              70              75              80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85              90              95
Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
      100              105              110
Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
      115              120              125
Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
      130              135              140
Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
145              150              155              160
Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
      165              170              175
Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Arg Glu Ser Tyr
      180              185              190
Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro Thr
      195              200              205
Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu Arg
      210              215              220
Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser Ser
225              230              235              240
His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn Tyr
      245              250              255
Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val Ser
      260              265              270
Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys Ser
      290              295              300
Ala Xaa Ser Lys Val
305

```

&lt;210&gt; 1550

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g467 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1550

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
      20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
      35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
      85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100      105      110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115      120      125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
      130      135      140

```



Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser  
 145 150 155 160  
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly  
 165 170 175  
 Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala  
 195 200 205  
 Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala  
 210 215 220  
 Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr  
 225 230 235 240  
 Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser  
 245 250 255  
 Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys  
 260 265 270  
 Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu  
 290 295 300  
 Leu Gly Lys Gly Arg Glu Val Gly  
 305 310

&lt;210&gt; 1551

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g468 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(82)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1551

Gly Glu Arg Leu Lys Thr Leu Asn Thr Cys Val Ser His Ile Tyr Ala  
 1 5 10 15  
 Val Leu Ile Phe Tyr Val Pro Met Val Ser Val Ser Met Val His Arg  
 20 25 30  
 Phe Gly Arg His Ala Pro Glu Tyr Val His Lys Phe Met Ser Phe Val  
 35 40 45  
 Pro Pro Met Leu Tyr Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile  
 50 55 60  
 Arg Arg Arg Leu His Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Arg  
 65 70 75 80  
 Lys Thr

&lt;210&gt; 1552

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g469 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1552

Met Glu Val Gly Asn Cys Thr Ile Leu Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Ala Asp Ser Gln Trp Gln Pro Ile Leu Phe Gly Val Phe Leu

```

      20      25      30
Met Leu Tyr Leu Ile Thr Leu Ser Gly Asn Met Thr Leu Val Ile Leu
  35      40      45
Ile Arg Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Ile Gly
  50      55      60
Asn Leu Ser Phe Leu Asp Phe Trp Tyr Thr Ser Val Tyr Thr Pro Lys
  65      70      75      80
Ile Leu Ala Ser Cys Val Ser Glu Asp Lys Arg Ile Ser Leu Ala Gly
      85      90      95
Cys Gly Ala Gln Leu Phe Phe Ser Cys Val Val Ala Tyr Thr Glu Cys
  100      105      110
Tyr Leu Leu Ala Ala Met Ala Tyr Asp Arg His Ala Ala Ile Cys Asn
  115      120      125
Pro Leu Leu Tyr Ser Gly Thr Met Ser Thr Ala Leu Cys Thr Gly Leu
  130      135      140
Val Ala Gly Ser Tyr Ile Gly Gly Phe Leu Asn Ala Ile Ala His Thr
  145      150      155      160
Ala Asn Thr Phe Arg Leu His Phe Cys Gly Lys Asn Ile Ile Asp His
      165      170      175
Phe Phe Cys Asp Ala Pro Pro Leu Val Lys Met Ser Cys Thr Asn Thr
      180      185      190
Arg Val Tyr Glu Lys Val Leu Leu Gly Val Val Gly Phe Thr Val Leu
  195      200      205
Ser Ser Ile Leu Ala Ile Leu Ile Ser Tyr Val Asn Ile Leu Leu Ala
  210      215      220
Ile Leu Arg Ile His Ser Ala Ser Gly Arg His Lys Ala Phe Ser Thr
  225      230      235      240
Cys Ala Ser His Leu Ile Ser Val Met Leu Phe Tyr Gly Ser Leu Leu
      245      250      255
Phe Met Tyr Ser Arg Pro Ser Ser Thr Tyr Ser Leu Glu Arg Asp Lys
      260      265      270
Val Ala Ala Leu Phe Tyr Thr Val Ile Asn Pro Leu Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Glu Ala Phe Arg Lys Ala
  290      295      300
Thr Gln Thr Ile Gln Pro Gln Thr
  305      310

```

&lt;210&gt; 1553

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g470 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1553

```

Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
  1      5      10      15
Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
      20      25      30
Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
      35      40      45
Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
      50      55      60
Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
  65      70      75      80
Pro Gln Ala Leu Ala Ile Phe Trp Phe Arg Ala Gly Asp Ile Ser Leu
      85      90      95
Asp Arg Cys Ile Thr Gln Leu Phe Phe Ile His Ser Thr Phe Ile Ser
      100      105      110

```

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys  
 130 135 140  
 Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro  
 145 150 155 160  
 Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile  
 165 170 175  
 Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn  
 180 185 190  
 Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr  
 195 200 205  
 Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu  
 210 215 220  
 His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu  
 225 230 235 240  
 Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser  
 245 250 255  
 Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro  
 260 265 270  
 Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met  
 275 280 285  
 Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln  
 290 295 300  
 Val Val Gln Phe Leu Phe Ile Lys Gln Lys Ile Thr Leu Val  
 305 310 315

&lt;210&gt; 1554

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g471 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1554

Met Glu Ala Ala Asn Glu Ser Ser Glu Gly Ile Ser Phe Val Leu Leu  
 1 5 10 15  
 Gly Leu Thr Thr Ser Pro Gly Gln Gln Arg Pro Leu Phe Val Leu Phe  
 20 25 30  
 Leu Leu Leu Tyr Val Ala Ser Leu Leu Gly Asn Gly Leu Ile Val Ala  
 35 40 45  
 Ala Ile Gln Ala Ser Pro Ala Leu His Ala Pro Met Tyr Phe Leu Leu  
 50 55 60  
 Ala His Leu Ser Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro  
 65 70 75 80  
 Lys Met Leu Ala Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp  
 100 105 110  
 Ser Cys Leu Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Arg  
 115 120 125  
 His Pro Leu Pro Tyr Ala Thr Arg Met Ser Arg Ala Met Cys Ala Ala  
 130 135 140  
 Leu Val Gly Met Ala Trp Leu Val Ser His Val His Ser Leu Leu Tyr  
 145 150 155 160  
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro  
 165 170 175  
 His Phe Phe Cys Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp  
 180 185 190  
 Thr His His Ile Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val

```

      195      200      205
Val Thr Pro Phe Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala
  210      215      220
Ala Val L u Gln Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser
  225      230      235      240
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val
      245      250      255
Ile Ala Val Tyr Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Ile Ile Tyr Ser Leu Trp Asn Arg Asp Val Gln Gly Ala Leu Arg Ala
      290      295      300
Leu Leu Ile Gly Arg Arg Ile Ser Ala Ser
  305      310

```

&lt;210&gt; 1555

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g472 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1555

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
  1      5      10      15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
      20      25      30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
      35      40      45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
      50      55      60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
  65      70      75      80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
      85      90      95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
      100      105      110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
      115      120      125
Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val
      130      135      140
Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn
  145      150      155      160
Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser
      165      170      175
Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala
      180      185      190
Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu
      195      200      205
Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu
      210      215      220
Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys
  225      230      235      240
Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr
      245      250      255

```

Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp  
                   260                  265                  270  
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro  
                   275                  280                  285  
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg  
                   290                  295                  300  
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile  
 305                  310                  315

&lt;210&gt; 1556

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g473 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1556

His Thr Glu Pro Trp Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
 1                  5                  10                  15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser  
                   20                  25                  30  
 Arg Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ile Ile Leu  
                   35                  40                  45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro  
 65                  70                  75                  80  
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
                   85                  90                  95  
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu  
                   100                  105                  110  
 Asp Met Leu Leu Thr Ala Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
                   115                  120                  125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Ser Val Phe  
                   130                  135                  140  
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
 145                  150                  155                  160  
 Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser  
                   165                  170                  175  
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
                   180                  185                  190  
 Ser Val Ile Asn Ser Ile Phe Leu Tyr Phe Asp Ser Thr Met Phe Gly  
                   195                  200                  205  
 Phe Leu Pro Ile Ser Arg Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro  
 210                  215                  220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser  
 225                  230                  235                  240  
 Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly  
                   245                  250                  255  
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Ser Gly  
                   260                  265                  270  
 Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro  
                   275                  280                  285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg  
                   290                  295                  300  
 Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser

```
<210> 1558
<211> 330
<212> PRT
```

<213> Unknown (H38g475 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1558

His	Thr	Glu	Pro	Arg	His	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Val
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Gly	Gly	Val	Ser
		20					25					30			
Leu	Ser	Met	Tyr	Gly	Val	Thr	Val	Ile	Arg	Asn	Val	Leu	Ile	Ile	Leu
	35					40					45				
Gly	Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55				60					
Ser	Asn	Val	Trp	Trp	Ala	Asp	Ile	Ser	Phe	Thr	Ser	Ala	Gly	Val	Pro
65					70				75					80	
Lys	Met	Thr	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Tyr	Tyr	Ala
		85						90					95		
Gly	Cys	Met	Thr	Arg	Met	Ser	Phe	Phe	Val	Leu	Leu	Ala	Cys	Ile	Glu
		100					105						110		
Asp	Met	Leu	Val	Cys	Val	Met	Ala	Xaa	Glu	Cys	Phe	Val	Ala	Met	Cys
	115					120						125			
Arg	Pro	Val	Gln	Tyr	Thr	Val	Ile	Val	Asn	Pro	His	Leu	Cys	Val	Phe
	130					135					140				
Arg	Val	Gly	Val	Ser	Phe	Leu	Gln	Ser	Val	Leu	Tyr	Ser	Gln	Val	His
145					150				155					160	
Arg	Xaa	Ser	Val	Ser	Gln	Phe	Thr	Phe	Phe	Lys	Asn	Val	Glu	Ile	Ser
		165						170					175		
His	Phe	Val	Cys	Glu	Pro	Ser	Gln	Phe	Leu	His	Phe	Ala	Cys	Cys	Asp
		180						185					190		
Ser	Phe	Ile	Lys	Ser	Ile	Phe	Met	Tyr	Phe	Asp	Ser	Asn	Met	Phe	Gly
	195					200						205			
Phe	Leu	Pro	Ile	Thr	Gly	Ile	Phe	Leu	Ser	Xaa	Tyr	Lys	Ser	Val	Pro
	210					215					220				
Ser	Ile	Ile	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
225					230				235					240	
Thr	Cys	Gly	Ser	His	Val	Ala	Val	Val	Cys	Leu	Leu	Tyr	Gly	Thr	Gly
			245					250					255		
Ile	Gly	Val	Tyr	Met	Thr	Ser	Gly	Val	Ala	Pro	Pro	Pro	Ser	Asn	Gly
		260					265						270		
Val	Val	Ala	Ser	Val	Lys	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Thr	Pro
		275					280					285			
Phe	Ile	Tyr	Ser	Val	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Pro	Leu	Trp	Ser
	290					295					300				
Val	Cys	Ser	Ser	Thr	Val	Lys	Ser	Phe	Asp	Val	Ser	His	Leu	Phe	Cys
305					310				315					320	
Val	Trp	Val	Arg	Lys	Gly	Thr	His	Ile	Lys						
			325					330							

<210> 1559

<211> 170

<212> PRT

<213> Unknown (H38g476 protein)

<220>

<223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(170)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1559

```

His Thr Gln Pro Arg Gly Leu Thr Arg Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Gln Asp Pro Gln Leu Gln Pro Val Leu Ser Gly Leu Ser
          20           25           30
Leu Cys Met Cys Leu Gly Thr Gln Leu Gly Asn Leu Leu Ile Ile Leu
          35           40           45
Gly Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Ser Phe Leu
          50           55           60
Ser Asn Leu Ser Gly Ala Asp Ile Ser Phe Thr Ser Thr Thr Gly Pro
65          70          75          80
Lys Leu Ile Val Asp Ile His Ser Tyr Thr Arg Asp Ile Ser Tyr Ala
          85          90          95
Arg Cys Leu Thr His Thr Pro Leu Phe Ala Ile Phe Gly Gly Val Glu
          100          105          110
Arg Asp Met Leu Leu Arg Val Met Gly Tyr Asp Arg Val Val Asp Ile
          115          120          125
Cys Asp Pro Leu Tyr His Ser His Ala Met Asn Pro Cys Val Cys Gly
          130          135          140
Ser Leu Asp Leu Trp Ser Leu Phe Phe Leu Thr Leu Leu Tyr Thr His
145          150          155          160
Leu His Asn Ser Ile Ala Leu His Met Thr
          165          170

```

&lt;210&gt; 1560

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g477 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1560

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
          20           25           30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
          35           40           45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
          85          90          95
Arg Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
          100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
          130          135          140
Phe Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys Ile Asp Thr
          180          185          190

```



Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu  
 195 200 205  
 Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile L u Val Thr  
 210 215 220  
 Val Arg Asn Ser Ser Ser Val Ser Met Val Lys Ala Cys Ser Thr Leu  
 225 230 235 240  
 Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala  
 260 265 270  
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met  
 275 280 285  
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg  
 290 295 300  
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe  
 305 310 315 320  
 Leu Glu

&lt;210&gt; 1561

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g478 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1561

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Phe Val Val Phe Ser  
 20 25 30  
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
 35 40 45  
 Val Leu Ser Thr Ser His Leu His Ser Arg Thr Tyr Phe Leu Leu Ser  
 50 55 60  
 Asn Leu Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met  
 65 70 75 80  
 Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys  
 85 90 95  
 Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val  
 100 105 110  
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro  
 115 120 125  
 Leu Arg Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val  
 130 135 140  
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu  
 145 150 155 160  
 Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile  
 180 185 190  
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Thr Ala Leu  
 195 200 205  
 Thr Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Thr  
 210 215 220  
 Ile Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser

```

                260                265                270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
      275                280                285
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
      290                295                300
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305                310

```

<210> 1562  
 <211> 198  
 <212> PRT  
 <213> Unknown (H38g479 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(198)  
 <223> Xaa = Any Amino Acid

```

<400> 1562
Met Asn Pro Cys Leu Cys Gly Phe Arg Val Val Val Ser Phe Phe Phe
 1                5                10                15
His Ser Leu Leu Gly Ala Gln Val His Asn Leu Ser Ala Ser Gln Met
      20                25                30
Thr Cys Phe Glu Tyr Val Glu Ile His Asn Phe Leu Trp Ala Leu Ser
      35                40                45
Gln Leu Pro His Arg Ala Trp Cys Asp Thr Phe Pro Asn Asn Ile Ile
      50                55                60
Val Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ala Gly Thr
      65                70                75                80
Leu Phe Ser Xaa Tyr Glu Ser Val Ser Ser Ile Glu Arg Val Ser Ser
      85                90                95
Xaa Gly Gly Glu Tyr Lys Ala Phe Pro Thr Cys Gly Ser His Leu Ser
      100                105                110
Val Val Cys Xaa Leu Tyr Gly Thr Gly Val Gly Gly His Leu Ser Ser
      115                120                125
Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
      130                135                140
Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Met Arg Asn
      145                150                155                160
Arg Asp Thr Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
      165                170                175
Phe Xaa Tyr Leu Leu Ile Cys Pro Ile Pro Phe Val Val Trp Val Lys
      180                185                190
Lys Gly Arg Lys Val Lys
      195

```

<210> 1563  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g480 protein)

<220>  
 <223> Synthetic construct

```

<400> 1563
Met Leu Gly Leu Asn Gly Thr Pro Phe Gln Pro Ala Thr Leu Gln Leu
 1                5                10                15
Thr Gly Ile Pro Gly Ile Gln Thr Gly Leu Thr Trp Val Ala Leu Ile
      20                25                30

```

Phe Cys Ile Leu Tyr Met Ile Ser Ile Val Gly Asn Leu Ser Ile Leu  
 35 40 45  
 Thr Leu Val Phe Trp Glu Pro Ala Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Met Leu Ala Leu Asn Asp Leu Gly Val Ser Phe Ser Thr Leu  
 65 70 75 80  
 Pro Thr Val Ile Ser Thr Phe Cys Phe Asn Tyr Asn His Val Ala Phe  
 85 90 95  
 Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Ser Phe Met  
 100 105 110  
 Glu Ser Gly Ile Leu Leu Ala Met Ser Leu Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg Tyr Val Thr Val Leu Thr His Asn Arg Ile Leu  
 130 135 140  
 Ala Met Gly Leu Gly Ile Leu Thr Lys Ser Phe Thr Thr Leu Phe Pro  
 145 150 155 160  
 Phe Pro Phe Val Val Lys Arg Leu Pro Phe Cys Lys Gly Asn Val Leu  
 165 170 175  
 His His Ser Tyr Cys Leu His Pro Asp Leu Met Lys Val Ala Cys Gly  
 180 185 190  
 Asp Ile His Val Asn Asn Ile Tyr Gly Leu Leu Val Ile Ile Phe Thr  
 195 200 205  
 Tyr Gly Met Asp Ser Thr Phe Ile Leu Leu Ser Tyr Ala Leu Ile Leu  
 210 215 220  
 Arg Ala Met Leu Val Ile Ile Ser Gln Glu Gln Arg Leu Lys Ala Leu  
 225 230 235 240  
 Asn Thr Cys Met Ser His Ile Cys Ala Val Leu Ala Phe Tyr Val Pro  
 245 250 255  
 Ile Ile Ala Val Ser Met Ile His Arg Phe Trp Lys Ser Ala Pro Pro  
 260 265 270  
 Val Val His Val Met Met Ser Asn Val Tyr Leu Phe Val Pro Pro Met  
 275 280 285  
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Glu Ile Arg Lys Gly  
 290 295 300  
 Ile Leu Lys Phe Phe His Lys Ser Gln Ala  
 305 310

&lt;210&gt; 1564

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g481 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1564

Met Gly Leu Phe Asn Val Thr His Pro Ala Phe Phe Leu Leu Thr Gly  
 1 5 10 15  
 Ile Pro Gly Leu Glu Ser Ser His Ser Trp Leu Ser Gly Pro Leu Cys  
 20 25 30  
 Val Met Tyr Ala Val Ala Leu Gly Gly Asn Thr Val Ile Leu Gln Ala  
 35 40 45  
 Val Arg Val Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 Met Leu Ser Phe Ser Asp Val Ala Ile Ser Met Ala Thr Leu Pro Thr  
 65 70 75 80  
 Val Leu Arg Thr Phe Cys Leu Asn Ala Arg Asn Ile Thr Phe Asp Ala  
 85 90 95  
 Cys Leu Ile Gln Met Phe Leu Ile His Phe Phe Ser Met Met Glu Ser  
 100 105 110  
 Gly Ile Leu Leu Ala Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Asp

```

      115      120      125
Pro Leu Arg Tyr Ala Thr Val Leu Thr Thr Glu Val Ile Ala Ala Met
  130      135      140
Gly Leu Gly Ala Ala Ala Arg Ser Phe Ile Thr Leu Phe Pro Leu Pro
145      150      155      160
Phe Leu Ile Lys Arg Leu Pro Ile Cys Arg Ser Asn Val Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Pro Asp Met Met Arg Leu Ala Cys Ala Asp Ile
      180      185      190
Ser Ile Asn Ser Ile Tyr Gly Leu Phe Val Leu Val Ser Thr Phe Gly
      195      200      205
Met Asp Leu Phe Phe Ile Phe Leu Ser Tyr Val Leu Ile Leu Arg Ser
210      215      220
Val Met Ala Thr Ala Ser Arg Glu Glu Arg Leu Lys Ala Leu Asn Thr
225      230      235      240
Cys Val Ser His Ile Leu Ala Val Leu Ala Phe Tyr Val Pro Met Ile
      245      250      255
Gly Val Ser Thr Val His Arg Phe Gly Lys His Val Pro Cys Tyr Ile
      260      265      270
His Val Leu Met Ser Asn Val Tyr Leu Phe Val Pro Pro Val Leu Asn
275      280      285
Pro Leu Ile Tyr Ser Ala Lys Thr Lys Glu Ile Arg Arg Ala Ile Phe
290      295      300
Arg Met Phe His His Ile Lys Ile
305      310

```

&lt;210&gt; 1565

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g482 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1565

```

Met Glu Ser Asn Gln Thr Trp Ile Thr Glu Val Ile Leu Leu Gly Phe
  1      5      10      15
Gln Val Asp Pro Ala Leu Glu Leu Phe Leu Phe Gly Phe Phe Leu Leu
      20      25      30
Phe Tyr Ser Leu Thr Leu Met Gly Asn Gly Ile Ile Leu Gly Leu Ile
      35      40      45
Tyr Leu Asp Ser Arg Leu His Thr Pro Met Tyr Val Phe Leu Ser His
      50      55      60
Leu Ala Ile Val Asp Met Ser Tyr Ala Ser Ser Thr Val Pro Lys Met
65      70      75      80
Leu Ala Asn Leu Val Met His Lys Lys Val Ile Ser Phe Ala Pro Cys
      85      90      95
Ile Leu Gln Thr Phe Leu Tyr Leu Ala Phe Ala Ile Thr Glu Cys Leu
      100      105      110
Ile Leu Val Met Met Cys Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115      120      125
Leu Ala Tyr Thr Pro Ile Ile Met Asn Trp Arg Val Cys Thr Val Leu
      130      135      140
Ala Ser Thr Cys Trp Ile Phe Ser Phe Leu Leu Ala
145      150      155

```

&lt;210&gt; 1566

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g483 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1566

```

Met Glu Cys Asn Gln Thr Trp Ile Thr Asp Ile Thr Leu Leu Gly Phe
 1           5           10           15
Gln Val Gly Pro Ala Leu Ala Ile Leu Ile Tyr Glu Leu Phe Ser Val
      20           25           30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
      35           40           45
Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
      50           55           60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
      65           70           75           80
Leu Ala Asn Leu Met Asn Gln Lys Arg Thr Ile Ser Phe Val Pro Cys
      85           90           95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu
      100          105          110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115          120          125
Phe Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Val
      130          135          140
Leu Thr Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Glu Ile
      145          150          155          160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu
      165          170          175
Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
      180          185          190
Val Asn Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly
      195          200          205
Pro Leu Ser Leu Ile Leu Val Ser Tyr Met His Ile Leu Gly Ala Ile
      210          215          220
Leu Lys Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys
      225          230          235          240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val
      245          250          255
Val Tyr Met Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met
      260          265          270
Leu Ser Leu Phe His Ser Val Leu Asn Pro Met Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Ala Gln Leu Lys Gly Ala Leu His Arg Ala Leu
      290          295          300
Gln Arg Lys Arg Ser Met Arg Thr Val Tyr Gly Leu Cys Leu Xaa Asn
      305          310          315          320
Met Trp Phe Ala Glu Ala Arg Ile Leu
      325

```

&lt;210&gt; 1567

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g484 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1567

```

Met Gly Val Asn Gln Ser Trp Ser Pro Glu Phe Ile Leu Val Glu Ser
 1          5          10          15
Gln Leu Ser Ala Glu Met Glu Val Leu Leu Phe Xaa Ile Phe Ser Leu
 20          25          30
Leu Tyr Ile Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
 35          40          45
Cys Leu Asp His Ile Leu Pro Thr Pro Met Tyr Phe Phe Leu Ser His
 50          55          60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65          70          75          80
Leu Ala Asn Leu Met Asn Lys Lys Arg Thr Ile Ser Phe Leu Pro Cys
 85          90          95
Ile Met Gln Thr Tyr Leu Tyr Phe Ser Phe Ala Ala Thr Glu Cys Leu
 100         105         110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
 115         120         125
Leu Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Ala
 130         135         140
Leu Thr Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Ala Ile
 145         150         155         160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu
 165         170         175
Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ser Asp Thr Trp
 180         185         190
Val Asn Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly
 195         200         205
Pro Leu Cys Leu Met Leu Val Ser Tyr Met His Ile Leu Leu Ala Ile
 210         215         220
Leu Lys Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys
 225         230         235         240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val
 245         250         255
Val Tyr Ile Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met
 260         265         270
Leu Ser Leu Phe His Ser Val Leu Asn Pro Ile Leu Asn Pro Leu Ile
 275         280         285
Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu His Arg Ala Leu
 290         295         300
Gln Arg Thr Leu Ser Met Xaa Gly Val
 305         310

```

&lt;210&gt; 1568

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g485 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1568

```

Met Cys Tyr Leu Ser Gln Leu Cys Leu Ser Leu Gly Glu His Thr Leu
 1          5          10          15
His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe
 20          25          30
Ile Leu Leu Gly Phe Ser Asp Tyr Pro Gln Leu Gln Lys Val Leu Phe
 35          40          45
Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr
 50          55          60

```

```

Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr
65          70          75          80
Phe Phe Leu Ser His Leu Ser Phe Leu Tyr Arg Cys Phe Thr Ser Ser
          85          90          95
Val Ile Pro Gln Leu Leu Val Asn Leu Trp Glu Pro Met Lys Thr Ile
          100         105         110
Ala Tyr Gly Gly Cys Leu Val His Leu Tyr Asn Ser His Ala Leu Gly
          115         120         125
Ser Thr Glu Cys Val Leu Pro Ala Val Met Ser Cys Asp Arg Tyr Val
          130         135         140
Ala Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ile His Leu
145          150         155         160
Cys Met Ala Leu Ala Ser Met Ala Trp Leu Ser Gly Ile Ala Thr Thr
          165         170         175
Leu Val Gln Ser Thr Leu Thr Leu Gln Leu Pro Phe Cys Gly His Arg
          180         185         190
Gln Val Asp His Phe Ile Cys Glu Val Pro Val Leu Ile Lys Leu Ala
          195         200         205
Cys Val Gly Thr Thr Phe Asn Glu Ala Glu Leu Phe Val Ala Ser Ile
          210         215         220
Leu Phe Leu Ile Val Pro Val Ser Phe Ile Leu Val Ser Ser Gly Tyr
225          230         235         240
Ile Ala His Ala Val Leu Arg Ile Lys Ser Ala Thr Arg Arg Gln Lys
          245         250         255
Ala Phe Gly Thr Cys Phe Ser His Leu Thr Val Val Thr Ile Phe Tyr
          260         265         270
Gly Thr Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Arg Ser Arg
          275         280         285
Asp Gln Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val Thr Arg Met
          290         295         300
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Ile Lys Glu Val Lys Gly Ala
305          310         315         320
Leu Lys Lys Val Leu Ala Lys Ala Leu Gly Val Asn Ile Leu
          325         330

```

&lt;210&gt; 1569

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g486 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1569

```

Met Glu Gly Asn Lys Thr Trp Ile Thr Asp Ile Thr Leu Pro Arg Phe
1          5          10         15
Gln Val Gly Pro Ala Leu Glu Ile Leu Leu Cys Gly Leu Phe Ser Ala
          20         25         30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
          35         40         45
Cys Leu Asp Cys Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
          50         55         60
Leu Ala Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met
65          70         75         80
Leu Thr Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys
          85         90         95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu
          100        105        110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro
          115        120        125
Leu Arg Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala

```

130	135	140
Val Ala Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Phe Ser		
145	150	155
Ser Gln Ser Leu Arg Cys Met Asn Val Leu		160
165	170	

<210> 1570  
 <211> 308  
 <212> PRT  
 <213> Unknown (H38g487 protein)

<220>  
 <223> Synthetic construct

<400> 1570

Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly														
1	5					10					15			
Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu														
20						25					30			
Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu														
35						40					45			
Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser														
50					55					60				
Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys														
65				70				75						80
Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser														
85							90							95
Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr														
100						105						110		
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr														
115					120						125			
Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu														
130					135						140			
Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr														
145					150						155			160
Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His														
165							170							175
Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr														
180							185							190
Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Val Ile Leu														
195						200						205		
Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr														
210					215						220			
Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser Lys Ala Phe Ser Thr														
225					230						235			240
Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly Ser Thr Val														
245														255
Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala Leu Asp Leu Ile Lys														
260							265							270
Ala Val His Val Leu Asn Thr Val Val Thr Pro Val Leu Asn Pro Phe														
275							280							285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Glu Thr Leu Leu Lys Lys														
290						295								300
Trp Lys Gly Lys														
305														

<210> 1571  
 <211> 223  
 <212> PRT  
 <213> Unknown (H38g488 protein)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(223)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1571

```

Lys Glu Met Gly Cys His Gln Ser Met Val Thr Glu Phe Ile Leu Val
 1           5           10           15
Gly Phe Gln Leu Ser Ala Glu Met Glu Val Leu Leu Phe Trp Ser Phe
           20           25           30
Ser Leu Gly Ile Ala Leu Glu Leu Ile Cys Leu Asp His Ser Leu His
 35           40           45
Thr Pro Tyr Phe Phe Leu Ser His Leu Ala Val Ile Asp Met Ala Tyr
 50           55           60
Ala Ser Asn Asn Val Pro Lys Met Leu Val Asp Leu Ala Asn Xaa Lys
 65           70           75           80
Ser Thr Met Cys Phe Phe Pro Cys Ile Met Gln Thr Phe Leu Tyr Leu
           85           90           95
Ala Phe Ala His Ile Glu Cys Leu Ile Leu Val Val Leu Ser Tyr Asp
           100          105          110
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Asn Val Leu Met Ser
 115          120          125
Trp Arg Glu Cys Thr Val Leu Ala Val Ala Ser Trp Val Phe Ser Phe
 130          135          140
Leu Leu Ala Leu Val His Leu Val Leu Ile Leu Arg Leu Pro Phe Ser
 145          150          155          160
Gly Pro His Glu Ile Asn His Tyr Cys Glu Ile Leu Ser Val Leu Lys
           165          170          175
Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile Phe Ala Ser
           180          185          190
Cys Met Phe Ile Leu Val Gly Xaa Leu Cys Leu Val Leu Val Ser Tyr
 195          200          205
Leu Gly Ile Trp Arg His Leu Arg Ser Val Ala Lys Pro Lys Arg
 210          215          220

```

&lt;210&gt; 1572

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g489 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1572

```

Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu
           20           25           30
Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile Ile
 35           40           45
Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln
 65           70           75           80
Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly
           85           90           95
Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys
           100          105          110
Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys

```

```

      115      120      125
Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu
  130      135      140
Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala
 145      150      155      160
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His
      165      170      175
Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr
      180      185      190
Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val
      195      200      205
Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala
      210      215      220
Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr
 225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile
      245      250      255
Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys
      260      265      270
Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu
      290      295      300
Leu Ser Gly Lys Leu
305

```

&lt;210&gt; 1573

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g490 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(337)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1573

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Val Phe Leu Leu Leu
 1      5      10      15
Gly Thr Thr Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Ile Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115      120      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130      135      140
Phe Leu Val Leu Leu Ser Phe Phe Ser Val Leu Ser Leu Leu Asp Ser
 145      150      155      160
Gln Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val
      165      170      175

```

Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala  
 180 185 190  
 Cys Cys Asp Thr Phe Thr Asn Lys Ile Ile Met Tyr Phe Pro Ala Ala  
 195 200 205  
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys  
 210 215 220  
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Val Tyr  
 245 250 255  
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Asp Val Ser Ser Ser  
 260 265 270  
 Pro Arg Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro  
 275 280 285  
 Met Pro Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser  
 290 295 300  
 Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu  
 305 310 315 320  
 Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Arg Lys Val  
 325 330 335  
 Lys

<210> 1574

<211> 293

<212> PRT

<213> Unknown (H38g491 protein)

<220>

<223> Synthetic construct

<400> 1574

Met Gly Phe Ser Asn Ser Trp Asp Ile Gln Ile Val His Ala Ala Leu  
 1 5 10 15  
 Phe Phe Leu Val Tyr Leu Ala Ala Val Ile Gly Asn Leu Leu Ile Ile  
 20 25 30  
 Ile Leu Thr Thr Leu Asp Val His Leu Gln Thr Pro Met Tyr Phe Phe  
 35 40 45  
 Leu Arg Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ile Ser Val Thr Ile  
 50 55 60  
 Pro Lys Ser Ile Val Ser Ser Leu Thr His Asp Thr Ser Ile Ser Phe  
 65 70 75 80  
 Phe Gly Cys Ala Leu Gln Ala Phe Phe Phe Met Asp Leu Ala Thr Thr  
 85 90 95  
 Glu Val Ala Ile Leu Thr Val Met Ser Tyr Asp Arg Tyr Met Ala Ile  
 100 105 110  
 Cys Arg Pro Leu His Tyr Glu Val Ile Ile Asn Gln Gly Val Cys Leu  
 115 120 125  
 Arg Met Met Ala Met Ser Trp Leu Ser Gly Val Ile Cys Gly Phe Met  
 130 135 140  
 His Val Ile Ala Thr Phe Ser Leu Pro Phe Cys Gly Arg Asn Arg Ile  
 145 150 155 160  
 Arg Gln Phe Phe Cys Asn Ile Pro Gln Leu Leu Ser Leu Leu Asp Pro  
 165 170 175  
 Lys Val Ile Thr Ile Glu Ile Gly Val Met Val Phe Gly Thr Ser Leu  
 180 185 190  
 Val Ile Ile Ser Phe Val Val Ile Thr Leu Ser Tyr Met Tyr Ile Phe  
 195 200 205  
 Ser Val Ile Met Arg Ile Pro Ser Lys Glu Gly Arg Ser Lys Thr Phe  
 210 215 220  
 Ser Thr Cys Ile Pro His Leu Val Val Val Thr Leu Phe Met Ile Ser



Tyr Ala Gln Lys Xaa Leu Ser Ala Gln Lys Asn Glu Xaa Glu Asn Ser  
 305 310 315 320  
 Xaa Met Cys Val Leu Ser Ile Ser Met Leu Asn Ala Xaa Arg Ile Leu  
 325 330 335  
 Met Arg Trp Phe Pro  
 340

<210> 1576  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g493 protein)

<220>  
 <223> Synthetic construct

<400> 1576  
 Met Lys Trp Ala Asn Gln Thr Ala Val Thr Glu Tyr Val Leu Met Gly  
 1 5 10 15  
 Leu His Glu His Cys Asn Leu Glu Val Val Leu Phe Val Phe Cys Leu  
 20 25 30  
 Gly Ile Tyr Ser Val Asn Val Leu Gly Asn Ala Leu Leu Ile Gly Leu  
 35 40 45  
 Asn Val Leu His Pro Arg Leu His Asn Pro Met Tyr Phe Phe Ser Asn  
 50 55 60  
 Leu Ser Leu Met Asp Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Met  
 65 70 75 80  
 Leu Asp Asn Phe Leu Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys  
 85 90 95  
 Ala Leu Gln Met Tyr Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu  
 100 105 110  
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro  
 115 120 125  
 Leu Arg Tyr Pro Glu Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala  
 130 135 140  
 Ala Leu Ser Trp Gly Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile  
 145 150 155 160  
 Leu Val Trp His Leu Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr  
 165 170 175  
 Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn  
 180 185 190  
 Ala Leu Ala Leu Met Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu  
 195 200 205  
 Leu Leu Ile Cys Leu Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg  
 210 215 220  
 Val Pro Ser Ala Ala Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala  
 225 230 235 240  
 His Arg Thr Val Val Val Phe Tyr Gly Thr Ile Ser Phe Met Tyr  
 245 250 255  
 Phe Lys Pro Lys Ala Lys Asp Pro Asn Val Asp Lys Thr Val Ala Leu  
 260 265 270  
 Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Ile Ile Tyr Ser Leu  
 275 280 285  
 Arg Asn Ala Glu Val Lys Ala Ala Val Leu Thr Leu Leu Arg Gly Gly  
 290 295 300  
 Leu Leu Ser Arg Lys Ala Ser  
 305 310

<210> 1577  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g494 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1577

```

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1           5           10           15
Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
          20           25           30
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
          35           40           45
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
65          70           75           80
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
          85           90           95
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
          100          105          110
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
          115          120          125
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
          130          135          140
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
145          150          155          160
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
          165          170          175
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
          195          200          205
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
          210          215          220
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
225          230          235          240
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
          245          250          255
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
          260          265          270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
          275          280          285
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
          290          295          300
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
305          310          315

```

&lt;210&gt; 1578

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g495 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1578

```

Met Met Val Leu Ser Ile Val Leu Thr Ser Leu Phe Gly Asn Ser Leu
 1           5           10           15
Met Ile L u Leu Ile His Trp Asp His Arg Phe His Thr Pro Met Tyr
          20           25           30
Phe Leu Leu Ser Gln Leu Ser Leu Met Asp Val Met Leu Val Ser Thr
          35           40           45

```

```

Thr Val Pro Lys Met Ala Ala Asp Tyr Leu Thr Gly Ser Lys Ala Ile
 50          55          60
Ser Arg Ala Gly Cys Gly Ala Gln Ile Phe Phe Leu Pro Thr Leu Gly
 65          70          75          80
Gly Gly Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala
          85          90          95
Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu
          100          105          110
Cys Leu Arg Met Asn Leu Ser Cys Trp Leu Leu Gly Ala Ala Asp Gly
          115          120          125
Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His
 130          135          140
Glu Ile Asp His Phe Phe Cys Glu Thr Pro Val Leu Val Arg Leu Ala
 145          150          155          160
Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val
          165          170          175
Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu
          180          185          190
Ile Leu Ala Ala Val Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys
          195          200          205
Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe Tyr
 210          215          220
Gly Ala Ala Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr
 225          230          235          240
Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro Leu
          245          250          255
Leu Asn Pro Leu Ile Tyr Ser Val
          260

```

&lt;210&gt; 1579

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g496 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1579

```

Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
 1          5          10          15
Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
          20          25          30
Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
          35          40          45
Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
 50          55          60
Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
 65          70          75          80
Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
          85          90          95
Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
          100          105          110
Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
          115          120          125
Met Leu Val Glu Ala Ile Thr Phe Ala Leu Gly Val Ala Leu Leu Leu
 130          135          140
Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr Gly Val Ile Ala Ala Ala
 145          150          155          160
Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
          165          170          175
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile

```

```
<210> 1581
<211> 314
<212> PRT
<213> Unknown (H38g498 protein)
```



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1581

```

Met Glu Arg Gly Asn Trp Thr Leu Val Thr Glu Phe Ile Leu Val Gly
 1           5           10           15
Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Val Ile Phe Tyr
           20           25           30
Pro Ala Tyr Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu
           35           40           45
Ile Leu Val Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser
           50           55           60
Asn Leu Ser Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys
           65           70           75           80
Met Leu Glu Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu
           85           90           95
Cys Ser Ala Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe
           100          105          110
Ile Pro Phe Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser
           115          120          125
Pro Leu Gln Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu
           130          135          140
Val Ile Leu Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr
           145          150          155          160
Ile Leu Lys Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His
           165          170          175
Phe Phe Cys Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile
           180          185          190
Arg Ala Ile Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu
           195          200          205
Ser Ser Leu Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr
           210          215          220
Ile Leu Lys Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr
           225          230          235          240
Cys Ala Ser His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile
           245          250          255
Phe Val Tyr Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys
           260          265          270
Ile Leu Phe Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe
           275          280          285
Val Phe Ser Leu Trp Asn Glu Pro Met Lys Asp Ala Leu Lys Asp Ala
           290          295          300
Val Gly Arg Arg Thr Glu Leu Ala Gln Arg
           305          310

```

&lt;210&gt; 1582

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g499 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1582

```

Met Ala Asn Leu Thr Ile Val Thr Glu Phe Ile Leu Met Gly Phe Ser
 1           5           10           15
Thr Asn Lys Asn Met Cys Ile Leu His Ser Ile Leu Phe Leu Leu Ile
           20           25           30
Tyr Leu Cys Ala Leu Met Gly Asn Val Leu Ile Ile Met Ile Thr Thr
           35           40           45
Leu Asp His His Leu His Thr Pro Val Tyr Phe Phe Leu Lys Asn Leu

```

50 55 60  
 Ser Phe Leu Asp Leu Cys Leu Ile Ser Val Thr Ala Pro Lys Ser Ile  
 65 70 75 80  
 Ala Asn Ser Leu Ile His Asn Asn Ser Ile Ser Phe Leu Gly Cys Val  
 85 90 95  
 Ser Gln Val Phe Leu Leu Leu Ser Ser Ala Ser Ala Glu Leu Leu Leu  
 100 105 110  
 Leu Thr Val Met Ser Phe Asp Arg Tyr Thr Ala Ile Cys His Pro Leu  
 115 120 125  
 His Tyr Asp Val Ile Met Asp Arg Ser Thr Cys Val Gln Arg Ala Thr  
 130 135 140  
 Val Ser Trp Leu Tyr Gly Gly Leu Ile Ala Val Met His Thr Ala Gly  
 145 150 155 160  
 Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Met Val His Gln Phe Phe  
 165 170 175  
 Cys Asp Ile Pro Gln Leu Leu Ala Ile Ser Cys Ser Glu Asn Leu Ile  
 180 185 190  
 Arg Glu Ile Ala Leu Ile Leu Ile Asn Val Val Leu Asp Phe Cys Cys  
 195 200 205  
 Phe Ile Val Ile Ile Ile Thr Tyr Val His Val Phe Ser Thr Val Lys  
 210 215 220  
 Lys Ile Pro Ser Thr Glu Gly Gln Ser Lys Ala Tyr Ser Ile Cys Leu  
 225 230 235 240  
 Pro His Leu Leu Val Val Leu Phe Leu Ser Thr Gly Phe Ile Ala Tyr  
 245 250 255  
 Leu Lys Pro Ala Ser Glu Ser Pro Ser Ile Leu Asp Ala Val Ile Ser  
 260 265 270  
 Val Phe Tyr Thr Met Leu Pro Pro Thr Phe Asn Pro Ile Ile Tyr Ser  
 275 280 285  
 Leu Arg Asn Lys Ala Ile Lys Val Ala Leu Gly Met Leu Ile Lys Gly  
 290 295 300  
 Lys Leu Thr Lys Lys  
 305

&lt;210&gt; 1583

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g500 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1583

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly  
 1 5 10 15  
 Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala  
 20 25 30  
 Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu  
 35 40 45  
 Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys  
 65 70 75 80  
 Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly  
 85 90 95  
 Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly  
 100 105 110  
 Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln  
 115 120 125  
 Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met  
 130 135 140

Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr  
 145 150 155 160  
 Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His  
 165 170 175  
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr  
 180 185 190  
 Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met  
 195 200 205  
 Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala  
 210 215 220  
 Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr  
 225 230 235 240  
 Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val  
 245 250 255  
 Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn  
 260 265 270  
 Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val  
 290 295 300  
 Leu Ser Arg Ala Gly Leu Arg Gln Met Cys  
 305 310

&lt;210&gt; 1584

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g501 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1584

Met Asp Leu Lys Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Phe Gly Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser  
 20 25 30  
 Leu Ile Tyr Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr  
 35 40 45  
 Val Thr Cys Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys  
 65 70 75 80  
 Met Ile Ile Asp Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly  
 85 90 95  
 Cys Val Thr Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met  
 100 105 110  
 Thr Leu Leu Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe  
 130 135 140  
 Ala Ile Leu Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile  
 145 150 155 160  
 Val Leu Thr Met Asn Leu Pro Phe Cys Gly His Asn Val Ile Asn Asn  
 165 170 175  
 Ile Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Ile Glu Thr  
 180 185 190  
 Tyr Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe  
 195 200 205  
 Thr Cys Phe Ile Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser  
 210 215 220  
 Val Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu

<400>	1585																
Met	Pro	Thr	Asp	Lys	Gln	Met	Glu	Lys	Gln	Asn	Gln	Ser	Met	Val	Pro		
1				5					10					15			
Glu	Phe	Ile	Leu	Tyr	Gly	Ile	Gln	Lys	Ser	His	Glu	Leu	Gln	Ile	Phe		
			20					25					30				
Phe	Ile	Leu	Phe	Phe	His	Ser	Leu	His	Ile	Ala	Xaa	Leu	Ser	Asn	Leu		
		35					40					45					
Ile	Ile	Ile	Phe	Val	Val	Lys	Leu	Asp	Pro	Gln	Leu	His	Ser	Pro	Met		
		50				55					60						
Tyr	Phe	Leu	Leu	Ala	Asn	Leu	Ser	Ser	Thr	Asp	Met	Pro	Leu	Ala	Ser		
65					70					75					80		
Phe	Ala	Thr	Pro	Lys	Lys	Ile	Asp	Asn	Val	Ile	Ser	Glu	Tyr	Arg	Thr		
				85					90					95			
Ile	Ser	Tyr	Glu	Gly	Cys	Met	Thr	Xaa	Arg	Phe	Phe	Leu	His	Phe	Leu		
			100					105					110				
Ser	Gly	Ser	Glu	Met	Val	Leu	Leu	Leu	Ala	Met	Ala	Ile	Asp	Arg	Xaa		
		115					120					125					
Phe	Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Lys	Ser	Ile	Ala	Ser	Asp	Leu		
		130				135					140						
Leu	Leu	Ala	Ser	Trp	Thr	Met	Asp	Phe	Met	His	Thr	Met	Ser	Gln	Ile		
145					150					155					160		
Val	Leu	Thr	Val	Thr	Leu	Pro	Phe	Cys	Gly	Leu	Ser	Val	Val	Asp	Ile		
				165					170					175			
Phe	Val	Cys	Asp	Val	Ile	Cys	Leu	Val	Ile	Lys	Leu	Ala	Cys	Thr	Asp		
			180					185					190				
Thr	Tyr	Ile	Leu	Glu	Leu	Xaa	Val	Ile	Ala	Asp	Ser	Gly	Leu	Leu	Ser		
		195				200						205					
Leu	Leu	Cys	Phe	Met	Phe	Leu	Leu	Ile	Ser	Tyr	Ser	Thr	Val	Leu	Ile		
		210				215					220						
Ile	Ile	Xaa	His	His	Ser	Ser	Arg	Gly	Ser	Ser	Lys	Thr	Leu	Ser	Thr		
225					230					235					240		
Leu	Ser	Ala	His	Ile	Met	Val	Val	Val	Leu	Phe	Phe	Gly	Ala	Cys	Ile		
				245					250					255			
Phe	Thr	Cys	Glu	Arg	Pro	Phe	Ser	Thr	Val	Ser	Ile	Asp	Ser	Val	Phe		
			260					265					270				
Xaa	Thr	Ile	Phe	Ala	Pro	Leu	Leu	Asn	Pro	Ile	Ile	Tyr	Thr	Phe	Arg		
		275					280					285					

Asn Asn Asp Met Lys Lys Ala Leu Arg Lys Met Lys Ile Asn Phe Val  
 290 295 300  
 Ser Ser Arg Ser Thr Xaa Xaa Leu Lys Tyr Tyr Asn His Xaa Lys His  
 305 310 315 320  
 His His Tyr Cys Cys  
 325

<210> 1586  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g503 protein)

<220>  
 <223> Synthetic construct

<400> 1586  
 Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly  
 1 5 10 15  
 Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Phe Ser  
 20 25 30  
 Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr  
 35 40 45  
 Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe  
 130 135 140  
 Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu  
 145 150 155 160  
 Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr  
 180 185 190  
 Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu  
 195 200 205  
 Ala Ser Phe Leu Ile Leu Ile Ser Tyr Ile Phe Ile Leu Val Thr  
 210 215 220  
 Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu  
 225 230 235 240  
 Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe  
 245 250 255  
 Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Arg Cys Ser Gln  
 290 295 300  
 Phe Val Asn Tyr Ser Lys Ile Phe  
 305 310

<210> 1587  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g504 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1587

```

Met Asn Arg Asp Asn Gln Ser Val Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Asn Ser Trp Glu Ile Lys Ile Phe Leu Phe Cys Phe Ser Cys
          20           25           30
Leu Phe Tyr Val Ser Gly Val Met Ala Asn Leu Ile Val Val Val Ile
          35           40           45
Val Thr Ser Asp Pro Tyr Leu His Ser Ser Leu Tyr Ile Leu Leu Ala
          50           55           60
Asn Leu Ser Val Ile Asp Leu Thr Phe Cys Ser Ile Ala Ala Arg Lys
65           70           75           80
Met Ile Cys Asp Ile Phe Arg Lys Gln Lys Val Ile Ser Phe Trp Gly
          85           90           95
Cys Val Ala Gln Ile Phe Phe Ser His Ala Val Gly Gly Thr Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Val Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met His Pro Arg Met Cys Ile Leu Ile
          130          135          140
Leu Val Ala Ser Trp Ala Ile Gly Leu Ile His Ser Leu Val Gln Leu
145          150          155          160
Ser Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Ile Pro Gln Leu Ile Lys Leu Ala Cys Thr Asn Thr
          180          185          190
Tyr Lys Leu Gln Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
          195          200          205
Ser Ala Phe Phe Leu Leu Ile Leu Ser Tyr Ile Phe Ile Leu Ala Thr
          210          215          220
Leu Gln Lys His Ser Ser Gly Gly Ser Ser Lys Ala Val Ser Thr Leu
225          230          235          240
Ser Ala His Ile Thr Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
          245          250          255
Phe Tyr Val Trp Pro Ser Pro Pro Thr His Leu Asn Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Ile Phe Thr Pro Phe Leu Asn Pro Val Ile Tyr Thr
          275          280          285
Phe Arg Asn Arg Glu Met Lys Ile Ala Ile Arg Arg Val Phe Gly Gln
          290          295          300
Phe Met Gly Phe Arg Lys Thr Thr Xaa Val Ala Leu Leu Lys His Arg
305          310          315          320
Ile Ser

```

&lt;210&gt; 1588

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g505 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1588

```

Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1          5          10          15
Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Val Phe Ser Ser
      20          25          30
Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr
      35          40          45
Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
      50          55          60
Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys
      65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly
      85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
      115          120          125
Pro Leu Gln Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Met Phe Phe
      130          135          140
Leu Val Ala Ala Trp Val Thr Gly Leu Ile His Ser Val Val Gln Leu
      145          150          155          160
Val Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Ser Asp Ser
      165          170          175
Phe Tyr Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Thr Asp Ser
      180          185          190
Tyr Arg Leu Glu Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
      195          200          205
Gly Ser Phe Phe Ile Leu Ile Ile Ser Tyr Val Val Ile Ile Leu Thr
      210          215          220
Val Leu Lys His Ser Ser Ala Gly Leu Ser Lys Ala Leu Ser Thr Leu
      225          230          235          240
Ser Ala His Val Ser Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
      245          250          255
Val Tyr Thr Trp Pro Ser Pro Ser Thr His Leu Asp Lys Phe Leu Ala
      260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
      275          280          285
Phe Arg Asn
      290

```

&lt;210&gt; 1589

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g506 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1589

```

Met Asn Gly Met Asn His Ser Val Val Ser Glu Phe Val Phe Met Gly
 1          5          10          15
Leu Thr Asn Ser Arg Glu Ile Gln Leu Leu Phe Val Phe Ser Leu
      20          25          30
Leu Phe Tyr Phe Ala Ser Met Met Gly Asn Leu Val Ile Val Phe Thr
      35          40          45
Val Thr Met Asp Ala His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
      50          55          60
Asn Leu Ser Ile Ile Asp Met Ala Phe Cys Ser Ile Thr Ala Pro Lys
      65          70          75          80
Met Ile Cys Asp Ile Phe Lys Lys His Lys Ala Ile Ser Phe Arg Gly
      85          90          95
Cys Ile Thr Gln Ile Phe Phe Ser His Ala Leu Gly Gly Thr Glu Met

```

```

      100      105      110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Tyr Phe
      130      135      140
Leu Ala Thr Ser Ser Ile Ile Gly Leu Ile His Ser Leu Val Gln Leu
145      150      155      160
Val Phe Val Val Asp Leu Pro Phe Cys Gly Pro Asn Ile Phe Asp Ser
      165      170      175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asn Thr
      180      185      190
Gln Glu Leu Glu Phe Met Val Thr Val Asn Ser Gly Leu Ile Ser Val
      195      200      205
Gly Ser Phe Val Leu Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
      210      215      220
Val Trp Lys His Ser Ser Gly Gly Leu Ala Lys Ala Leu Ser Thr Leu
225      230      235      240
Ser Ala His Val Thr Val Val Ile Leu Phe Phe Gly Pro Leu Met Phe
      245      250      255
Phe Tyr Thr Trp Pro Ser Pro Thr Ser His Leu Asp Lys Tyr Leu Ala
      260      265      270
Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu Asn Pro Val Ile Tyr Thr
      275      280      285
Phe Arg Asn Lys Asp Met Lys Val Ala Met Arg Arg Leu Cys Ser Arg
      290      295      300
Leu Ala His Phe Thr Lys Ile Leu
305      310

```

&lt;210&gt; 1590

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g507 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1590

```

Met Glu Gln Arg Lys Asn Val Thr Glu Phe Val Leu Val Gly Leu Thr
 1      5      10      15
Gln Ser Pro Gln Gly Gln Lys Ile Leu Phe Leu Val Phe Leu Leu Ile
      20      25      30
Tyr Val Val Thr Met Val Gly Asn Ile Phe Ile Val Val Thr Val Val
      35      40      45
Val Ser Pro Thr Leu Gly Cys Pro Met Tyr Phe Phe Leu Gly Tyr Leu
      50      55      60
Ser Phe Met Asp Ala Val His Ser Thr Thr Val Thr Pro Asn Met Ile
65      70      75      80
Ile Asp Leu Leu Tyr Glu Lys Lys Thr Ile Ser Phe Gln Ala Cys Ile
      85      90      95
Thr Gln Ile Phe Ile Gly His Leu Phe Gly Gly Ala Glu Ile Leu Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Gly Tyr Val Thr Ile Cys Lys Pro Leu
      115      120      125
His Tyr Leu Thr Ile Met Asn Gln Arg Val Cys Ile Leu Leu Leu Leu
      130      135      140
Leu Ala Trp Ala Gly Gly Phe Leu His Ala Val Val Gln Leu Leu Phe
145      150      155      160

```



```

Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
      165                      170                      175
Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr Tyr Val
      180                      185                      190
Thr Gly Leu Thr Val Val Ala Asn Asp Gly Ala Ile Cys Val Val Ile
      195                      200                      205
Phe Met Leu Leu Leu Phe Ser Tyr Gly Val Ile Leu His Ser Leu Lys
      210                      215                      220
Asn Leu Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Gly Ser
      225                      230                      235                      240
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245                      250                      255
Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr Val Phe
      260                      265                      270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275                      280                      285
Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg Lys Arg
      290                      295                      300
Lys Xaa Gly Gly Asp Lys Cys Ile Ile Tyr Phe Gln Xaa Arg Val Ala
      305                      310                      315                      320
Pro Ser Arg Lys Ala Ile Cys
      325

```

&lt;210&gt; 1591

&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g508 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1591

```

Met Asn Leu Lys Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly
  1          5          10          15
Phe Phe Gly Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser
      20          25          30
Leu Ile Tyr Gly Ala Thr Val Val Gly Asn Ile Leu Ile Met Val Thr
      35          40          45
Val Thr Cys Ser Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly
      50          55          60
Asn Leu Ser Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys
      65          70          75          80
Met Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr Gln Lys Phe
      85          90          95
Phe Met His Phe Phe Gly Ser Ala Glu Met Thr Leu Leu Ile Ile Met
      100          105          110
Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His Tyr Arg Thr
      115          120          125
Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu Ser Trp Ile
      130          135          140
Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr Met Asn Leu
      145          150          155          160
Pro Phe Cys Gly His Asn Val Ile Asn Asn Ile Phe Cys Asp Leu Pro
      165          170          175
Leu Val Ile Lys Leu Ala Cys Ile Glu Thr Tyr Thr Leu Glu Leu Phe
      180          185          190
Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr Cys Phe Ile Leu Leu
      195          200          205
Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val Pro Lys Lys Ser Ser
      210          215          220
His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ile Ile Val

```

225					230					235					240
Val	Thr	Leu	Phe	Phe	Gly	Pro	Cys	Ile	Phe	Ile	Tyr	Val	Trp	Pro	Phe
				245					250					255	
Ser	Ser	Leu	Ala	Ser	Asn	Lys	Thr	Leu	Ala	Val	Phe	Tyr	Thr	Val	Ile
				260					265					270	
Thr	Pro	Leu	Leu	Asn	Pro	Ser	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Lys	Met
				275					280					285	
Gln	Glu	Ala	Ile	Arg	Lys	Leu	Arg	Phe	Gln	Tyr	Val	Ser	Ser	Ala	Gln
				290					295					300	
Asn	Phe														
305															

```
<210> 1592
<211> 336
<212> PRT
<213> Unknown (H38g509 protein)
```

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(336)
<223> Xaa = Any Amino Acid
```

<400>	1592															
Ser	Thr	Asp	Pro	Gln	Asn	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu	
1				5					10					15		
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Xaa	Gln	Pro	Val	Leu	Ala	Gly	Leu	Phe	
			20					25					30			
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	
		35					40					45				
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Ile	Phe	Phe	
	50					55					60					
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro	
65					70					75					80	
Lys	Met	Thr	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	
				85					90					95		
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu	
			100					105					110			
Glu	Asn	Met	Phe	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	
		115				120						125				
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	
	130					135				140						
Phe	Leu	Val	Leu	Leu	Ser	Phe	Phe	Phe	Ser	Leu	Ser	Leu	Leu	Asp	Val	
145					150					155					160	
Gln	Leu	Arg	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	
				165					170					175		
Glu	Ile	Pro	Asn	Phe	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	
		180						185					190			
Cys	Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Leu	Tyr	Phe	Pro	Ala	Ala	
		195				200						205				
Ile	Phe	Gly	Phe	Leu	Pro	Ile	Leu	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	
	210					215					220					
Ile	Val	Phe	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	
225				230						235					240	
Ala	Phe	Ser	Thr	Cys	Val	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	
				245					250					255		
Gly	Thr	Gly	Val	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser	Ser	Ser	Pro	
		260						265					270			
Arg	Lys	Ala	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	
		275					280						285			

Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val  
 290 295 300  
 Leu Arg Arg Pro His Ser Ser Thr Val Xaa Ser Xaa Tyr Leu Leu Ile  
 305 310 315 320  
 Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys  
 325 330 335

<210> 1593

<211> 319

<212> PRT

<213> Unknown (H38g510 protein)

<220>

<223> Synthetic construct

<400> 1593

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu  
 1 5 10 15  
 Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val  
 20 25 30  
 Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Leu  
 35 40 45  
 Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro  
 65 70 75 80  
 Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly  
 85 90 95  
 Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu  
 100 105 110  
 Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly  
 130 135 140  
 Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly  
 145 150 155 160  
 Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp  
 165 170 175  
 His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp  
 180 185 190  
 Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val  
 195 200 205  
 Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg  
 210 215 220  
 Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile  
 245 250 255  
 Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly  
 260 265 270  
 Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His  
 290 295 300  
 Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln  
 305 310 315

<210> 1594

<211> 304

<212> PRT

<213> Unknown (H38g511 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1594

```

Met Glu Arg Ala Asn His Ser Val Val Ser Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Lys Ser Gln Asn Leu Gln Ile Leu Phe Phe Leu Gly Phe Ser
          20          25          30
Val Val Phe Val Gly Ile Val Leu Gly Asn Leu Leu Ile Leu Val Thr
          35          40          45
Val Thr Phe Asp Ser Leu Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50          55          60
Asn Leu Ser Cys Ile Asp Met Ile Leu Ala Ser Phe Ala Thr Pro Lys
65          70          75          80
Met Ile Val Asp Phe Leu Arg Glu Arg Lys Thr Ile Ser Trp Trp Gly
          85          90          95
Cys Tyr Ser Gln Met Phe Phe Met His Leu Leu Gly Gly Ser Glu Met
          100          105          110
Met Leu Leu Val Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu His Tyr Met Thr Ile Met Ser Pro Arg Val Leu Thr Gly Leu
          130          135          140
Leu Leu Ser Ser Tyr Ala Val Gly Phe Val His Ser Ser Ser Gln Met
145          150          155          160
Ala Phe Met Leu Thr Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Lys Asp Thr
          180          185          190
Tyr Ile Leu Gln Leu Leu Val Ile Ala Asp Ser Gly Leu Leu Ser Leu
          195          200          205
Val Cys Phe Leu Leu Leu Leu Val Ser Tyr Gly Val Ile Ile Phe Ser
          210          215          220
Val Arg Tyr Arg Ala Ala Ser Arg Ser Ser Lys Ala Phe Ser Thr Leu
225          230          235          240
Ser Ala His Ile Thr Val Val Thr Leu Phe Phe Ala Pro Cys Val Phe
          245          250          255
Ile Tyr Val Trp Pro Phe Ser Arg Tyr Ser Val Asp Lys Ile Leu Ser
          260          265          270
Val Phe Tyr Thr Ile Phe Thr Pro Leu Leu Asn Pro Ile Ile Tyr Thr
          275          280          285
Leu Arg Asn Gln Glu Val Lys Ala Ala Ile Lys Lys Arg Leu Cys Ile
290          295          300

```

&lt;210&gt; 1595

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g512 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1595

```

Met Val Asn Leu Thr Ser Met Ser Gly Phe Leu Leu Met Gly Phe Ser
 1          5          10          15
Asp Glu Arg Lys Leu Gln Ile Leu His Ala Leu Val Phe Leu Val Thr
          20          25          30
Tyr Leu Leu Ala Leu Thr Gly Asn Leu Leu Ile Ile Thr Ile Ile Thr
          35          40          45
Val Asp Arg Arg Leu His Ser Pro Met Tyr Tyr Phe Leu Lys His Leu
50          55          60

```

Ser Leu Leu Asp Leu Cys Phe Ile Ser Val Thr Val Pro Gln Ser Ile  
 65 70 75 80  
 Ala Asn Ser Leu Met Gly Asn Gly Tyr Ile Ser Leu Val Gln Cys Ile  
 85 90 95  
 Leu Gln Val Phe Phe Phe Ile Ala Leu Ala Ser Ser Glu Val Ala Ile  
 100 105 110  
 Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu  
 115 120 125  
 His Tyr Glu Thr Ile Met Asp Pro Arg Ala Cys Arg His Ala Val Ile  
 130 135 140  
 Ala Val Trp Ile Ala Gly Gly Leu Ser Gly Leu Met His Ala Ala Ile  
 145 150 155 160  
 Asn Phe Ser Ile Pro Leu Cys Gly Lys Arg Val Ile His Gln Phe Phe  
 165 170 175  
 Cys Asp Val Pro Gln Met Leu Lys Leu Ala Cys Ser Tyr Glu Phe Ile  
 180 185 190  
 Asn Glu Ile Ala Leu Ala Ala Phe Thr Thr Ser Ala Ala Phe Ile Cys  
 195 200 205  
 Leu Ile Ser Ile Val Leu Ser Tyr Ile Arg Ile Phe Ser Thr Val Leu  
 210 215 220  
 Arg Ile Pro Ser Ala Glu Gly Arg Thr Lys Val Phe Ser Thr Cys Leu  
 225 230 235 240  
 Pro His Leu Phe Val Ala Thr Phe Phe Leu Ser Ala Ala Gly Phe Glu  
 245 250 255  
 Phe Leu Arg Leu Pro Ser Asp Ser Ser Ser Thr Val Asp Leu Val Phe  
 260 265 270  
 Ser Val Phe Tyr Thr Val Ile Pro Pro Thr Leu Asn Pro Val Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Asp Ser Met Lys Ala Ala Leu Arg Lys Met Leu Ser  
 290 295 300  
 Lys Glu Glu Leu Pro Gln Arg Lys Met Cys Leu Lys Ala Met Phe Lys  
 305 310 315 320  
 Leu

&lt;210&gt; 1596

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g513 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1596

Met Asp Pro Gln Asn Tyr Ser Leu Val Ser Glu Phe Val Leu His Gly  
 1 5 10 15  
 Leu Cys Thr Ser Arg His Leu Gln Asn Phe Phe Phe Ile Phe Phe Phe  
 20 25 30  
 Gly Val Tyr Val Ala Ile Met Leu Gly Asn Leu Leu Ile Leu Val Thr  
 35 40 45  
 Val Ile Ser Asp Pro Cys Leu His Ser Ser Pro Met Tyr Phe Leu Leu  
 50 55 60  
 Gly Asn Leu Ala Phe Leu Asp Met Trp Leu Ala Ser Phe Ala Thr Pro  
 65 70 75 80  
 Lys Met Ile Arg Asp Phe Leu Ser Asp Gln Lys Leu Ile Ser Phe Gly  
 85 90 95  
 Gly Cys Met Ala Gln Ile Phe Phe Leu His Phe Thr Gly Gly Ala Glu  
 100 105 110  
 Met Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Lys Pro Leu His Tyr Met Thr Leu Met Ser Trp Gln Thr Cys Ile Arg

```

      130              135              140
Leu Val Leu Ala Ser Trp Val Val Gly Phe Val His Ser Ile Ser Gln
145              150              155              160
Val Ala Phe Thr Val Asn Leu Pro Tyr Cys Gly Pro Asn Glu Val Asp
      165              170              175
Ser Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Met Asp
      180              185              190
Thr Tyr Val Leu Gly Ile Ile Met Ile Ser Asp Ser Gly Leu Leu Ser
      195              200              205
Leu Ser Cys Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Leu
      210              215              220
Ala Ile Arg Gln Arg Ala Ala Gly Ser Thr Ser Lys Ala Leu Ser Thr
225              230              235              240
Cys Ser Ala His Ile Met Val Val Thr Leu Phe Phe Gly Pro Cys Ile
      245              250              255
Phe Val Tyr Val Arg Pro Phe Ser Arg Phe Ser Val Asp Lys Leu Leu
      260              265              270
Ser Val Phe Tyr Thr Ile Phe Thr Pro Leu Leu Asn Pro Ile Ile Tyr
      275              280              285
Thr Leu Arg Asn Glu Glu Met Lys Ala Ala Met Lys Lys Leu Gln Asn
      290              295              300
Arg Arg Val Thr Phe Gln
305              310

```

&lt;210&gt; 1597

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g514 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1597

```

Met Glu Arg Lys Asn Gln Thr Ala Ile Thr Glu Phe Ile Ile Leu Gly
1      5      10      15
Phe Ser Asn Leu Asn Glu Leu Gln Phe Leu Leu Phe Thr Ile Phe Phe
      20      25      30
Leu Thr Tyr Phe Cys Thr Leu Gly Gly Asn Ile Leu Ile Ile Leu Thr
      35      40      45
Thr Val Thr Asp Pro His Leu His Thr Pro Met Tyr Tyr Phe Leu Gly
      50      55      60
Asn Leu Ala Phe Ile Asp Ile Cys Tyr Thr Thr Ser Asn Val Pro Gln
65      70      75      80
Met Met Val His Leu Leu Ser Lys Lys Lys Ser Ile Ser Tyr Val Gly
      85      90      95
Cys Val Val Gln Leu Phe Ala Phe Val Phe Phe Val Gly Ser Glu Cys
      100      105      110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Ser Val Ile Leu Ser Lys Val Leu Cys Asn Gln Leu
      130      135      140
Ala Ala Ser Cys Trp Ala Ala Gly Phe Leu Asn Ser Val Val His Thr
145      150      155      160
Val Leu Thr Phe Cys Leu Pro Phe Cys Gly Asn Asn Gln Ile Asn Tyr
      165      170      175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Ile Leu Ser Cys Gly Asn Thr
      180      185      190
Ser Val Asn Glu Leu Ala Leu Leu Ser Thr Gly Val Phe Ile Gly Trp
      195      200      205
Thr Pro Phe Leu Cys Ile Val Leu Ser Tyr Ile Cys Ile Ile Ser Thr
210      215      220

```

```

Ile Leu Arg Ile Gln Ser Ser Glu Gly Arg Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ala Ile Val Phe Leu Phe Tyr Gly Ser Ala Ile
          245          250          255
Phe Thr Tyr Val Arg Pro Ile Ser Thr Tyr Ser Leu Lys Lys Asp Arg
          260          265          270
Leu Val Ser Val Leu Tyr Ser Val Val Thr Pro Met Leu Asn Pro Ile
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asp Ile Lys Glu Ala Val Lys Thr Ile
          290          295          300
Gly Ser Lys Trp Gln Pro Pro Ile Ser Ser Leu Asp Ser Lys Leu
305          310          315

```

&lt;210&gt; 1598

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g515 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1598

```

Met Arg Glu Phe Phe Leu Ser Gly Phe Ser Gln Thr Pro Ser Ile Glu
1          5          10          15
Ala Gly Leu Phe Val Leu Phe Leu Phe Phe Tyr Met Ser Ile Trp Val
          20          25          30
Gly Asn Val Leu Ile Met Val Thr Val Ala Ser Asp Lys Tyr Leu Asn
          35          40          45
Ser Ser Pro Met Tyr Phe Leu Leu Gly Asn Leu Ser Phe Leu Asp Leu
          50          55          60
Cys Tyr Ser Thr Val Thr Thr Pro Lys Leu Leu Ala Asp Phe Phe Asn
          65          70          75          80
His Glu Lys Leu Ile Ser Tyr Asp Gln Cys Ile Val Gln Leu Phe Phe
          85          90          95
Leu His Phe Val Gly Ala Ala Glu Met Phe Leu Leu Thr Val Met Ala
          100          105          110
Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Thr Thr Val
          115          120          125
Met Ser Arg Gly Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly
          130          135          140
Gly Phe Val His Ser Thr Val Gln Thr Ile Leu Thr Val His Leu Pro
          145          150          155          160
Phe Cys Gly Pro Asn Gln Val Glu Asn Phe Phe Cys Asp Val Pro Pro
          165          170          175
Val Ile Lys Leu Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met
          180          185          190
Val Ser Asn Ser Gly Leu Ile Ser Thr Ile Ser Phe Val Val Leu Ile
          195          200          205
Ser Ser Tyr Thr Thr Ile Leu Val Lys Ile Arg Ser Lys Glu Gly Arg
          210          215          220
Arg Lys Ala Leu Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu
          225          230          235          240
Phe Phe Gly Pro Cys Ile Phe Ile Tyr Ala Arg Pro Phe Ser Thr Phe
          245          250          255
Ser Val Asp Lys Met Val Ser Val Leu Tyr Asn Val Ile Thr Pro Met
          260          265          270
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala
          275          280          285
Met Gln Lys Leu Trp Val Arg Asn Gly Leu Thr Trp Lys Lys Gln
          290          295          300

```

<210> 1599  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g516 protein)

<220>  
 <223> Synthetic construct

<400> 1599  
 Met Glu Asn Val Thr Thr Met Asn Glu Phe Leu Leu Leu Gly Leu Thr  
 1 5 10 15  
 Gly Val Gln Glu Leu Gln Pro Phe Phe Phe Gly Ile Phe Leu Ile Ile  
 20 25 30  
 Tyr Leu Ile Asn Leu Ile Gly Asn Gly Ser Ile Leu Val Met Val Val  
 35 40 45  
 Leu Glu Pro Gln Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu  
 50 55 60  
 Ser Cys Leu Asp Ile Ser Tyr Ser Ser Val Thr Leu Pro Lys Leu Leu  
 65 70 75 80  
 Val Asn Leu Val Cys Ser Arg Arg Ala Ile Ser Phe Leu Gly Cys Ile  
 85 90 95  
 Thr Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Ile Leu  
 100 105 110  
 Leu Ala Ile Met Ala Phe Asp Arg Phe Val Ala Ile Cys Asn Pro Leu  
 115 120 125  
 Arg Tyr Thr Val Ile Met Asn Pro Gln Val Cys Ile Leu Leu Ala Ala  
 130 135 140  
 Ala Ala Trp Leu Ile Ser Phe Phe Tyr Ala Leu Met His Ser Val Met  
 145 150 155 160  
 Thr Ala His Leu Ser Phe Cys Gly Ser Gln Lys Leu Asn His Phe Phe  
 165 170 175  
 Tyr Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Ser Asp Thr Leu Leu  
 180 185 190  
 Asn Gln Trp Leu Leu Ser Ile Val Thr Gly Ser Ile Ser Met Gly Ala  
 195 200 205  
 Phe Phe Leu Thr Leu Leu Ser Cys Phe Tyr Val Ile Gly Phe Leu Leu  
 210 215 220  
 Phe Lys Asn Arg Ser Cys Arg Ile Leu His Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Ala Ser His Phe Met Val Val Cys Leu Phe Tyr Gly Pro Val Gly Phe  
 245 250 255  
 Thr Tyr Ile Arg Pro Ala Ser Ala Thr Ser Met Ile Gln Asp Arg Ile  
 260 265 270  
 Met Ala Ile Met Tyr Ser Ala Val Thr Pro Val Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Met Met Ala Leu Lys Lys Ile Phe  
 290 295 300  
 Gly Arg Lys Leu Phe Lys Asp Trp Gln Gln His  
 305 310 315

<210> 1600  
 <211> 322  
 <212> PRT  
 <213> Unknown (H38g517 protein)

<220>  
 <223> Synthetic construct

<400> 1600  
 Met Asn Glu Thr Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly  
 1 5 10 15



Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser  
                   20                  25                  30  
 Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr  
           35                  40                  45  
 Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala  
           50                  55                  60  
 Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Phe Ala Thr Pro Lys  
   65                  70                  75                  80  
 Met Ile Ala Asp Phe Leu Val Glu Arg Lys Thr Ile Ser Phe Asp Ala  
                   85                  90                  95  
 Cys Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met  
                   100                  105                  110  
 Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
           115                  120                  125  
 Pro Leu His Tyr Met Thr Val Met Ser Arg Arg Val Cys Val Val Leu  
           130                  135                  140  
 Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu  
   145                  150                  155                  160  
 Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser  
                   165                  170                  175  
 Phe Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys Ile Asp Thr  
                   180                  185                  190  
 Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu  
           195                  200                  205  
 Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr  
           210                  215                  220  
 Val Arg Asn Arg Ser Ser Ala Ser Met Ala Lys Ala Arg Ser Thr Leu  
   225                  230                  235                  240  
 Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe  
                   245                  250                  255  
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala  
                   260                  265                  270  
 Val Phe Tyr Thr Ile Phe Thr Leu Ile Leu Asn Pro Val Ile Tyr Thr  
           275                  280                  285  
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg  
   290                  295                  300  
 Tyr Leu Lys Pro Ser Gln Val Ser Val Val Ile Arg Asn Val Leu Phe  
   305                  310                  315                  320  
 Leu Glu

&lt;210&gt; 1601

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g518 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1601

Glu Arg Leu Leu Leu Pro Met Tyr Cys Phe Leu Thr Ile Leu Ser Ala  
   1                  5                  10                  15  
 Thr Asp Leu Gly Leu Ser Ile Ser Thr Leu Val Thr Met Leu Ser Ile  
           20                  25                  30  
 Phe Trp Phe Asn Val Arg Glu Ile Ser Phe Asn Ala Cys Leu Ser His  
           35                  40                  45  
 Met Phe Phe Ile Lys Phe Phe Thr Val Met Glu Ser Ser Val Leu Leu  
           50                  55                  60  
 Ala Met Ala Phe Asp Arg Phe Val Ala Val Ser Asn Pro Leu Arg Tyr  
   65                  70                  75                  80  
 Ala Met Ile Leu Thr Asp Ser Arg Ile Ala Gln Ile Gly Val Ala Ser

```

      85              90              95
Val Ile Arg Gly Leu Leu Met Leu Thr Pro Met Val Ala Leu Leu Ile
      100              105              110
Arg Leu Ser Tyr Cys His Ser Arg Val Leu His His Ser Tyr Cys Tyr
      115              120              125
His Pro Asp Val Met Lys Phe Ser Cys Thr Asp Ala Arg Ile Asn Ser
      130              135              140
Ala Val Gly Leu Thr Ala Met Phe Ser Thr Val Gly Val Asp Leu Leu
      145              150              155              160
Leu Ile Leu Leu Ser Tyr Val Leu Ile Ile Arg Thr Val Leu Asn Val
      165              170              175
Ala Ser Pro Glu Glu Arg Arg Lys Pro Phe Ser Thr Cys Val Ser His
      180              185              190
Ile Gly Gly Phe Cys
      195

```

&lt;210&gt; 1602

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g519 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1602

```

Met Ser Pro Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
  1              5              10              15
Leu Pro Ile Arg Pro Glu Gln Gln Ala Val Phe Phe Thr Leu Phe Leu
      20              25              30
Gly Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu
      35              40              45
Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50              55              60
His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys
      65              70              75              80
Met Leu Met Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu
      85              90              95
Cys Ile Ser Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser
      100              105              110
Phe Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu
      130              135              140
Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr
      145              150              155              160
Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His
      165              170              175
Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile
      180              185              190
Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr
      195              200              205
Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr
      210              215              220
Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr
      225              230              235              240
Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe
      245              250              255
Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val
      260              265              270
Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285

```

Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu  
 290 295 300  
 Phe Ser Arg Ala Thr Phe Phe Ser Trp  
 305 310

<210> 1603  
 <211> 196  
 <212> PRT  
 <213> Unknown (H38g520 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(196)  
 <223> Xaa = Any Amino Acid

<400> 1603  
 Arg Leu Leu Leu Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Leu Leu  
 1 5 10 15  
 Asp Leu Cys Leu Pro Ser Ile Pro Val Pro Lys Met Leu Gln Asn Leu  
 20 25 30  
 Leu Thr Gln Arg Xaa Thr Ile Ser Met Trp Tyr Cys Ile Val Gln Ser  
 35 40 45  
 Phe Phe Leu Ile Phe Ser Gly Ser Thr Glu Ala Cys Leu Leu Leu Ala  
 50 55 60  
 Met Ala Cys Asp His Ser Thr Ser Asn Cys His Pro Arg Leu Asn Asp  
 65 70 75 80  
 Val Val Met Asn Gln Pro Val Cys Val Arg Met Val Ile Ala Ala Trp  
 85 90 95  
 Ala Val Gly Phe Leu Asn Ser Leu Thr Lys Asn Leu Phe Ile Tyr Asn  
 100 105 110  
 Leu His Phe Cys Gly Pro Ser Val Ile Pro His Phe Cys Cys Glu Leu  
 115 120 125  
 Pro Ser Leu Phe Pro Leu Ser Cys Ile Asp Pro Ala Ala Ser Glu Val  
 130 135 140  
 Leu Pro Ala Gly Ser Cys Thr Leu Leu Gly Phe Val Thr Cys Arg Cys  
 145 150 155 160  
 Val Leu Phe Ser Tyr Ser Asn Thr Ile Ser Ala Val Leu Ala Ile Trp  
 165 170 175  
 Phe Ser Glu Gly Gln Gly Lys Ala Phe Ser Thr Cys Ser Ser His Leu  
 180 185 190  
 Thr Val Val Leu  
 195

<210> 1604  
 <211> 306  
 <212> PRT  
 <213> Unknown (H38g521 protein)

<220>  
 <223> Synthetic construct

<400> 1604  
 Met Ser Pro Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Arg Pro Glu Gln Gln Ala Val Phe Phe Ala Leu Phe Leu  
 20 25 30  
 Gly Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu  
 35 40 45  
 Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser

```

      50              55              60
His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys
65              70              75              80
Met Leu Met Asn Met Gln Thr Gln His Leu Ala Val Phe Tyr Lys Gly
      85              90              95
Cys Ile Ser Gln Thr Tyr Phe Phe Ile Phe Phe Ala Asp Leu Asp Ser
      100              105              110
Phe Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu His Tyr Ala Thr Ile Met Thr Gln Ser Gln Cys Val Met Leu
      130              135              140
Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu His Thr
145              150              155              160
Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp His Ile Ile Pro His
      165              170              175
Tyr Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr
      180              185              190
Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Ala Leu Thr Ala Ile Met
      195              200              205
Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly His Ile Gly Val Thr
      210              215              220
Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys Lys Ala Leu Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr Tyr Arg Thr Ile Ile
      245              250              255
Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr Asn Asp Lys Asn Ile
      260              265              270
Ile Ala Ser Val Ile Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu
      290              295              300
Leu Ser
305

```

&lt;210&gt; 1605

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g522 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1605

```

Leu Leu Leu Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Leu Met Asp
1              5              10              15
Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Ile Leu Asp Asn Phe Leu
      20              25              30
Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr
      35              40              45
Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu Leu Ala Val Met
      50              55              60
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu
65              70              75              80
Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly
      85              90              95
Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu
      100              105              110
Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val
      115              120              125
Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn Ala Leu Ala Leu Met
      130              135              140

```

Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu Leu Leu Ile Cys Leu  
 145 150 155 160  
 Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala  
 165 170 175  
 Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val  
 180 185 190  
 Val Val Phe Tyr Gly  
 195

<210> 1606

<211> 328

<212> PRT

<213> Unknown (H38g523 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1606

Val Asn Gly Trp Ser Asn Lys Ser Val Val Thr Glu Phe Asn Leu Leu  
 1 5 10 15  
 Gly Leu Ser Ser Ser Trp Glu Leu Gln Val Phe Phe Phe Phe Ile Phe  
 20 25 30  
 Ser Val Phe Tyr Gly Ala Ala Val Leu Gly Asn Ile Leu Ile Ile Ile  
 35 40 45  
 Thr Val Ile Ile Asp Ser His Leu His Ser Pro Met Tyr Phe Leu Leu  
 50 55 60  
 Ser Asn Leu Ser Ser Ile Asp Val Cys Gln Ala Thr Phe Ala Thr Pro  
 65 70 75 80  
 Lys Met Ile Ala Asp Phe Leu Asn Glu His Lys Thr Thr Thr Phe Gln  
 85 90 95  
 Gly Cys Met Ser Gln Ile Phe Phe Leu His Val Phe Gly Gly Ser Glu  
 100 105 110  
 Met Val Leu Val Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys  
 115 120 125  
 Lys Pro Leu His Tyr Met Thr Ile Met Asn Arg Arg Val Xaa Thr Val  
 130 135 140  
 Leu Val Gly Val Ser Trp Ala Ile Gly Ile Ser His Ser Ala Thr His  
 145 150 155 160  
 Leu Ala Phe Lys Val Asn Leu Pro Phe Cys Gly Pro Asn Arg Val Asp  
 165 170 175  
 Asn Phe Phe Cys Asp Leu Leu Leu Val Ile Lys Leu Ala Cys Leu Asp  
 180 185 190  
 Thr Tyr Gly Phe Glu Ile Leu Val Leu Thr Asn Ser Gly Leu Leu Ser  
 195 200 205  
 Leu Met Cys Phe Leu Leu Leu Ile Ser Asp Thr Ile Ile Leu Ala  
 210 215 220  
 Thr Val His Arg Gln Ala Ser Asp Gly Met Ser Lys Ala Leu Ser Thr  
 225 230 235 240  
 Leu Ser Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Leu Ile  
 245 250 255  
 Phe Ile Tyr Ile Trp Pro Phe Glu Ser Phe Pro Ile Asp Lys Phe Ile  
 260 265 270  
 Ser Val Phe Phe Thr Val Phe Thr Pro Leu Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Asp Ile Lys Glu Ala Met Arg Lys Leu Arg Arg  
 290 295 300  
 Xaa His Val Gly Ser Lys Gln Gly Phe Xaa Thr Thr Thr Lys Lys Xaa

305 310 315 320

Tyr Lys Phe Leu Leu Leu Gly Phe  
325

<210> 1607  
<211> 260  
<212> PRT  
<213> Unknown (H38g524 protein)

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(260)  
<223> Xaa = Any Amino Acid

<400> 1607

Met Tyr Phe Phe Leu Ser Phe Leu Ser Leu Thr Asp Ile Cys Phe Thr  
1 5 10 15  
Thr Ser Val Val Pro Lys Met Leu Met Asn Phe Leu Ser Glu Lys Lys  
20 25 30  
Thr Ile Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Tyr Ala  
35 40 45  
Leu Gly Asn Ser Asp Ser Cys Leu Leu Ser Xaa Met Ala Phe Asp Arg  
50 55 60  
Tyr Val Ala Val Cys Asp Pro Phe His Tyr Val Thr Thr Met Ser His  
65 70 75 80  
His His Cys Val Leu Leu Val Ala Phe Ser Cys Ser Phe Thr Tyr Leu  
85 90 95  
His Ser Leu Leu His Thr Leu Leu Leu Asn Arg Leu Thr Phe Cys Asp  
100 105 110  
Ser Asn Val Ile His His Phe Leu Cys Asp Leu Ser Pro Val Leu Lys  
115 120 125  
Leu Ser Cys Ser Ser Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu  
130 135 140  
Ala Pro Ile Val Leu Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr  
145 150 155 160  
Ile Arg Ile Leu Thr Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys  
165 170 175  
Arg Lys Ala Phe Ser Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu  
180 185 190  
Phe Tyr Gly Ser Ile Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr  
195 200 205  
Ala Val Lys Asp His Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser  
210 215 220  
Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln  
225 230 235 240  
Gly Leu Arg Lys Leu Met Ser Lys Arg Ser Xaa Glu Ala Pro Ser Xaa  
245 250 255  
Lys Thr Arg Lys  
260

<210> 1608  
<211> 192  
<212> PRT  
<213> Unknown (H38g525 protein)

<220>  
<223> Synthetic construct

**<400> 1608**

Tyr Tyr Tyr Tyr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Phe Leu  
 1 5 10 15  
 Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln Leu Leu Ala Asn Leu  
 20 25 30  
 Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly Cys Val Val Gln Phe  
 35 40 45  
 Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys Val Leu Leu Ala Thr  
 50 55 60  
 Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu His Tyr Thr  
 65 70 75 80  
 Val Ile Met His Pro Gln Leu Cys Leu Gly Leu Ala Leu Ala Ser Trp  
 85 90 95  
 Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser Thr Leu Thr Met Leu  
 100 105 110  
 Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His Phe Phe Cys Glu Met  
 115 120 125  
 Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met  
 130 135 140  
 Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu  
 145 150 155 160  
 Ile Leu Val Ser Tyr Gly His Ile Ala Glu Ala Gly Leu Lys Asn Lys  
 165 170 175  
 Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Phe His Val  
 180 185 190

&lt;210&gt; 1609

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g526 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1609

Met Asp Ile Arg Asn Ser Ser Ile Ile Thr Glu Phe Val Leu Leu Glu  
 1 5 10 15  
 Phe Ile Ser Thr Trp Glu Leu Glu Ile Leu Phe Leu Ile Ile Phe Leu  
 20 25 30  
 Leu Ala Tyr Ala Ala Ile Met Ala Gly Asn Leu Thr Ala Ile Ala Val  
 35 40 45  
 Thr Ser Asn Pro Pro Leu Cys Ser Thr Pro Met Tyr Phe Leu Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Ser Met Phe Ile Ser Thr Val Thr Ile Ser Lys  
 65 70 75 80  
 Met Val Leu Asp Val Leu Arg Glu Asn Lys Thr Thr Ser Ser Trp Gly  
 85 90 95  
 Cys Met Ala Gln Met Leu His Phe Leu Gly Gly Ser Glu Met Thr Leu  
 100 105 110  
 Leu Ile Phe Met Ala Val Asp Gln His Ile Ala Ile Cys Arg Pro Leu  
 115 120 125  
 His Cys Arg Thr Ile Thr Asn Cys Arg Val Leu Met Ala Thr His Gly  
 130 135 140  
 Leu Cys Val Leu Ser Arg Ala Val Gly Phe Val His Thr Ile Ser Gln  
 145 150 155 160  
 Ile Val Phe Ile Ile Thr Leu Pro Phe Cys Gly Pro Ser Val Val Asp  
 165 170 175  
 Asn Leu Phe Xaa Asp Leu Pro Leu Val Leu Lys Leu Ala Cys Thr Glu

```

      180      185      190
Thr Tyr Asp Leu Glu Leu Leu Val Ile Ala Lys Ser Gly Gln Leu Ser
      195      200      205
Phe Ile Cys Phe Ile Val Leu Leu Ile Phe Tyr Thr Ile Ile Leu Val
      210      215      220
Thr Val Gln His Arg Ser Ser Asp Ala Leu Ser Lys Ala Leu Ser Thr
225      230      235      240
Leu Ser Ala His Ile Thr Ala Val Thr Leu Phe Phe Glu Pro Cys Val
      245      250      255
Tyr Ile Tyr Thr Trp Pro Phe Arg Ser Phe Ser Val Asp Thr Phe Leu
      260      265      270
Ser Val Phe Tyr Ser Val Thr Pro Leu Leu Asn Pro Ile Thr Tyr Ser
      275      280      285
Leu Arg Xaa Lys His Ala Ile His Gln Leu Arg Thr Gln His Ile Ile
      290      295      300
Ser Arg Gln Thr Phe Ser
305      310

```

&lt;210&gt; 1610

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g527 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1610

```

Leu Leu Leu Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Leu Val Asp
1      5      10      15
Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met Val Gly Phe Leu
      20      25      30
Thr Gly Asp Lys Phe Ile Leu Tyr Asn Ala Cys Ala Thr Gln Phe Phe
      35      40      45
Phe Phe Val Ala Phe Ile Thr Ala Glu Ser Phe Leu Leu Ala Ser Met
      50      55      60
Ala Tyr Asp Arg Tyr Ala Ala Leu Cys Lys Pro Leu His Tyr Thr Thr
65      70      75      80
Thr Met Thr Thr Asn Val Cys Ala Arg Leu Ala Ile Gly Ser Tyr Ile
      85      90      95
Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asn Thr Phe Arg Leu
      100      105      110
Ser Phe Cys Arg Ser Asn Val Val Glu His Phe Phe Cys Asp Ala Pro
      115      120      125
Pro Leu Leu Thr Leu Ser Cys Ser Asp Asn Tyr Ile Ser Glu Met Val
      130      135      140
Ile Phe Phe Val Val Gly Phe Asn Asp Leu Phe Ser Ile Leu Val Ile
145      150      155      160
Leu Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Met Lys Met Arg Ser
      165      170      175
Pro Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr
      180      185      190
Ala Val Ser Ile Phe Tyr
      195

```

&lt;210&gt; 1611

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g528 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 1611

```

Met Glu Ala Met Lys Leu Leu Asn Gln Ser Gln Val Ser Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Thr Ser Ser Gln Asp Val Glu Phe Leu Leu Phe Ala
 20           25           30
Leu Phe Ser Val Ile Tyr Val Val Thr Val Leu Gly Asn Leu Leu Ile
 35           40           45
Ile Val Thr Val Phe Asn Thr Pro Asn Leu Asn Thr Pro Met Tyr Phe
 50           55           60
Leu Leu Gly Asn Leu Ser Phe Val Asp Met Thr Leu Ala Ser Phe Ala
 65           70           75           80
Thr Pro Lys Val Ile Leu Asn Leu Leu Lys Lys Gln Lys Val Ile Ser
 85           90           95
Phe Ala Gly Cys Phe Thr Gln Ile Phe Leu Leu His Leu Leu Gly Gly
100          105          110
Val Glu Met Val Leu Leu Val Ser Met Ala Phe Asp Arg Tyr Val Ala
115          120          125
Ile Cys Lys Pro Leu His Tyr Met Thr Ile Met Asn Lys Lys Val Cys
130          135          140
Val Leu Leu Val Val Thr Ser Trp Leu Leu Gly Leu Leu His Ser Gly
145          150          155          160
Phe Gln Ile Pro Phe Ala Val Asn Leu Pro Phe Cys Gly Pro Asn Val
165          170          175
Val Asp Ser Ile Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys
180          185          190
Ile Asp Ile Tyr Phe Val Gln Val Val Ile Val Ala Asn Ser Gly Ile
195          200          205
Ile Ser Leu Ser Cys Phe Ile Ile Leu Leu Ile Ser Tyr Ser Leu Ile
210          215          220
Leu Ile Thr Ile Lys Asn His Ser Pro Thr Gly Gln Ser Lys Ala Arg
225          230          235          240
Ser Thr Leu Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro
245          250          255
Cys Ile Phe Ile Tyr Ile Trp Pro Phe Gly Asn His Ser Val Asp Lys
260          265          270
Phe Leu Ala Val Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Ile
275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Met Lys Ile Ser Met Lys Lys Leu
290          295          300
Trp Arg Ala Phe Val Asn Ser Arg Glu Asp Thr
305          310          315

```

&lt;210&gt; 1612

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g529 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1612

```

Met Glu Pro Gln Asn Thr Ser Thr Val Thr Asn Phe Gln Leu Leu Gly
 1           5           10           15
Phe Gln Asn Leu Leu Glu Trp Gln Ala Leu Leu Phe Val Ile Phe Leu
 20           25           30
Leu Ile Tyr Cys Leu Thr Ile Ile Gly Asn Val Val Ile Ile Thr Val
 35           40           45
Val Ser Gln Gly Leu Arg Leu His Ser Pro Met Tyr Met Phe Leu Gln
 50           55           60
His Leu Ser Phe Leu Glu Val Trp Tyr Thr Ser Thr Thr Val Pro Leu

```

```

65          70          75          80
Leu Leu Ala Asn Leu Leu Ser Trp Gly Gln Ala Ile Ser Phe Ser Ala
      85          90          95
Cys Met Ala Gln Leu Tyr Phe Phe Val Phe Leu Gly Ala Thr Glu Cys
      100         105         110
Phe Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Ser
      115         120         125
Pro Leu Arg Tyr Pro Phe Leu Met His Arg Gly Leu Cys Ala Arg Leu
      130         135         140
Val Val Val Ser Trp Cys Thr Gly Val Ser Thr Gly Phe Leu His Ser
145         150         155         160
Met Met Ile Ser Arg Leu Asp Phe Cys Gly Arg Asn Gln Ile Asn His
      165         170         175
Phe Phe Cys Asp Leu Pro Pro Leu Met Gln Leu Ser Cys Ser Arg Val
      180         185         190
Tyr Ile Thr Glu Val Thr Ile Phe Ile Leu Ser Ile Ala Val Leu Cys
      195         200         205
Ile Cys Phe Phe Leu Thr Leu Gly Pro Tyr Val Phe Ile Val Ser Ser
      210         215         220
Ile Leu Arg Ile Pro Ser Thr Ser Gly Arg Arg Lys Thr Phe Ser Thr
225         230         235         240
Cys Gly Ser His Leu Ala Val Val Thr Leu Tyr Tyr Gly Thr Met Ile
      245         250         255
Ser Met Tyr Val Cys Pro Ser Pro His Leu Leu Pro Glu Ile Asn Lys
      260         265         270
Ile Ile Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val
      275         280         285
Ile Tyr Ser Leu Arg Asn Lys Asp Phe Lys Glu Ala Val Arg Lys Val
      290         295         300
Met Arg Arg Lys Cys Gly Ile Leu Trp Ser Thr Ser Lys
305         310         315

```

&lt;210&gt; 1613

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g530 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1613

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Gly Ser Ser Glu Asp Pro Glu Trp Gln Pro Val Leu Thr Gly Leu Cys
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100     105     110
Glu Asn Met Leu Leu Ser Val Ile Ala Tyr Glu Arg Phe Val Ala Ile
      115     120     125

```

```

Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130                      135                      140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
145                      150                      155                      160
Leu His Asn Leu Ile Ala Leu Gln Arg Thr Cys Phe Lys Asp Val Glu
                      165                      170                      175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Tyr
                      180                      185                      190
Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
                      195                      200                      205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile
                      210                      215                      220
Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225                      230                      235                      240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
                      245                      250                      255
Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
                      260                      265                      270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Ile Pro Met Pro
                      275                      280                      285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val Leu
290                      295                      300
Gln Arg Pro His Gly Ser Thr Ile Ser Ser Gln Tyr Leu Leu Ile Cys
305                      310                      315                      320
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
                      325                      330                      335

```

&lt;210&gt; 1614

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g531 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(330)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1614

```

His Thr Glu Pro Gln Asn Leu Thr Gly Ile Xaa Glu Phe Leu Leu Leu
 1                      5                      10                      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
                      20                      25                      30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Thr Leu
                      35                      40                      45
Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu
50                      55                      60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Ile Val Pro
65                      70                      75                      80
Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
                      85                      90                      95
Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
                      100                      105                      110
Asp Met Phe Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
115                      120                      125
Arg Pro Leu Tyr Tyr Pro Val Ile Ile Asn Pro His Leu Cys Val Phe
130                      135                      140
Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
145                      150                      155                      160
Ser Trp Ile Val Xaa Gln Phe Thr Phe Ser Lys Asn Val Glu Ile Ser

```

Asn	Phe	Val	Cys	Glu	Pro	Ser	Gln	Leu	Leu	Tyr	Leu	Ala	Cys	Ser	Asp
			180					185					190		
Ser	Ile	Ile	Asn	Ser	Ile	Phe	Ile	Tyr	Phe	Asp	Ser	Thr	Met	Phe	Gly
		195					200					205			
Phe	Leu	Pro	Ile	Ser	Arg	Ile	Leu	Leu	Ser	Tyr	Tyr	Lys	Ile	Val	Pro
	210					215					220				
Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Thr
225					230					235					240
Thr	Cys	Gly	Ser	His	Leu	Ala	Val	Val	Cys	Leu	Phe	Asp	Gly	Thr	Gly
			245						250					255	
Ile	Gly	Met	Tyr	Leu	Thr	Ser	Ala	Val	Ala	Pro	Pro	Pro	Arg	Asn	Gly
		260						265					270		
Val	Val	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Asn	Pro
	275						280					285			
Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Asn	Thr	Leu	Trp	Arg
	290					295					300				
Leu	Arg	Ser	Arg	Arg	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro	Phe	Phe
305					310					315					320
Val	Trp	Val	Arg	Lys	Gly	Asn	His	Ile	Lys						
			325						330						

&lt;210&gt; 1615

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g532 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1615

Ser	Thr	Asp	Pro	Gln	Asn	Leu	Ile	Asp	Val	Phe	Val	Phe	Leu	Leu	Leu
1					5				10					15	
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Arg	Gln	Leu	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70				75						80
Lys	Leu	Ile	Val	Asp	Ile	Gln	Ser	Tyr	Ser	Arg	Val	Ile	Ser	Tyr	Ala
			85					90						95	
Gly	Cys	Leu	Thr	Gln	Thr	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
		100						105					110		
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Val	Tyr	Asp	Arg	Phe	Val	Ala	Ile
	115					120						125			
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Val	Met	Asn	Pro	Cys	Phe	Cys	Gly
	130					135					140				
Phe	Leu	Val	Leu	Leu	Ser	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ala	Gln
145					150				155						160
Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	Glu
			165						170					175	
Ile	Pro	Asn	Phe	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys
		180						185					190		
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile
	195						200					205			

```

Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Glu Ile
 210                215                220
Val Ser Ser Ile Leu Arg Val Ser Ser Xaa Gly Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
                245                250                255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
                260                265                270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
                275                280                285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Thr Lys Ser Val Leu
                290                295                300
Arg Arg Pro His Gly Ser Thr Val Xaa Ser Xaa Tyr Leu Leu Ile Cys
305                310                315                320
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Arg Lys Val Lys
                325                330                335

```

&lt;210&gt; 1616

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g533 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1616

```

His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1                5                10                15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
                20                25                30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
                35                40                45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
                50                55                60
Ser Asn Leu Cys Trp Ala Asp Ile Ser Phe Thr Ser Ala Thr Val Pro
65                70                75                80
Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
                85                90                95
Gly Cys Leu Thr Arg Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu
                100                105                110
Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys
                115                120                125
Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe
130                135                140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
145                150                155                160
Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
                165                170                175
His Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
                180                185                190
Ser Phe Ile Asn Ser Ile Phe Met Tyr Phe Asp Ser Thr Met Phe Gly
195                200                205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
210                215                220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
225                230                235                240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly

```

<400> 1617															
Ile	Ser	Leu	Leu	Phe	Trp	Val	Leu	Leu	Leu	Val	Ile	Ser	Arg	Val	Leu
1				5					10					15	
Val	Ala	Met	Ala	Xaa	Gly	Asn	Ser	Thr	Glu	Val	Thr	Glu	Phe	Cys	Leu
			20					25					30		
Leu	Gly	Phe	Gly	Ala	Xaa	Gln	Glu	Phe	Trp	Cys	Ile	Leu	Phe	Ile	Ile
		35					40					45			
Phe	Leu	Leu	Ile	Tyr	Val	Thr	Ser	Ile	Met	Gly	Asn	Ser	Gly	Ile	Ile
	50					55					60				
Leu	Leu	Ile	Asn	Thr	Asp	Ser	Arg	Phe	Gln	Thr	Pro	Met	Tyr	Phe	Phe
65					70					75					80
Leu	Gln	His	Leu	Ala	Phe	Val	Asp	Ile	Cys	Tyr	Thr	Ser	Ala	Ile	Thr
				85					90					95	
Pro	Lys	Met	Leu	Gln	Ser	Phe	Thr	Glu	Glu	Lys	Asn	Leu	Ile	Ser	Phe
			100					105					110		
Trp	Gly	Cys	Met	Ile	Gln	Leu	Leu	Val	Tyr	Ala	Thr	Phe	Ala	Thr	Ser
		115					120					125			
Asp	Cys	Tyr	Leu	Leu	Ala	Met	Ile	Ala	Val	Asp	His	Tyr	Val	Ala	Ile
	130					135					140				
Cys	Lys	Pro	Leu	His	Tyr	Thr	Val	Ile	Thr	Ser	Gln	Thr	Val	Cys	Ile
145					150					155					160
His	Leu	Val	Ala	Gly	Ser	Tyr	Ile	Met	Gly	Ser	Ile	Asn	Ala	Ser	Val
				165					170					175	
His	Thr	Gly	Phe	Ala	Phe	Ser	Leu	Ser	Phe	Cys	Lys	Ser	Asn	Asn	Ile
			180					185					190		
Asn	His	Phe	Phe	Cys	Asp	Gly	Pro	Pro	Ile	Leu	Ala	Leu	Ser	Cys	Ser
		195					200					205			
Asn	Ile	Asp	Ile	Asn	Ile	Met	Leu	Leu	Val	Val	Phe	Val	Gly	Phe	Asn
	210					215					220				
Leu	Met	Phe	Thr	Gly	Leu	Val	Val	Ile	Phe	Ser	Tyr	Ile	Tyr	Ile	Met
225				230						235					240
Ala	Thr	Ile	Leu	Lys	Met	Ser	Ser	Ser	Ala	Gly	Arg	Lys	Lys	Ser	Phe
				245					250					255	
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Thr	Val	Ala	Ile	Phe	Tyr	Gly	Thr
			260					265					270		
Leu	Ser	Tyr	Met	His	Leu	Gln	Ser	His	Ser	Asn	Asn	Ser	Gln	Glu	Asn
		275					280					285			
Met	Lys	Val	Ala	Ser	Ile	Phe	Tyr	Gly	Thr	Val	Ile	Pro	Met	Leu	Asn
	290					295					300				

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys  
 305 310 315 320  
 Leu Ile Gly Lys Lys Phe Phe  
 325

<210> 1618

<211> 309

<212> PRT

<213> Unknown (H38g535 protein)

<220>

<223> Synthetic construct

<400> 1618

Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly  
 1 5 10 15  
 Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu  
 20 25 30  
 Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu  
 35 40 45  
 Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln  
 50 55 60  
 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Met Leu Phe Gln Gly  
 85 90 95  
 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys  
 100 105 110  
 Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu  
 130 135 140  
 Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr  
 145 150 155 160  
 Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val  
 180 185 190  
 Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile  
 195 200 205  
 Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr  
 210 215 220  
 Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser  
 245 250 255  
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys  
 260 265 270  
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Val Ile  
 290 295 300  
 Gly Lys Lys Leu Phe  
 305

<210> 1619

<211> 298

<212> PRT

<213> Unknown (H38g536 protein)

<220>

&lt;223&gt; Synthetic construct

&lt;400&gt; 1619

```

Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly
 1           5           10           15
Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu
 20           25           30
Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu
 35           40           45
Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln
 50           55           60
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65           70           75           80
Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly
 85           90           95
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
 100          105          110
Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys
 115          120          125
Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu
 130          135          140
Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr
 145          150          155          160
Gly Phe Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Lys Ile Asn His
 165          170          175
Phe Phe Cys Asp Gly Leu Pro Ile Leu Ala Leu Ser Cys Ser Asn Ile
 180          185          190
Asp Ile Asn Ile Ile Leu Asp Val Val Phe Val Gly Phe Asp Leu Met
 195          200          205
Phe Thr Glu Leu Val Ile Ile Phe Ser Tyr Ile Tyr Ile Met Val Thr
 210          215          220
Ile Leu Lys Met Ser Ser Thr Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225          230          235          240
Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245          250          255
Tyr Met Tyr Leu Gln Pro Gln Ser Asn Asn Ser Gln Glu Asn Met Lys
 260          265          270
Val Ala Ser Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Gly Lys
 290          295

```

&lt;210&gt; 1620

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g537 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(148)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1620

```

Thr Tyr Asp Gly Ala Arg Ala Gly Leu Cys Ile Val Ser Tyr Asn Thr
 1           5           10           15
Cys Lys Ser Thr Met Met Ser Ile Lys Ile Gln Leu Lys Tyr Met Xaa
 20           25           30
Xaa Lys Xaa Leu Leu Ile Tyr Ala Gly Val Tyr Leu Asn Val Thr Met
 35           40           45

```



Leu Ile Val Thr Phe Lys Tyr Thr His Ile Phe His His Pro Glu Leu  
 50 55 60  
 Ala Leu Cys Tyr Val Ser Phe Ser Ala Val Val Phe His Leu Thr Ala  
 65 70 75 80  
 Val Thr Ile Phe Phe Gly Ala Leu Ser Tyr Met Asp Leu Gln Pro Glu  
 85 90 95  
 Ser Thr Val Phe Gln Glu Gln Glu Lys Pro Ala Ser Ile Phe Cys Gly  
 100 105 110  
 Ile Met Thr Leu Val Leu Asn Phe Leu Ile Tyr Cys Leu Xaa Asn Xaa  
 115 120 125  
 Glu Val Lys Glu Ala Leu Gln Leu Thr Arg Lys Lys Tyr Xaa Tyr Met  
 130 135 140  
 Xaa Thr Glu Gly  
 145

<210> 1621

<211> 296

<212> PRT

<213> Unknown (H38g538 protein)

<220>

<223> Synthetic construct

<400> 1621

Met Leu Val Ser Gln Gln Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu  
 1 5 10 15  
 Gly Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala  
 20 25 30  
 Ile Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 35 40 45  
 Asn Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys  
 50 55 60  
 Met Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly  
 65 70 75 80  
 Cys Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn  
 85 90 95  
 Cys Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln  
 100 105 110  
 Pro Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met  
 115 120 125  
 Leu Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr  
 130 135 140  
 Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His  
 145 150 155 160  
 Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 165 170 175  
 His Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr  
 180 185 190  
 Val Pro Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala  
 195 200 205  
 Val Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr  
 210 215 220  
 Cys Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met  
 225 230 235 240  
 Gly Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser  
 245 250 255  
 Arg Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe  
 260 265 270  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu  
 275 280 285  
 Phe Val Ser Gly Lys Thr Phe Phe

290

295

<210> 1622  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g539 protein)

<220>  
 <223> Synthetic construct

<400> 1622  
 Met Lys Arg Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Asp  
 1 5 10 15  
 Leu Pro Ile Trp Pro Glu Gln Gln Ala Val Phe Phe Thr Leu Phe Leu  
 20 25 30  
 Gly Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Phe Phe Phe Leu Ser  
 50 55 60  
 His Leu Ala Leu Thr Asp Ile Ser Leu Ser Ser Val Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Leu Ser Met Gln Thr Gln Asp Gln Ser Ile Leu Tyr Ala Gly  
 85 90 95  
 Cys Val Thr Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Asn  
 100 105 110  
 Phe Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Thr Thr Ile Met Lys Glu Gly Leu Cys Asn Leu Leu  
 130 135 140  
 Val Thr Val Ser Trp Ile Leu Ser Cys Thr Asn Ala Leu Ser His Thr  
 145 150 155 160  
 Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Leu Val Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile  
 180 185 190  
 Ser Leu Asn Glu Leu Val Ile Phe Thr Val Gly Gln Ala Val Ile Thr  
 195 200 205  
 Leu Pro Leu Ile Cys Ile Leu Ile Ser Tyr Gly His Ile Gly Val Thr  
 210 215 220  
 Ile Leu Lys Ala Pro Ser Thr Lys Gly Ile Phe Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Thr Ile Ile  
 245 250 255  
 Gly Leu Tyr Phe Leu Pro Ser Ser Ser Ala Ser Ser Asp Lys Asp Val  
 260 265 270  
 Ile Ala Ser Val Met Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Leu Glu Arg Leu  
 290 295 300  
 Phe Asn Arg Ala Thr Val Leu Ser Gln  
 305 310

<210> 1623  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g540 protein)

<220>  
 <223> Synthetic construct

<400> 1623

```

Met Glu Asn Gln Ser Ser Ile Ser Glu Phe Phe Leu Arg Gly Ile Ser
 1          5          10          15
Ala Pro Pro Glu Gln Gln Gln Ser Leu Phe Gly Ile Phe Leu Cys Met
          20          25          30
Tyr Leu Val Thr Leu Thr Gly Asn Leu Leu Ile Ile Leu Ala Ile Gly
          35          40          45
Ser Asp Leu His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu
          50          55          60
Ser Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu
          65          70          75          80
Val Asn Ile Gln Thr Arg His His Thr Ile Ser Tyr Thr Gly Cys Leu
          85          90          95
Thr Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe
          100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
          115          120          125
Cys Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala
          130          135          140
Leu Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu
          145          150          155          160
Met Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe
          165          170          175
Cys Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile
          180          185          190
Asn Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro
          195          200          205
Phe Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu
          210          215          220
Arg Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser
          225          230          235          240
Ser His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala
          245          250          255
Tyr Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala
          260          265          270
Ala Ala Met Tyr Thr Ile Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Lys Arg Leu Phe Ser
          290          295          300
His Arg Ser Ile Val Ser Ser
          305          310

```

&lt;210&gt; 1624

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g541 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1624

```

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Val Gly Pro Ala Leu Ala Ile Leu Leu Cys Gly Leu Phe Ser Val
          20          25          30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
          35          40          45
Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His

```

```

      50              55              60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
65              70              75              80
Leu Ala Asn Leu Met Asn Gln Lys Ser Thr Ile Ser Phe Val Pro Cys
      85              90              95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu
      100              105              110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115              120              125
Phe Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Ala
      130              135              140
Ser Thr Cys Trp Ile Ile Ser Phe Leu Met Ala Leu Val His Ile Thr
145              150              155              160
His Ile Leu Arg Pro Pro Phe Cys Gly Pro Gln Lys Ile Asn His Phe
      165              170              175
Ile Cys Gln Ile Met Ser Val Phe Lys Leu Ala Cys Ala Gly Pro Arg
      180              185              190
Leu Asn Gln Val Val Leu Tyr Ala Gly Ser Ala Phe Ile Val Glu Gly
      195              200              205
Pro Leu Cys Leu Glu Leu Val Ser Asn Leu His Ile Leu Ser Ala Ile
      210              215              220
Leu Arg Ile Gln Asn Gly Glu Gly Arg Arg Pro Thr Tyr Ser Ser Cys
225              230              235              240
Ser Ser His Leu Cys Met Val Gly Leu Leu Phe Gly Ser Thr Met Val
      245              250              255
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val
      260              265              270
Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275              280              285
Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys Arg Val Leu
      290              295              300
Trp Lys Gln Arg Ser Lys Xaa Gly Met Pro
305              310

```

&lt;210&gt; 1625

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g542 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(193)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1625

```

Leu Lys Val Tyr Xaa Lys Ala Ile Xaa Val Gln Lys Gln Gly Lys Phe
1      5      10      15
Phe Val Ile Ile Phe Cys Xaa Xaa Cys Glu Met Xaa Gly Lys Asn Ile
      20      25      30
Gln Leu Xaa Gly Cys Leu Thr Val Leu Leu Glu Thr Ser Phe Ala Leu
      35      40      45
Gln Arg Pro Leu Cys Gly Asn Leu Ile Asp Asp Thr Cys Glu Ile Leu
      50      55      60
Glu Val Leu Lys Leu Val Cys Ser Ser Ser Leu Leu Met Asp Met Ile
65              70              75              80
Met Met Val Val Asn Ile Leu Leu Leu Pro Ile Pro Met Tyr Leu Phe
      85              90              95
Ile Thr Met Cys Ser Val Ile Leu Phe Leu Lys Arg Ser Tyr Gly Asn
      100              105              110

```

Leu Pro Arg Glu Phe Ser Phe Cys Ile Ser Trp Ser Ile Trp Val Phe  
           115                  120                  125  
 Val Tyr Cys Leu Ala Ile Ile Phe Arg Ala Leu Tyr Lys Leu Thr Lys  
           130                  135                  140  
 Ile Trp Gly Ser Thr Met Asn Glu Ile Val Arg Trp Met Tyr Xaa Tyr  
 145                  150                  155                  160  
 Xaa Thr Tyr Xaa Tyr Xaa Ile Val Xaa His Lys Leu Ala Leu Lys Tyr  
                   165                  170                  175  
 Asn His Lys Leu Val Ser Thr Met Leu Gln Ala Leu Leu Ser Phe Leu  
                   180                  185                  190  
 Lys

<210> 1626

<211> 314

<212> PRT

<213> Unknown (H38g543 protein)

<220>

<223> Synthetic construct

<400> 1626

Met Ala Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly  
 1                  5                  10                  15  
 Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe  
                   20                  25                  30  
 Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu  
                   35                  40                  45  
 Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly  
 50                  55                  60  
 Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys  
 65                  70                  75                  80  
 Met Leu Glu Asn Phe Phe Ser Glu Asn Lys Arg Ile Ser Leu Tyr Glu  
                   85                  90                  95  
 Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys  
                   100                  105                  110  
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
                   115                  120                  125  
 Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met  
                   130                  135                  140  
 Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val  
 145                  150                  155                  160  
 Gly Leu Val Phe Arg Leu Val Phe Cys Gly Ser Asn His Ile Asn His  
                   165                  170                  175  
 Phe Tyr Cys Asp Ile Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro  
                   180                  185                  190  
 Tyr Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val  
                   195                  200                  205  
 Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr  
                   210                  215                  220  
 Ile Phe Lys Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr  
 225                  230                  235                  240  
 Cys Ala Ser His Phe Leu Ser Val Ser Leu Phe Tyr Gly Ser Leu Phe  
                   245                  250                  255  
 Phe Met Tyr Val Arg Pro Asn Leu Leu Glu Glu Gly Asp Lys Asp Ile  
                   260                  265                  270  
 Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe  
                   275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Arg Glu Val Ile Ser Val Leu Arg Lys Ile  
                   290                  295                  300  
 Leu Met Lys Glu Ile Ile Ser Arg Arg Trp

305

310

&lt;210&gt; 1627

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g544 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1627

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1          5          10          15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
 20          25          30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
 35          40          45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
 50          55          60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
 65          70          75          80
Leu Leu Val Asn Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
 85          90          95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
 100         105         110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115         120         125
Pro Leu Arg Tyr Ser Ile Ile Met Asn Arg Cys Val Cys Ala Arg Met
 130         135         140
Ala Thr Val Ser Trp Val Thr Gly Cys Leu Thr Ala Leu Leu Glu Thr
 145         150         155         160
Ser Phe Ala Leu Gln Ile Pro Leu Cys Gly Asn Leu Ile Asp His Phe
 165         170         175
Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Thr Ser Ser Leu
 180         185         190
Leu Met Asn Thr Ile Met Leu Val Val Ser Ile Leu Leu Leu Pro Ile
 195         200         205
Pro Met Leu Leu Val Cys Ile Ser Tyr Ile Phe Ile Leu Ser Thr Ile
 210         215         220
Leu Arg Ile Thr Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser Thr Cys
 225         230         235         240
Gly Ala His Leu Thr Val Val Ile Leu Tyr Tyr Gly Ala Ala Leu Ser
 245         250         255
Met Tyr Leu Lys Pro Ser Ser Ser Asn Ala Gln Lys Ile Asp Lys Ile
 260         265         270
Ile Ser Leu Leu Tyr Gly Val Leu Thr Pro Met Leu Asn Pro Ile Ile
 275         280         285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Met Lys Lys Leu Leu
 290         295         300
Gly Lys Ile Thr Leu His Gln Thr His Glu His Leu
305          310          315

```

&lt;210&gt; 1628

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g545 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1628

Met Met Gly Arg Arg Asn Asn Thr Asn Val Ala Asp Phe Ile Leu Met  
 1 5 10 15  
 Gly Leu Thr Leu Ser Glu Glu Ile Gln Met Ala Leu Phe Met Leu Phe  
 20 25 30  
 Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu  
 35 40 45  
 Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro  
 65 70 75 80  
 Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly  
 85 90 95  
 Cys Phe Ala Gln Met Phe Phe Phe Ala Phe Leu Gly Thr Ala Glu Cys  
 100 105 110  
 Tyr Leu Leu Ser Ser Met Ala His Asp Arg Tyr Ala Ala Ile Cys Ser  
 115 120 125  
 Pro Leu His Tyr Thr Val Ile Met Ser Lys Arg Leu Cys Leu Ala Leu  
 130 135 140  
 Ile Thr Gly Pro Tyr Val Ile Gly Phe Ile Asp Ser Phe Val Asn Val  
 145 150 155 160  
 Val Ser Met Ser Arg Leu His Phe Tyr Asp Ser Asn Val Ile His His  
 165 170 175  
 Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr  
 180 185 190  
 Tyr Asn Thr Glu Ile Leu Ile Phe Ile Ile Val Gly Ser Thr Leu Met  
 195 200 205  
 Val Ser Leu Phe Thr Ile Ser Ala Ser Tyr Val Phe Ile Leu Phe Thr  
 210 215 220  
 Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Ser Thr Leu Ile  
 245 250 255  
 Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln  
 260 265 270  
 Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Val Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Val Ile Arg Val  
 290 295 300  
 Met Gln Arg Arg Gln Asp Ser Arg  
 305 310

&lt;210&gt; 1629

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g546 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1629

Thr Met Phe Tyr Lys Ile Ser Ala Leu Phe Xaa Cys Leu Cys Ile Thr  
 1 5 10 15  
 Leu Phe Xaa Xaa Lys Leu Ser Lys Gln Lys Ile Tyr Trp Val Leu Thr  
 20 25 30  
 Ile Phe Gly Phe Leu Glu Ala Phe Ile Ala Met Asn Lys Leu Xaa Lys  
 35 40 45  
 Leu Tyr Ser Ser Leu Ile Cys Leu Tyr Phe Ile Ile Xaa Ile Phe Lys

```

      50              55              60
Phe Ser Asn Met Phe Ile Phe Tyr Asn Met Asn Ile Ser Val His Tyr
65              70              75              80
Phe Leu Lys Cys Ile Phe Phe Phe Cys Ile Cys Cys Leu Xaa Leu Leu
      85              90              95
Ile Phe Asp Ser Phe Ser Thr His Pro Pro Leu Pro Leu Leu Xaa Glu
      100              105              110
Ala Asp Ile Cys Ala Asn Ser Xaa Pro Cys Tyr Thr Asn Thr Thr Ala
      115              120              125
Ser Xaa Xaa His Phe Tyr Ile Ile Leu Asn Phe Cys Leu Ser Tyr Xaa
      130              135              140
Pro Ser Val Ser Ser Met Leu Tyr Gly Arg Leu Phe Leu Met Tyr Leu
145              150              155              160
Met Pro Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe Tyr
      165              170              175
Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Trp Ser Pro Arg Asn
      180              185              190
Lys Asp Val Thr Ser Ala Leu Arg Lys Val Met Val Asn Arg Lys Gln
      195              200              205
Ala Leu Phe Cys
210

```

&lt;210&gt; 1630

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g547 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(228)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1630

```

Cys Met Phe Ser Phe Tyr Phe Asn Phe Tyr His Phe Phe Ser Thr Xaa
1              5              10              15
Lys Val Leu Gln Ser Leu Arg Asn Ala Glu Ile Asn Xaa Leu Val Xaa
      20              25              30
Ser Lys Val Ser Asp Xaa Xaa Asn Leu Leu Xaa Asn Xaa Leu Ala Phe
      35              40              45
Ser Trp Thr Ile Arg Leu Cys Thr Thr Thr Ser Tyr Ser Asn Met Gln
      50              55              60
Phe Ser Phe Gln Cys Cys Met Thr Gln Tyr Pro Ala Leu Gln Ser Thr
65              70              75              80
Phe Phe Phe Leu Gly Arg Ser Gln Val Phe Leu Leu Leu Leu Met Ala
      85              90              95
Tyr Asp Asn Tyr Arg Ala Ile Xaa Lys Ser Leu Gln Tyr Leu Val Val
      100              105              110
Met Lys Gln Trp Leu Cys Val Val Leu Leu Val Val Pro Trp Ala Gly
      115              120              125
Gly Phe Leu His Thr Val Ile Gln Leu Gly Leu Ile His Gly Leu Pro
      130              135              140
Ser Tyr Asp Pro Asn Val Ile Gly Arg Phe Val Cys Asp Met Asp Pro
145              150              155              160
Leu Met Lys Leu Val Cys Asp Tyr Thr Leu Asn Arg Phe Val Tyr Phe
      165              170              175
Ala Gly His Asp Leu Asn Tyr Xaa Val Leu Tyr Ile Ser Phe Ile Phe
      180              185              190
Arg Leu Asp Cys Phe Leu Leu Val Ile Xaa L u Trp Tyr Pro Phe Val
195              200              205

```



Ile Phe Ser Leu Glu Arg His Asp Ser Ile Asn Leu Val Ile His Ser  
 210 215 220  
 Tyr Tyr Pro Cys  
 225

<210> 1631

<211> 299

<212> PRT

<213> Unknown (H38g548 protein)

<220>

<223> Synthetic construct

<400> 1631

Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr  
 1 5 10 15  
 Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe  
 20 25 30  
 Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr  
 35 40 45  
 Val Ser Glu Thr Leu Gly Ser Pro Met Ser Phe Phe Leu Ala Gly Leu  
 50 55 60  
 Thr Phe Ile Asp Ile Ile Tyr Ser Ser Ser Ile Ser Pro Arg Leu Ile  
 65 70 75 80  
 Ser Asp Leu Phe Phe Gly Asn Asn Ser Ile Ser Phe Gln Ser Phe Met  
 85 90 95  
 Ala Gln Leu Phe Ile Glu His Leu Phe Gly Gly Ser Glu Val Phe Leu  
 100 105 110  
 Leu Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Leu Val  
 130 135 140  
 Val Ser Trp Val Gly Gly Phe Leu Gln Ser Val Phe Gln Leu Ser Ile  
 145 150 155 160  
 Ile Tyr Gly Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe  
 165 170 175  
 Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr His Val  
 180 185 190  
 Ile Gly Leu Leu Val Val Ala Asn Gly Gly Leu Ser Cys Thr Ile Ala  
 195 200 205  
 Phe Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys  
 210 215 220  
 Lys Leu Ser Gln Lys Gly Arg Gln Lys Ala His Ser Thr Cys Ser Ser  
 225 230 235 240  
 His Ile Thr Val Val Val Phe Phe Phe Val Pro Cys Ile Phe Met Cys  
 245 250 255  
 Ala Arg Pro Ala Arg Thr Phe Ser Ile Asp Lys Ser Val Ser Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ser Glu Met Thr Ser Ala Met Lys Lys Leu  
 290 295

<210> 1632

<211> 315

<212> PRT

<213> Unknown (H38g549 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1632

```

Met Ser Pro Asp Gly Asn His Ser Ser Asp Pro Thr Glu Phe Val Leu
 1          5          10          15
Ala Gly Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val
          20          25          30
Phe Leu Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val
          35          40          45
Gly Val Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Gly Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile
65          70          75          80
Pro Lys Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe
          85          90          95
Ala Ala Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser
          100          105          110
Glu Phe Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe
          130          135          140
Arg Val Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly
145          150          155          160
Pro Thr Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val
          165          170          175
Val Gln His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu
          195          200          205
Val Ile Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile
          210          215          220
Val Leu Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala
225          230          235          240
Phe Ser Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly
          245          250          255
Ser Ala Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp
          260          265          270
Thr Asn Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu
          275          280          285
Asn Pro Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu
          290          295          300
Lys Asp Met Phe Arg Lys Val Val Ala Gly Val
305          310          315

```

&lt;210&gt; 1633

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g550 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(260)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1633

```

Val Leu Cys Val Ile Phe Cys Lys Xaa Asn His His Ile Ser Leu Leu
 1          5          10          15
Ser Phe Phe Glu Tyr Leu Met Thr Xaa Xaa Lys Lys Tyr Gly Ser Ile
          20          25          30
Cys Ser Thr Met Leu Val Ser Ile Arg Ile Lys Tyr Leu Glu Val Phe
          35          40          45

```

Ala Glu Asn Leu Phe Gly Ala Ala Glu Ile Ile Pro Leu Met Trp Met  
 50 55 60  
 Val His Gly Cys Tyr Val Thr Val Cys Asn Tyr Met Thr Ile Val Asn  
 65 70 75 80  
 Gln Tyr Arg Cys Ser His Leu Thr Gly Met Ala Trp Thr Glu Ser Phe  
 85 90 95  
 Ile His Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr  
 100 105 110  
 Asp Pro Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Phe Leu  
 115 120 125  
 Lys Leu Leu Cys Met Gly Thr Thr Asn Thr Ile Gly Phe Phe Val Ala  
 130 135 140  
 Ala Asn Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val  
 145 150 155 160  
 Ser Xaa Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu  
 165 170 175  
 Arg Cys Xaa Ser Leu Ser Thr Cys Ile Ser His Thr Thr Met Val Ile  
 180 185 190  
 Leu Phe Phe Glu Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu  
 195 200 205  
 Leu Pro Ile Asn Lys Ala Met Ala Val Phe His Thr Val Ile Asn Pro  
 210 215 220  
 Met Leu Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser  
 225 230 235 240  
 Ala Leu Arg Lys Val Trp Val Lys Arg Xaa Pro Glu Glu Arg Asn Asn  
 245 250 255  
 Leu Asn Ile Arg  
 260

&lt;210&gt; 1634

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g551 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1634

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly  
 1 5 10 15  
 Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe  
 20 25 30  
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile  
 35 40 45  
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser  
 65 70 75 80  
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly  
 85 90 95  
 Cys Ala Val Gln Met Phe Leu Ser Leu Ala Met Gly Thr Thr Glu Cys  
 100 105 110  
 Val Leu Leu Gly Val Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met  
 130 135 140  
 Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Thr  
 145 150 155 160  
 Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His  
 165 170 175  
 Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile

<210> 1635  
<211> 333  
<212> PRT  
<213> Unknown (H38g552 protein)

```
<221> VARIANT
<222> (1)...(333)
<223> Xaa = Any Amino Acid
```

886

```

Ser Ala His Met Thr Val Val Ile Val Phe Tyr Gly Thr Ile Leu Phe
                245                250                255
Met Tyr Met Lys Ala Lys Ser Lys Asp Ser Ala Phe Asp Lys Leu Ile
                260                265                270
Ala Leu Phe Tyr Gly Ile Val Thr Pro Met Leu Asn Pro Ile Ile Tyr
                275                280                285
Ser Leu Arg Asn Thr Glu Val His Gly Ala Met Arg Lys Leu Met Ser
                290                295                300
Arg His Leu Val Leu Glu Glu Met Met Thr His Xaa His Leu Xaa Val
305                310                315                320
Tyr Ala Gln Asn Thr Leu Thr Ser Leu Arg Gln His Phe
                325                330

```

&lt;210&gt; 1636

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g553 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1636

```

His Thr Glu Pro Trp Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
1                5                10                15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
                20                25                30
Leu Ser Leu Ser Met Cys Leu Val Met Val Leu Arg Asn Leu Leu Ser
35                40                45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Val Tyr Phe
50                55                60
Phe Leu Ser Lys Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr
65                70                75                80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
85                90                95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Ile Leu Phe Ala Cys
100               105               110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
115               120               125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
130               135               140
Val Ser Phe Leu Leu Val Ser Phe Phe Leu Ser Met Leu Asp Ser Gln
145               150               155               160
Leu His Ser Xaa Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
165               170               175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
180               185               190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asn Ser Thr Met
195               200               205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Cys Lys Ile
210               215               220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225               230               235               240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Arg
245               250               255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
260               265               270
Asn Gly Val Val Ala Ser Ala Met Phe Ser Val Val Thr Pro Met Leu

```

275                      280                      285  
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu  
 290                      295                      300  
 Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Tyr Asp Leu Phe His Pro  
 305                      310                      315                      320  
 Phe Ser

&lt;210&gt; 1637

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g554 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1637

Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly  
 1                      5                      10                      15  
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu  
 20                      25                      30  
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu  
 35                      40                      45  
 Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg  
 50                      55                      60  
 Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg  
 65                      70                      75                      80  
 Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln  
 85                      90                      95  
 Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu  
 100                      105                      110  
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115                      120                      125  
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala  
 130                      135                      140  
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His  
 145                      150                      155                      160  
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro  
 165                      170                      175  
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly  
 180                      185                      190  
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile  
 195                      200                      205  
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly  
 210                      215                      220  
 Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser  
 225                      230                      235                      240  
 Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala  
 245                      250                      255  
 Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp  
 260                      265                      270  
 Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro  
 275                      280                      285  
 Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His  
 290                      295                      300  
 Leu Val Lys Arg Gln Arg Pro Ser  
 305                      310

&lt;210&gt; 1638

&lt;211&gt; 310

&lt;212&gt; PRT

<213> Unknown (H38g555 protein)

<220>

<223> Synthetic construct

<400> 1638

```

Met Ala Gly Asn Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1           5           10          15
Phe Ala Asn His Pro Glu Leu Gln Val Ser Leu Phe Leu Met Phe Leu
          20          25          30
Phe Ile Tyr Leu Phe Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
          35          40          45
Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys
65          70          75          80
Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly
          85          90          95
Cys Phe Val Gln Met Tyr Phe Phe Val Gly Leu Val Cys Cys Glu Cys
          100         105         110
Phe Leu Leu Gly Ser Met Ala Tyr Asn Arg Tyr Ile Ala Ile Cys Asn
          115         120         125
Pro Leu Leu Tyr Ser Val Val Met Ser Gln Lys Val Ser Asn Trp Leu
          130         135         140
Gly Val Met Pro Tyr Val Ile Gly Phe Thr Ser Ser Leu Ile Ser Val
145         150         155         160
Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His Phe
          165         170         175
Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr Phe
          180         185         190
Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu Ser
          195         200         205
Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ser Ala Ile
          210         215         220
Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys
225         230         235         240
Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile Phe
          245         250         255
Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln Val
          260         265         270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
          275         280         285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile
          290         295         300
His Arg Lys Leu Phe Pro
305          310

```

<210> 1639

<211> 157

<212> PRT

<213> Unknown (H38g556 protein)

<220>

<223> Synthetic construct

<400> 1639

```

Ile Cys Ser Pro Leu Leu Tyr Ser Val Ile Ile Ser Asn Lys Ala Cys
 1           5           10          15
Phe Ser Leu Ile Leu Gly Val Tyr Ile Ile Gly Leu Val Cys Ala Ser
          20          25          30
Val His Thr Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Leu

```

```

      35      40      45
Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Leu Leu Lys Leu Ser Cys
  50      55      60
Ser Ser Ile Tyr Val Asn Lys Leu Leu Ile Leu Cys Val Gly Ala Phe
  65      70      75      80
Asn Ile Leu Val Pro Ser Leu Thr Ile Leu Cys Ser Tyr Ile Phe Ile
      85      90      95
Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser Lys Ala
      100      105      110
Phe Ser Thr Cys Ser Ser His Met Leu Ala Val Val Ile Phe Phe Gly
      115      120      125
Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Ile Ser Ser Met Asp
      130      135      140
Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Ile Ile Val
  145      150      155

```

&lt;210&gt; 1640

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g557' protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(178)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1640

```

Leu Ala Pro Ser Ser Ser Leu Ala Leu Gly Thr Trp Arg Trp Gln Trp
  1      5      10      15
His Ser Met Thr Glu Leu Val Leu Leu Val Leu Ser Gly Phe Gly Ser
      20      25      30
Val Arg Gly Leu Leu Phe Trp Ala Val Leu Cys Lys His Leu Val Thr
      35      40      45
Leu Leu Asp Asn Ser Leu Ile Val Val Leu Ala Leu Val Ser Leu Cys
      50      55      60
Leu Arg Trp Pro Thr His Phe Leu Leu His His Phe Ser Leu Gly Glu
      65      70      75      80
Val Pro Arg His Ser Gly Gly Val Ser Asp Ala Gly Arg Phe Pro Ser
      85      90      95
Pro Ala Ala Leu Ala His Arg Xaa Ala Ala Ser Arg Cys Trp Val Phe
      100      105      110
Phe Ala Leu Pro Gly Ile Ala Glu Cys Cys Leu Arg Arg Ala Met Ala
      115      120      125
Tyr Arg Arg Cys Asp Ala Ile Cys Arg Pro Leu His Ser Thr Thr Xaa
      130      135      140
Gly Ala Leu Val Phe Arg Ala Arg Phe Ala Phe Thr Leu Pro Phe Cys
      145      150      155      160
Gly Ala Ala Arg Thr Arg Tyr Phe Arg Leu Asp Ser Arg Pro Val Leu
      165      170      175
Arg Pro

```

&lt;210&gt; 1641

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g558 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct



&lt;400&gt; 1641

```

Met Thr Arg Lys Asn Tyr Thr Ser Leu Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ala Asp Thr Leu Glu Leu Gln Ile Ile Leu Phe Leu Phe Phe Leu
 20          25          30
Val Ile Tyr Thr Leu Thr Val Leu Gly Asn Leu Gly Met Ile Leu Leu
 35          40          45
Ile Arg Ile Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Phe Val Asp Val Cys Asn Ser Thr Thr Ile Thr Pro Lys
 65          70          75          80
Met Leu Ala Asp Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
 85          90          95
Cys Phe Leu Gln Met Tyr Phe Phe Ile Ser Leu Ala Thr Thr Glu Cys
100          105          110
Ile Leu Phe Gly Leu Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
115          120          125
Pro Leu Leu Tyr Ser Leu Ile Met Ser Arg Thr Val Tyr Leu Lys Met
130          135          140
Ala Ala Gly Ala Phe Ala Ala Gly Leu Leu Asn Phe Met Val Asn Thr
145          150          155          160
Ser His Val Ser Ser Leu Ser Phe Cys Asp Ser Asn Val Ile His His
165          170          175
Phe Phe Cys Asp Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr
180          185          190
Ile Leu Lys Glu Ser Ile Ser Ser Ile Leu Ala Gly Val Asn Ile Val
195          200          205
Gly Thr Leu Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser
210          215          220
Ile Phe Ser Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Thr Ala Ile Ile Leu Phe Tyr Ala Thr Cys Ile
245          250          255
Tyr Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys
260          265          270
Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Ser Leu Arg Ser Lys Glu Val Lys Lys Ala Leu Ala Asn Val
290          295          300
Ile Ser Arg Lys Arg Thr Ser Ser Phe Leu
305          310

```

&lt;210&gt; 1642

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g559 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1642

```

Met Thr Arg Lys Asn Tyr Thr Ser Leu Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ala Asp Thr Leu Glu Leu Gln Ile Ile Leu Phe Leu Leu Phe Leu
 20          25          30
Val Ile Tyr Thr Leu Thr Val Leu Gly Asn Ile Gly Met Ile Leu Leu
 35          40          45
Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Val
 50          55          60
Asn Leu Ser Phe Val Asp Ile Cys Tyr Ser Thr Thr Ile Thr Pro Lys

```

```

65              70              75              80
Met Leu Ala Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
              85              90              95
Cys Phe Leu Gln Met Tyr Phe Phe Ile Ala Leu Ala Thr Thr Glu Cys
              100             105             110
Ile Leu Phe Gly Leu Met Ala Tyr Asp Arg Tyr Val Thr Ile Cys Arg
              115             120             125
Pro Leu Leu Tyr Ser Leu Ile Met Ser Arg Thr Val Cys Leu Lys Met
              130             135             140
Ala Ala Gly Ala Phe Ala Ala Gly Leu Leu Asn Ser Met Val Asn Thr
145              150             155             160
Ser Tyr Val Ser Ser Leu Ser Phe Cys Gly Ser Asn Val Ile His His
              165             170             175
Phe Phe Cys Asn Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr
              180             185             190
His Leu Lys Glu Ser Ile Phe Ser Thr Phe Ala Gly Val Asn Lys Val
              195             200             205
Gly Ala Leu Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser
              210             215             220
Ile Phe Ser Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr
225              230             235             240
Cys Ala Ser His Leu Thr Ala Ile Ile Leu Phe Tyr Thr Thr Ser Ile
              245             250             255
Tyr Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys
              260             265             270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Leu
              275             280             285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Ala Asn Val
290              295             300
Ile Ser Arg Lys Arg Ile Pro Ser Phe Leu
305              310

```

&lt;210&gt; 1643

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g560 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1643

```

Met Ser Gly Glu Asn Val Thr Lys Val Ser Thr Phe Ile Leu Val Gly
1              5              10              15
Leu Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu
              20              25              30
Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Ile
              35              40              45
Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser
50              55              60
Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys
65              70              75              80
Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly
              85              90              95
Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys
              100             105             110
Val Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115              120             125

```

Pro Leu Arg Tyr His Val Leu Val Thr Ala Gly Leu Cys Val Gln Leu  
 130 135 140  
 Val Gly Phe Ser Phe Val Ser Gly Phe Ser Ile Ser Met Ile Lys Val  
 145 150 155 160  
 Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe  
 180 185 190  
 Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val  
 195 200 205  
 Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala  
 210 215 220  
 Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu  
 245 250 255  
 Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys  
 260 265 270  
 Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu  
 275 280 285  
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala  
 290 295 300  
 Leu Gly Leu Gly Gln Thr Ser His Xaa Asp  
 305 310

&lt;210&gt; 1644

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g561 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1644

Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu Val  
 1 5 10 15  
 His Leu Leu Ser Arg Lys Lys Val Ile Val Phe Thr Leu Cys Ala Ala  
 20 25 30  
 Arg Leu Leu Phe Leu Leu Ile Gly Gly Cys Thr Gln Cys Ala Leu Leu  
 35 40 45  
 Gly Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg  
 50 55 60  
 Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr Ala  
 65 70 75 80  
 Pro Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe Thr  
 85 90 95  
 Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Trp Cys  
 100 105 110  
 Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala Ser  
 115 120 125  
 Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro Val  
 130 135 140  
 Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val Lys  
 145 150 155 160  
 Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr Tyr  
 180 185 190  
 Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val Phe  
 195 200 205  
 Tyr Pro Ile Val Thr Pro

210

&lt;210&gt; 1645

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g562 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1645

```

Met Leu Glu Ser Asn Tyr Thr Met Pro Thr Glu Phe Leu Phe Val Gly
 1           5           10           15
Phe Thr Asp Tyr Leu Pro Leu Arg Val Thr Leu Phe Leu Val Phe Leu
      20           25           30
Leu Val Tyr Thr Leu Thr Met Val Gly Asn Ile Leu Leu Ile Ile Leu
      35           40           45
Val Asn Ile Asn Ser Ser Leu Gln Ile Pro Met Tyr Tyr Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr Ala Ile Thr Pro Lys
      65           70           75           80
Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser Ile Ser Pro Tyr Gly
      85           90           95
Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe Ala Asp Ala Glu Cys
      100          105          110
Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
      115          120          125
Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg Val Cys Val Cys Phe
      130          135          140
Ile Val Leu Ala Tyr Phe Ser Gly Ser Thr Thr Ser Leu Val His Val
      145          150          155          160
Cys Leu Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Ile Val Asn His
      165          170          175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Thr Asp Thr
      180          185          190
Gln Ile Asn Gln Leu Leu Leu Phe Ala Leu Cys Ser Phe Ile Gln Thr
      195          200          205
Ser Thr Phe Val Val Ile Phe Ile Ser Tyr Phe Cys Ile Leu Ile Thr
      210          215          220
Val Leu Ser Ile Lys Ser Ser Gly Gly Arg Ser Lys Thr Phe Ser Thr
      225          230          235          240
Cys Ala Ser His Leu Ile Ala Val Thr Leu Phe Tyr Gly Ala Leu Leu
      245          250          255
Phe Met Tyr Leu Gln Pro Thr Thr Ser Tyr Ser Leu Asp Thr Asp Lys
      260          265          270
Val Val Ala Val Phe Tyr Thr Val Val Phe Pro Met Phe Asn Pro Ile
      275          280          285
Ile Tyr Ser Phe Arg Asn Lys Asp Val Lys Asn Ala Leu Lys Lys Leu
      290          295          300
Leu Glu Arg Ile Gly Tyr Ser Asn Glu Trp Tyr Leu
      305          310          315

```

&lt;210&gt; 1646

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g563 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1646

```

Met Ser Thr His Arg Met Glu Ile Ser Gln Cys Val Pro Leu Trp Glu
 1              5              10              15
Ser Met Leu Lys Gly Leu Glu Gly Gly Leu Glu Asn Gln Ala Leu Leu
      20              25              30
Phe Ala Val Phe Pro Gly Leu Tyr Met Val Thr Ile Pro Gly Asn Leu
      35              40              45
Thr Met Thr Met Val Ile Ile Leu Asp Thr His Leu His Phe Pro Val
      50              55              60
Asn Phe Phe Leu Gly Ala Ser Pro Phe Leu Asp Leu Gly His Ala Ser
65              70              75              80
Ile Ile Pro Asn Ala Leu Val Asn Phe Ser Ser Ser Ser Lys Val Val
      85              90              95
Thr Phe Ala Gly Cys Ala Ala Arg Phe Phe Phe Ser Leu Leu Ser Thr
      100             105             110
Thr Glu Thr Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Phe Val Ala
      115             120             125
Ile Cys Ser Leu Val Trp Cys Pro Val Thr Thr Cys Leu Ser Ile Cys
      130             135             140
Ile Ile Leu Gly Pro Gly Thr Tyr Cys Arg Val Cys Leu Ser Ser Ile
145             150             155             160
Val Gln Thr Gly Leu Met Phe Gln Leu Pro Ser Ala Gly Thr Asn His
      165             170             175
Ile Asp His Tyr Cys Asp Met Pro Gln Leu Leu Arg Leu Ala Cys Ala
      180             185             190
Cys Leu Ala Leu Asn Glu Leu Thr Lys Phe Ser Leu Cys Gly Leu Met
      195             200             205
Met Val Asn Ala Thr Leu Val Val Leu Val Ser Phe Gly Cys Val Thr
      210             215             220
Val Thr Ile Leu Arg Thr Pro Ser Gly Ser Gln Xaa His Lys Val Phe
225             230             235             240
Thr Cys Ser Ser His Val Met Thr Val Ser Leu Phe Asp Gly Thr Val
      245             250             255
Phe Val Thr Tyr Ala Gln Pro Gly Thr Met Glu Ser Met Glu Gln Gly
      260             265             270
Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Gly Pro
      275             280             285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Arg
      290             295             300
Leu Gly Gln Arg Gln Ala Leu Met Gly Arg
305              310

```

&lt;210&gt; 1647

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g564 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1647

```

Met Tyr Phe Phe Leu Gly Asn Leu Ser Phe Cys Asp Ile Cys Tyr Ser
 1              5              10              15
Thr Val Phe Ala Pro Lys Met Leu Val Asn Phe Leu Ser Lys His Lys
      20              25              30
Ser Ser Thr Phe Ser Gly Cys Val Leu Gln Ser Phe Pro Phe Ala Val
      35              40              45
Tyr Val Thr Thr Lys Asp Ile Leu Leu Ser Met Met Ala Tyr Asp His

```

```

      50              55              60
Tyr Val Ala Ile Ala Asn Pro Leu Leu Tyr Thr Val Ile Met Ala Gln
65              70              75              80
Lys Val Cys Ile Gln Met Val Leu Ala Ser Tyr Leu Gly Gly Leu Ile
      85              90              95
Asn Ser Leu Thr His Thr Ile Gly Leu Leu Lys Leu Asp Phe Cys Gly
      100              105              110
Pro Asn Ile Val Asn His Tyr Phe Cys Asp Val Pro Pro Leu Leu Arg
      115              120              125
Leu Ser Cys Ser Asp Ala His Ile Asn Glu Met Leu Pro Leu Val Phe
      130              135              140
Ser Gly Leu Ile Ala Met Phe Thr Phe Ile Val Ile Met Val Ser Tyr
145              150              155              160
Ile Cys Ile Ile Ile Ala Ile Gln Arg Ile His Ala Ala Glu Gly Arg
      165              170              175
Tyr Lys Ala Phe Ser Thr Cys Val Ser His Leu Thr Thr Val Thr Leu
      180              185              190
Phe Tyr Gly Ser Val Ser Phe Ser Tyr Ile Gln Pro Ser Ser Gln Tyr
      195              200              205
Ser Leu Glu Gln Glu Lys Val Leu Ala Val Phe Tyr Thr Leu Val Ile
      210              215              220
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
225              230              235              240
Asp Ala Ala Lys Arg Leu Ile Trp Trp Gly Glu Lys
      245              250

```

&lt;210&gt; 1648

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g565 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1648

```

Met Ser Gly Glu Asn Val Thr Arg Val Gly Thr Phe Ile Leu Val Gly
1              5              10              15
Phe Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu
      20              25              30
Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Thr
      35              40              45
Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser
      50              55              60
Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys
65              70              75              80
Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly
      85              90              95
Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys
      100              105              110
Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Cys Ala Ser Arg Leu
      130              135              140
Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val
145              150              155              160
Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His
      165              170              175
Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe
      180              185              190
Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val
195              200              205

```

Phe Pro Leu Leu Ala Thr Met Leu Ser Tyr Ala His Ile Thr Leu Ala  
 210 215 220  
 Val Leu Arg Ile Pro Ser Pro Arg Gly Cys Trp Arg Ala Phe Phe Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu  
 245 250 255  
 Phe Met Tyr Val Arg Pro Arg Pro Leu Tyr Ser Arg Ser Ser Asn Lys  
 260 265 270  
 Leu Ile Ser Val Leu Tyr Thr Val Ile Thr Pro Ile Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asn Ala Leu Lys Asn Ser  
 290 295 300  
 Arg Leu Asp Asp Cys Ala Val Glu Gly Arg Leu Ser Ser Leu Leu  
 305 310 315

&lt;210&gt; 1649

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g566 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1649

Met Ala Asp Val Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Glu  
 1 5 10 15  
 Leu Thr Asp Arg Ala Glu Leu Lys Met Val Leu Phe Val Leu Phe Leu  
 20 25 30  
 Leu Ile Tyr Thr Ile Ser Leu Val Gly Asn Ile Gly Met Leu Phe Leu  
 35 40 45  
 Ile Tyr Val Thr Pro Lys Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 Cys Leu Ser Phe Val Asp Ala Cys Tyr Ser Ser Val Phe Ala Pro Arg  
 65 70 75 80  
 Met Leu Leu Asn Phe Phe Val Glu Arg Glu Thr Ile Leu Phe Ser Ala  
 85 90 95  
 Cys Ile Val Gln Tyr Phe Leu Phe Val Ser Leu Leu Thr Thr Glu Gly  
 100 105 110  
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Met Ala Ile Val Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ala Met Thr Lys Ile Val Cys Ile Val Leu  
 130 135 140  
 Ala Phe Gly Ser Cys Met Gly Gly Leu Ile Asn Ser Leu Thr His Thr  
 145 150 155 160  
 Ile Gly Leu Val Lys Leu Ser Phe Cys Gly Pro Asn Val Ile Ser His  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Ser Glu Thr  
 180 185 190  
 Ser Met Asn Glu Leu Leu Leu Leu Ile Phe Ser Gly Ile Ile Ala Thr  
 195 200 205  
 Leu Thr Phe Leu Thr Val Val Ile Ser Tyr Ile Phe Ile Val Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Arg Xaa Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Ile Thr Val Thr Leu Phe Tyr Gly Ser Ile Ser  
 245 250 255  
 Phe Ser Tyr Ile Gln Pro Asn Ser Gln Tyr Ser Leu Glu Gln Glu Lys





<210> 1651  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g568 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(314)  
 <223> Xaa = Any Amino Acid

<400> 1651  
 Ile Xaa Met Ala Asp Arg Asn Val Thr Val Ile Thr Glu Phe Ile Leu  
 1 5 10 15  
 Leu Gly Leu Thr Asp Asn Pro Glu Met Asn Val Val Leu Ser Val Leu  
 20 25 30  
 Phe Leu Leu Ile Tyr Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile  
 35 40 45  
 Ile Ile Ile Leu Ala Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Gln Leu Ala Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile  
 65 70 75 80  
 Pro Lys Met Leu Val Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr  
 85 90 95  
 His Gly Cys Leu Leu Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr  
 100 105 110  
 Glu Cys Phe Leu Leu Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val  
 115 120 125  
 Cys His Pro Leu His Tyr Lys Gly Leu Met Thr Pro Thr Phe Xaa Ile  
 130 135 140  
 Tyr Leu Val Thr Val Ser Tyr Leu Leu Gly Ser Val Asn Ser Leu Thr  
 145 150 155 160  
 His Leu Ser Ser Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Val Ile  
 165 170 175  
 Asn Arg Tyr Phe Cys Asp Ile Pro Leu Leu Phe Gln Leu Ser Cys Ser  
 180 185 190  
 Asn Thr Gln His Ser Lys Ile Leu Phe Thr Val Leu Ser Gly Ala Thr  
 195 200 205  
 Ser Val Thr Thr Phe Leu Ile Val Val Ser Ser Tyr Leu Val Ile Leu  
 210 215 220  
 Leu Ile Val Leu Lys Ile His Ser Thr Arg Gly Arg Asn Lys Ala Ile  
 225 230 235 240  
 Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Tyr Arg Thr  
 245 250 255  
 Val Ile Phe Thr Tyr Leu Gly Ala Asn Pro Gly Tyr Ser Gln Asp Arg  
 260 265 270  
 Pro Lys Ile Leu Pro Val Glu Cys Thr Leu Leu Leu Ser Ile Leu Asn  
 275 280 285  
 Leu Leu Ile Tyr Ser Val Arg Asn Arg Glu Val Lys Glu Ala Ile Lys  
 290 295 300  
 Ile Ile Ile Lys Arg Lys Ile Leu Pro Gln  
 305 310

<210> 1652  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g569 protein)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1652

```

Met Leu Met Asn Tyr Ser Ser Ala Thr Glu Phe Tyr Leu Leu Gly Phe
 1          5          10          15
Pro Gly Ser Glu Leu His His Ile Leu Phe Ala Ile Phe Phe Phe
          20          25          30
Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Met Ile Val
          35          40          45
Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Gly His
          50          55          60
Leu Ser Ala Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Val Met
          65          70          75          80
Leu Trp Gly Leu Leu Leu Pro Gly Met Gln Thr Ile Tyr Leu Ser Ala
          85          90          95
Cys Val Val Gln Leu Phe Leu Tyr Leu Ala Val Gly Thr Thr Glu Phe
          100          105          110
Ala Leu Leu Gly Ala Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn
          115          120          125
Pro Leu Arg Tyr Asn Ile Ile Met Asn Arg His Thr Cys Asn Phe Val
          130          135          140
Val Leu Val Ser Trp Val Phe Gly Phe Leu Phe Gln Ile Trp Pro Val
          145          150          155          160
Tyr Val Met Phe Gln Leu Thr Tyr Cys Lys Ser Asn Val Val Asn Asn
          165          170          175
Phe Phe Cys Asp Arg Gly Gln Leu Leu Lys Leu Ser Cys Asn Asn Thr
          180          185          190
Leu Phe Thr Glu Phe Ile Leu Phe Leu Met Ala Val Phe Val Leu Phe
          195          200          205
Gly Ser Leu Ile Pro Thr Ile Val Ser Asn Ala Tyr Ile Ile Ser Thr
          210          215          220
Ile Leu Lys Ile Pro Ser Ser Ser Gly Arg Arg Lys Ser Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Phe Thr Cys Val Val Ile Gly Tyr Gly Ser Cys Leu
          245          250          255
Phe Leu Tyr Val Lys Pro Lys Gln Thr Gln Ala Ala Asp Tyr Asn Trp
          260          265          270
Val Val Ser Leu Met Val Ser Val Val Thr Pro Phe Leu Asn Pro Phe
          275          280          285
Ile Phe Thr Leu Arg Asn Asp Lys Val Ile Glu Ala Leu Arg Asp Gly
          290          295          300
Val Lys Arg Cys Cys Gln Leu Phe Arg Asn
          305          310

```

&lt;210&gt; 1653

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g570 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1653

```

Met Met Gly Arg Arg Asn Asp Thr Asn Val Ala Asp Phe Ile Leu Thr
 1          5          10          15
Gly Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Met Leu Phe
          20          25          30
Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Leu Leu
          35          40          45
Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60

```

```

Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro
65          70          75          80
Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly
          85          90          95
Cys Phe Ala Gln Met Phe Cys Phe Val Phe Leu Gly Thr Ala Glu Cys
          100         105         110
Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Ser
          115         120         125
Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu Cys Leu Ala Leu
          130         135         140
Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser Phe Val Asn Val
145          150         155         160
Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn Ile Ile His His
          165         170         175
Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr
          180         185         190
Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly Ser Thr Leu Met
          195         200         205
Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr
          210         215         220
Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr
225          230         235         240
Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile
          245         250         255
Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln
          260         265         270
Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
          275         280         285
Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala Leu Ile Arg Val
          290         295         300
Met Gln Arg Arg Gln Asp Ser Arg
305          310

```

&lt;210&gt; 1654

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g571 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(245)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1654

```

Met Ser Xaa Xaa Ile Phe Cys Leu Pro Lys Ile Ile Ile Thr Leu Leu
1          5          10          15
Gln Xaa Glu Trp Asp Ala Leu Asn Leu Glu Thr Arg Val Phe Leu Glu
          20          25          30
Glu Asp Phe Pro Cys Gly Phe Ser Leu Trp Ile Val Arg Gln Leu Ser
          35          40          45
Phe Phe Leu Glu Ile Asn Xaa Phe Ala His Leu Lys Lys Xaa Cys Arg
          50          55          60
Lys His Thr Ser Thr Phe Ser Leu Ser Asn Leu Ala Phe Xaa Asp Phe
65          70          75          80
Cys Tyr Ala Ser Val Ile Thr Ser Lys Met Phe Gly Ser Phe Leu Tyr
          85          90          95
Lys Gln Lys Lys Leu Thr Phe Asn Ala Leu Gly Cys Ser Leu Thr Phe
          100         105         110
Met Thr Thr Glu Cys Leu Leu Leu Ala Phe Met Ala Cys Asp Gln Tyr

```

115	120	125
Leu Val Ile Cys Asn Pro Pro Leu Tyr Met Val Thr Met Ser Pro Pro		
130	135	140
Gln Gly Val Cys Ile Gln Leu Met Pro Ala Ser Tyr Ser Tyr Ser Phe		
145	150	155
Leu Met Thr Leu Ser His Tyr Leu Ser Ala Phe Arg Leu Pro Tyr Cys		160
	165	170
Pro Ser Val Ser Leu Met Phe Asn Gly Ser Leu Phe Leu Tyr Cys Thr		175
	180	185
Xaa Cys Ser Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe		190
195	200	205
Tyr Thr Val Val Ile Pro Met Leu Ser Pro Leu Ile Trp Ser Leu Arg		
210	215	220
Asn Lys Asp Val Lys Asp Ala Leu Arg Lys Val Ile Val Asn Arg Asn		
225	230	235
Gln Ala Leu Phe Cys		240
	245	

&lt;210&gt; 1655

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g572 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1655

Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly		
1	5	10
Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu		15
	20	25
Val Leu Tyr Val Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu		30
	35	40
Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg		45
50	55	60
His Leu Ala Ile Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys		
65	70	75
Met Leu Met Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu		80
	85	90
Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val		95
	100	105
Met Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn,		110
	115	120
Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu		125
130	135	140
Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser		
145	150	155
Pro Cys Ile Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His		160
	165	170
Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr		175
	180	185
Tyr Ile Pro Glu Thr Ile Val Phe Ile Ser Ala Ala Thr Asn Leu Phe		190
	195	200
Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser		205
210	215	220
Ile Leu Arg Ile Arg Ser Pro Glu Gly Arg Lys Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Met Ile Ala Val Thr Val Phe Tyr Gly Thr Met Leu		240
	245	250
Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser Leu Asp Thr Asp Lys		255
	260	265
		270

Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu  
                   275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Asn Asp Val Asn Val Ala Leu Lys Lys Phe  
                   290                                  295                                  300  
 Met Glu Asn Pro Cys Tyr Ser Phe  
 305                                  310

<210> 1656  
 <211> 161  
 <212> PRT  
 <213> Unknown (H38g573 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(161)  
 <223> Xaa = Any Amino Acid

<400> 1656  
 Ile Cys Gly Ser His Ser Gly Val Thr Glu Phe Cys Leu Leu Gly Phe  
   1                                  5                                  10                                  15  
 Pro Gly Ser Gln Xaa Val Cys His Leu Leu Pro Ser Ser Phe Val Ser  
                   20                                  25                                  30  
 Ile Val Ile Arg Asn Tyr Val Ile Ile Val Cys Val Glu Lys Cys  
                   35                                  40                                  45  
 Leu Leu Phe Leu Leu Tyr Leu Phe Tyr Gly Asp Leu Ser Val Met Glu  
                   50                                  55                                  60  
 Ile Leu Ile Thr Tyr Thr Ala Val Pro Leu Met Leu Arg Gly Cys Tyr  
   65                                  70                                  75                                  80  
 Phe Pro Xaa Phe Lys Gln Tyr Leu Xaa Xaa His Val Ser Val Gln Leu  
                   85                                  90                                  95  
 Tyr Met Asn Phe Phe Gly Gly Thr Gln Glu Phe Ala Leu Leu Gly Val  
                   100                                  105                                  110  
 Met Thr Val Asn His Tyr Val Ala Leu Cys Asn Ser Leu Lys Xaa Asn  
                   115                                  120                                  125  
 Ile Ile Met Ser Ser Thr His Cys Ile Trp Leu Val Ile Val Leu Leu  
                   130                                  135                                  140  
 Ile Gly Phe Leu Ser Glu Ile Trp Ser Val Tyr Ala Thr Phe Gln Leu  
   145                                  150                                  155                                  160  
 Pro

<210> 1657  
 <211> 324  
 <212> PRT  
 <213> Unknown (H38g574 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 1657  
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu  
   1                                  5                                  10                                  15  
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser  
                   20                                  25                                  30  
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser

```

      35              40              45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
  50              55              60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met
  65              70              75              80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85              90              95
His Glu Gly Cys Leu Thr Gln Met Phe Phe Leu Val Leu Phe Ala Cys
      100              105              110
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115              120              125
Ile Cys Arg Pro Leu Asn Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130              135              140
Val Phe Phe Ile Leu Met Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
  145              150              155              160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165              170              175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180              185              190
Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
      195              200              205
Phe Ala Phe Leu Pro Ile Ser Ala Ile Leu Leu Ser Tyr Tyr Lys Ile
      210              215              220
Val Thr Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
  225              230              235              240
Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
      245              250              255
Thr Asp Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260              265              270
Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
      275              280              285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290              295              300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
  305              310              315              320
Phe Phe Leu Cys

```

&lt;210&gt; 1658

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g575 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1658

```

His Thr Lys Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu
      50              55              60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
  65              70              75              80

```

Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Glu  
                     85                    90                    95  
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Thr Glu  
                     100                    105                    110  
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys  
                     115                    120                    125  
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe  
                     130                    135                    140  
 Phe Ile Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His  
                     145                    150                    155                    160  
 Ser Xaa Val Val Leu Gln Phe Thr Phe Phe Asn Asn Val Glu Ile Ser  
                     165                    170                    175  
 Asn Phe Val Cys Glu Pro Ser Gln Leu Val Asn Leu Ala Ser Ser Asp  
                     180                    185                    190  
 Ser Val Val Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly  
                     195                    200                    205  
 Phe Leu Pro Ile Leu Gly Val Leu Leu Ser His Tyr Lys Ile Val Pro  
                     210                    215                    220  
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Val Phe Ala  
                     225                    230                    235                    240  
 Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr Gly  
                     245                    250                    255  
 Ile Asp Met Tyr Leu Thr Ser Ala Val Ser Pro Pro His Arg Asn Gly  
                     260                    265                    270  
 Val Val Ala Ser Val Met Tyr Ala Val Phe Thr Pro Met Leu Asn Pro  
                     275                    280                    285  
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg  
                     290                    295                    300  
 Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser  
                     305                    310                    315                    320

&lt;210&gt; 1659

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g576 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(270)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1659

Val Ser Leu Ile Thr Tyr Leu Ile Thr Val Met Ser Asn Leu Gly Met  
   1                    5                    10                    15  
 Asn Ile Leu Thr Lys Leu Asp Ser His Leu Tyr Thr Pro Val Val Tyr  
                     20                    25                    30  
 Phe Leu Ile Lys His Ile Phe Phe Ile Asp Phe Tyr Asn Cys Ile Val  
                     35                    40                    45  
 Ile Tyr Thr Asn Lys Met Leu Asn Phe Val Val Asp Gln Asn Asn Ile  
                     50                    55                    60  
 Ser Tyr Tyr Ala Cys Ala Thr His Met Thr Phe Phe Met Phe Ile Ile  
                     65                    70                    75                    80  
 Thr Glu Leu Leu Ile Leu Val Ser Met Ala Tyr Asp Cys Tyr Val Val  
                     85                    90                    95  
 Asn Ser Asn Pro Leu Phe Tyr Ile Val Ile Met Cys Leu Xaa Leu Xaa  
                     100                    105                    110  
 His Val Leu Met Ser Ile Pro Tyr Leu Cys Asn Thr Phe Gln Ser Leu  
                     115                    120                    125  
 Ile Ile Thr Ile Asp Leu Phe Leu Thr Phe Cys Ser Phe Ile Ile Ser

130		135		140
His Phe Tyr Cys Tyr	Asp Val Leu Phe Phe	His Met Leu Cys Ser Asn		
145	150	155	160	
Ala Gln Glu Arg Glu	Leu Leu Ile Thr Leu	Leu Thr Ala Phe Asn Leu		
	165	170	175	
Ile Pro Ser Leu Leu	Val Leu Leu Val Leu	Asn Ile Leu Ile Leu Leu		
	180	185	190	
Ala Ile Cys Xaa Met	His Ser Ala Leu Gly	Arg Lys Lys Ala Phe Ser		
195	200	205		
Met Cys Gly Ser His	Leu Thr Met Val Val	Met Phe Tyr Gly Ser Leu		
210	215	220		
Leu Phe Asp Met Asp	Lys Val Ala Ser Leu	Phe Tyr Thr Leu Met Ile		
225	230	235	240	
Leu Arg Phe Asn Leu	Ile Tyr Ser Phe Ser	Asn Leu Gly Val Lys		
	245	250	255	
Asn Val Phe Tyr Arg	Val Phe Lys Asn Xaa	Cys Lys Leu Cys		
260	265	270		

<210> 1660  
 <211> 128  
 <212> PRT  
 <213> Unknown (H38g577 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(128)  
 <223> Xaa = Any Amino Acid

<400> 1660
Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
1 5 10 15
Gln Leu Cys Ala Glu Met Glu Ile Phe Leu Ser Cys Ile Phe Ser Arg
20 25 30
Phe Tyr Ala Phe Ser Leu Leu Arg Asn Gly Met Asn Met Gly Leu Thr
35 40 45
Tyr Leu Asp Asp Arg Asp Asp Arg Leu His Thr Leu Ile Tyr Ile Phe
50 55 60
Leu Ser His Leu Ala Ile Asn Asp Met Tyr Tyr Ala Ser Asn Asn Val
65 70 75 80
Pro Lys Arg Gln Val Asn Gln Met Asn Gln Lys Lys Lys Asn Phe Val
85 90 95
Leu Trp Ile Lys Gln Ile Phe Leu Tyr Leu Ala Phe Ala His Thr Glu
100 105 110
Cys Leu Ile Xaa Ala Met Met Ser Cys Asn Arg Tyr Val Ala Ile Cys
115 120 125

<210> 1661  
 <211> 307  
 <212> PRT  
 <213> Unknown (H38g578 protein)

<220>  
 <223> Synthetic construct

<400> 1661
Met Gly Gln His Asn Leu Thr Val Leu Thr Glu Phe Ile Leu Met Glu
1 5 10 15
Leu Thr Arg Arg Pro Glu Leu Gln Ile Pro Leu Phe Gly Val Phe Leu
20 25 30



Val Ile Tyr Leu Ile Thr Val Val Gly Asn Leu Thr Met Ile Ile Leu  
 35 40 45  
 Thr Lys Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Ser Ile Arg  
 50 55 60  
 His Leu Ala Ser Val Asp Leu Gly Asn Ser Thr Val Ile Cys Pro Lys  
 65 70 75 80  
 Val Leu Ala Asn Phe Val Val Asp Arg Asn Thr Ile Ser Tyr Tyr Ala  
 85 90 95  
 Cys Ala Ala Gln Leu Ala Phe Phe Leu Met Phe Ile Ile Ser Glu Phe  
 100 105 110  
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Tyr Val Ile Met Ser Gln Arg Leu Cys His Val Leu  
 130 135 140  
 Val Gly Ile Gln Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Phe Thr  
 145 150 155 160  
 Ile Lys Ile Phe Thr Leu Thr Phe Cys Gly Ser Asn Val Ile Ser His  
 165 170 175  
 Phe Tyr Cys Asp Asp Val Pro Leu Leu Pro Met Leu Cys Ser Asn Ala  
 180 185 190  
 Gln Glu Ile Glu Leu Leu Ser Ile Leu Phe Ser Val Phe Asn Leu Ile  
 195 200 205  
 Ser Ser Phe Leu Ile Val Leu Val Ser Tyr Met Leu Ile Leu Leu Ala  
 210 215 220  
 Ile Cys Gln Met His Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Val Val Val Val Phe Tyr Gly Ser Leu Leu  
 245 250 255  
 Phe Met Tyr Met Gln Pro Asn Ser Thr His Phe Phe Asp Thr Asp Lys  
 260 265 270  
 Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Glu Glu Val Lys Asn Ala Phe Tyr Lys Leu  
 290 295 300  
 Phe Glu Asn  
 305

&lt;210&gt; 1662

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g579 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(218)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1662

Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Val Ile Phe Gly Gly Met Glu Glu Ser Met Leu  
 35 40 45  
 Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 65 70 75 80  
 Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ala Gln Leu His Asn Leu

Ile	Ala	Leu	Gln	Val	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe
			100					105					110		
Phe	Cys	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	Cys	Asp	Thr	Phe
		115					120					125			
Thr	Ile	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu
	130				135						140				
Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Ser	Lys	Ile	Val	Ser	Ser	Ile
145					150					155					160
Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Arg	Tyr	Lys	Ala	Leu	Ser	Thr	Cys
			165					170						175	
Gly	Ser	His	Val	Ser	Val	Val	Cys	Xaa	Val	Tyr	Gly	Thr	Gly	Val	Gly
		180						185					190		
Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser	Phe	Ser	Pro	Arg	Lys	Gly	Ala	Val
	195					200						205			
Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro						
	210					215									

&lt;210&gt; 1663

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g580 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(227)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1663

Met	Tyr	Phe	Phe	Phe	Ser	Asn	Leu	Ser	Leu	Pro	Asp	Asp	Gly	Phe	Thr
1				5					10					15	
Ser	Thr	Thr	Val	Pro	Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg
		20						25					30		
Val	Thr	Ser	Tyr	Ala	Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile
		35				40						45			
Phe	Gly	Gly	Met	Glu	Glu	Ser	Met	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp
	50				55						60				
Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu	Cys	His	Ser	Ala	Ile	Thr	Asn
65				70					75					80	
Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu	Leu	Ser	Phe	Phe	Phe	Leu	Ser
			85					90						95	
Leu	Leu	Asp	Ala	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Arg	Thr	Cys
		100						105					110		
Phe	Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe	Cys	Asp	Pro	Ser	Gln	Phe
	115					120						125			
Pro	Arg	Leu	Ala	Cys	Cys	Gly	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr
	130					135						140			
Phe	Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe
145				150						155				160	
Ser	Tyr	Asp	Lys	Ile	Val	Phe	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly
		165						170						175	
Gly	Lys	His	Lys	Ala	Phe	Ser	Thr	Arg	Gly	Ser	His	Leu	Ser	Val	Val
		180						185					190		
Cys	Xaa	Phe	Tyr	Gly	Thr	Gly	Ile	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val
	195					200						205			
Ser	Ser	Ser	Pro	Arg	Lys	Ala	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val
	210					215						220			
Ala	Ile	Pro													
	225														

<210> 1664  
 <211> 194  
 <212> PRT  
 <213> Unknown (H38g581 protein)

<220>  
 <223> Synthetic construct

<400> 1664  
 Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ile  
 1 5 10 15  
 Ser Cys Val Pro Gly Met Leu Val Asn Leu Trp Glu Pro Lys Lys Thr  
 20 25 30  
 Ile Ile Leu Leu Gly Cys Ser Val Gln Phe Phe Ile Phe Leu Ser Leu  
 35 40 45  
 Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr  
 50 55 60  
 Met Ala Ile Cys Gln Pro Leu His Tyr Ala Thr Ile Val His Pro Leu  
 65 70 75 80  
 Leu Cys Trp Gln Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Glu  
 85 90 95  
 Ser Val Val Gln Thr Pro Ser Thr Leu His Leu Pro Phe Cys Pro Asp  
 100 105 110  
 Arg Gln Val Asp Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu  
 115 120 125  
 Ser Cys Glu Asp Thr Ser Tyr Asn Glu Ile Gln Leu Ala Val Ala Ser  
 130 135 140  
 Val Phe Ile Leu Ala Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly  
 145 150 155 160  
 Ala Ile Ala Trp Ala Val Leu Arg Thr Asn Ser Ala Lys Gly Gln Arg  
 165 170 175  
 Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe  
 180 185 190  
 Tyr Ser

<210> 1665  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g582 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(320)  
 <223> Xaa = Any Amino Acid

<400> 1665  
 Met Val Ser Ser Asn Gln Thr Ser Pro Val Leu Gly Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile  
 20 25 30  
 Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu  
 35 40 45  
 Val Thr Ile Leu Asp Ser Arg Leu Asp Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Leu  
 65 70 75 80  
 Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Ala Cys Ala

```
<210> 1666
<211> 318
<212> PRT
<213> Unknown (H38g583 protein)
```

<220>  
<223> Synthetic construct

910

His Phe Thr Cys Glu Ile Leu Ala Val Gln Lys Leu Ala Cys Ala Asp  
 180 185 190  
 Ile Ser Val Asn Val Ile Ser Met Gly Val Thr Asn Val Ile Phe Leu  
 195 200 205  
 Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe Ile Ile Ala  
 210 215 220  
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr Gly Thr Ile  
 245 250 255  
 Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp  
 260 265 270  
 Lys Gln Asp Phe Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val  
 275 280 285  
 Thr Pro Met Leu Asn Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val  
 290 295 300  
 Lys Ala Ala Val Arg Asp Leu Ile Phe Gln Lys Cys Phe Ala  
 305 310 315

&lt;210&gt; 1667

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g584 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1667

Met Asn Arg Ser Asn Glu Ala Ser Pro Val Leu Gly Phe Val Leu Leu  
 1 5 10 15  
 Gly Leu Ser Ala His Pro Xaa Leu Glu Lys Thr Phe Phe Val Phe Ile  
 20 25 30  
 Leu Leu Val Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu  
 35 40 45  
 Val Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Leu  
 65 70 75 80  
 Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Ala Cys Ala  
 85 90 95  
 Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys Val Leu  
 100 105 110  
 Leu Ser Met Met Ala Phe Asp His Tyr Leu Asp Met Cys Asn Pro Leu  
 115 120 125  
 Arg Tyr Pro Val Val Met Ser Lys Ala Ala Tyr Met Pro Met Ala Val  
 130 135 140  
 Gly Ser Trp Ala Ala Gly Ile Thr Asn Ser Val Val Gln Ile Ser Leu  
 145 150 155 160  
 Ala Met Xaa Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His Phe Thr  
 165 170 175  
 Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile Cys Ile  
 180 185 190  
 Asn Val Ile Ser Met Val Val Thr Asn Met Ile Phe Leu Ala Leu Pro  
 195 200 205  
 Val Leu Phe Ile Phe Val Ser Tyr Val Phe Ile Ile Ala Thr Ile Leu  
 210 215 220  
 Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser

```

225          230          235          240
Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Met Ile Leu Phe Met
          245          250          255
Tyr Gly Lys Pro Lys Ser Lys Asp Pro Met Gly Ala Asp Lys Gln Asp
          260          265          270
Leu Ala Asp Lys Leu Ile Ser Ile Phe Tyr Gly Val Val Thr Pro Ile
          275          280          285
Leu Asn Pro Ile Ile Tyr Ser Pro Arg Asn Lys Asp Leu Lys Ala Ala
          290          295          300
Met Arg Asn Leu Val Ala Gln Lys His Leu Thr Glu Xaa Leu Ser Gln
305          310          315          320
Ile

```

<210> 1668  
 <211> 125  
 <212> PRT  
 <213> Unknown (H38g585 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(125)  
 <223> Xaa = Any Amino Acid

```

<400> 1668
Arg Leu Asn Val Ile Ser His Leu Pro Phe Tyr Gly Asp Ile Ile Asn
1          5          10          15
His Leu Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
          20          25          30
Ile Ser Ile Asn Met Ile Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala
          35          40          45
His Leu Thr Val Val Val Ile Phe Tyr Arg Thr Ile Leu Phe Thr His
          50          55          60
Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Phe
65          70          75          80
Ala Asp Lys Leu Ile Ser Leu Ser Tyr Gly Val Val Thr Pro Met Leu
          85          90          95
Asn Thr Ile Ile Tyr Ser Leu Arg Lys Lys Gly Val Lys Ala Ala Val
          100          105          110
Lys Asn Leu Val Phe Gln Lys Pro Leu Thr Glu Xaa Gln
          115          120          125

```

<210> 1669  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g586 protein)

<220>  
 <223> Synthetic construct

```

<400> 1669
Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu Val
1          5          10          15
Asn Ile Gln Thr Arg His His Thr Ile Thr Tyr Thr Gly Cys Leu Thr
          20          25          30
Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe Leu
          35          40          45
Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Cys
50          55          60

```

Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala Leu  
 65 70 75 80  
 Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu Met  
 85 90 95  
 Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys  
 100 105 110  
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn  
 115 120 125  
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe  
 130 135 140  
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg  
 145 150 155 160  
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser  
 165 170 175  
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr  
 180 185 190  
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala  
 195 200 205  
 Ala Met Tyr Thr Ile Val Thr Pro  
 210 215

<210> 1670

<211> 319

<212> PRT

<213> Unknown (H38g587 protein)

<220>

<223> Synthetic construct

<400> 1670

Met Glu Lys Ala Asn Glu Thr Ser Pro Val Met Gly Phe Val Leu Leu  
 1 5 10 15  
 Arg Leu Ser Ala His Pro Glu Leu Glu Lys Thr Phe Phe Val Leu Ile  
 20 25 30  
 Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu  
 35 40 45  
 Val Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Phe Thr Thr Ser Ser Val Pro  
 65 70 75 80  
 Leu Val Leu Asp Ser Phe Leu Thr Pro Gln Glu Thr Ile Ser Phe Ser  
 85 90 95  
 Ala Cys Ala Val Gln Met Ala Leu Ser Phe Ala Met Ala Gly Thr Glu  
 100 105 110  
 Cys Leu Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Ala Ala Tyr Met Pro  
 130 135 140  
 Met Ala Ala Ser Ser Trp Ala Ile Gly Gly Ala Ala Ser Val Val His  
 145 150 155 160  
 Thr Ser Leu Ala Ile Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn  
 165 170 175  
 His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp  
 180 185 190  
 Ile Ser Ile Asn Val Ile Ser Met Glu Val Thr Asn Val Ile Phe Leu  
 195 200 205  
 Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe Ile Ile Thr  
 210 215 220  
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Val Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu

**<400> 1672**



```

Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala
 1          5          10          15
Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr
          20          25          30
Gln Leu Tyr Phe Leu Ala Val Cys Gly Asn Met Asp Asn Phe Leu Leu
          35          40          45
Gly Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu Val Val Gly
          65          70          75          80
Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile Leu Leu Met
          85          90          95
Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His Phe Phe Cys
          100          105          110
Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115          120          125
Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val Thr Pro Phe
          130          135          140
Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val Leu Arg
          145          150          155          160
Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr Cys Gly Ser
          165          170          175
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr
          180          185          190
Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met Ala Ala Ala
          195          200          205
Val Met Tyr Pro Val Val Thr Pro
          210          215

```

&lt;210&gt; 1673

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g590 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1673

```

Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu
          35          40          45
Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly
          50          55          60
Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys
          65          70          75          80
Met Leu Ile Asn Phe Leu Ser Lys Asn His Met Leu Ser Met Ala Lys
          85          90          95
Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln Phe
          130          135          140
Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His Val

```

```

145          150          155          160
Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His Tyr
          165          170          175
Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn Pro
          180          185          190
Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln Val
          195          200          205
Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser Ala
          210          215          220
Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ala His Leu Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu Phe
          245          250          255
Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala Lys
          260          265          270
Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Asp Ala Leu Arg Arg Ile
          290          295          300
Met Lys Lys Xaa Ile Val Val Arg Gln His Ser Asn His Phe Phe Phe
305          310          315          320
Ile Phe Cys Xaa Arg Lys Pro Gln Val
          325

```

&lt;210&gt; 1674

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g591 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1674

```

Cys His Ser Gln Val Ser Arg Leu Ala Gly Leu Gly Tyr Leu Glu Gly
1      5      10      15
Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys Ala Ala Gln Met Phe Phe
20     25     30
Phe Val Ala Leu Ala Thr Val Glu Asn Ile Leu Leu Thr Ser Met Ala
35     40     45
Tyr Asp His Tyr Ile Ala Val Cys Lys Pro Leu His Tyr Thr Thr Thr
50     55     60
Thr Ile Ala Ser Val Cys Ala His Leu Val Ile Gly Ser Tyr Val Cys
65     70     75     80
Gly Phe Leu Asn Ala Ser Leu Arg Ile Val Asp Ile Phe Ser Leu Ser
85     90     95
Phe Cys Lys Ser Asn Leu Val His His Leu Phe Cys Asp Val Pro Pro
100    105    110
Val Met Ala Val Ser Cys Ser Gly Lys His Ile Ser Lys Lys Ile Leu
115    120    125
Val Phe Met Ser Ser Phe Asn Val Phe Leu Ala Leu Leu Val Ile Leu
130    135    140
Thr Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Lys Met His Ser Ala
145    150    155    160
Gln Gly His Leu Lys Ala Leu Ser Thr Cys Ala Ser His Leu Ile Ala
165    170    175
Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe Met Tyr Leu Gln Pro Ser
180    185    190
Ser Ser His Ser Met Asp Thr Asp Glu Met Ala Ser Leu Phe Tyr Ala
195    200    205
Val Phe Ile Ser
210

```

<210> 1675  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g592 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(314)  
 <223> Xaa = Any Amino Acid

<400> 1675  
 Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe  
 1 5 10 15  
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu  
 20 25 30  
 Leu Tyr Leu Phe Ser Leu Leu Gly Asn Gly Val Ile Phe Gly Leu Ile  
 35 40 45  
 Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His  
 50 55 60  
 Leu Ala Val Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met  
 65 70 75 80  
 Leu Ala Asn Leu Val Asn Gln Lys Arg Thr Ile Ser Phe Ile Ser Cys  
 85 90 95  
 Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Val Cys Leu  
 100 105 110  
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro  
 115 120 125  
 Leu His Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Val Leu Ala  
 130 135 140  
 Val Ala Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val His Leu Val  
 145 150 155 160  
 Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe  
 165 170 175  
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp  
 180 185 190  
 Leu Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly  
 195 200 205  
 Xaa Leu Cys Leu Val Leu Val Ser Tyr Leu His Ile Leu Ala Ala Ile  
 210 215 220  
 Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val  
 245 250 255  
 Met Tyr Met Ala Pro Lys Ser Ser His Ser Gln Glu Arg Arg Lys Ile  
 260 265 270  
 Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Ile Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys Arg Val Leu  
 290 295 300  
 Trp Lys Gln Arg Ser Ile Glu Glu Ser Phe  
 305 310

<210> 1676  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g593 protein)

<220>

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1676

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln  
 1 5 10 15  
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp Cys Leu Thr  
 20 25 30  
 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu  
 35 40 45  
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
 50 55 60  
 Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu  
 65 70 75 80  
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met  
 85 90 95  
 Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys  
 100 105 110  
 Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr Arg Val Asn  
 115 120 125  
 Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe  
 130 135 140  
 Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys  
 145 150 155 160  
 Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr  
 180 185 190  
 Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala  
 195 200 205  
 Met Met Tyr Thr Val Val Thr Pro  
 210 215

&lt;210&gt; 1677

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g594 protein)

&lt;220&gt;

## &lt;223&gt; Synthetic construct

&lt;400&gt; 1677

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly  
 1 5 10 15  
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser  
 35 40 45  
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys  
 115 120 125  
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe  
 130 135 140  
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu  
 145 150 155 160

Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val  
 195 200 205  
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr  
 210 215 220  
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu  
 225 230 235 240  
 Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe  
 245 250 255  
 Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr  
 275 280 285  
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln  
 290 295 300  
 Leu Val Ile Tyr Lys Arg Ile Ser  
 305 310

&lt;210&gt; 1678

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g595 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1678

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe  
 1 5 10 15  
 Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe  
 20 25 30  
 Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly  
 35 40 45  
 Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr  
 50 55 60  
 Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala  
 65 70 75 80  
 Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile  
 85 90 95  
 Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala  
 100 105 110  
 Asp Thr Glu Cys Ser Met Gln Leu Met Pro Lys Val Asn Gln Asn Val  
 115 120 125

&lt;210&gt; 1679

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g596 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1679

Met Thr Ile Val Leu Leu Ser Ala Leu Asp Ser Arg Leu His Thr Pro  
 1 5 10 15  
 Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Leu Asp Met Cys Phe Thr  
 20 25 30  
 Thr Gly Ser Ile Pro Gln Met Leu Tyr Asn Leu Trp Gly Pro Asp Lys

```

      35              40              45
Thr Ile Ser Tyr Val Gly Cys Ala Ile Gln Leu Tyr Phe Val Leu Ala
  50              55              60
Leu Gly Gly Val Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg
  65              70              75              80
Tyr Ala Ala Val Cys Lys Pro Leu His Tyr Thr Ile Ile Met His Pro
      85              90              95
Arg Leu Cys Gly Gln Leu Ala Ser Val Ala Trp Leu Ser Gly Phe Gly
      100              105              110
Asn Ser Leu Ile Met Ala Pro Gln Thr Leu Met Leu Pro Arg Cys Gly
      115              120              125
His Arg Arg Val Asp His Phe Leu Cys Glu Met Pro Ala Leu Ile Gly
      130              135              140
Met Ala Cys Val Asp Thr Met Met Leu Glu Ala Leu Ala Phe Ala Leu
      145              150              155              160
Ala Ile Phe Ile Ile Leu Ala Pro Leu Ile Leu Ile Leu Ile Ser Tyr
      165              170              175
Gly Tyr Val Gly Gly Thr Val Leu Arg Ile Lys Ser Ala Ala Gly Arg
      180              185              190
Lys Lys Ala Phe Asn Thr Cys Ser Ser His Leu Ile Val Val Ser Leu
      195              200              205
Phe Tyr Gly Thr Ile Ile Tyr Met Tyr Leu Gln Pro Ala Asn Thr Tyr
      210              215              220
Ser Gln Asp Gln Gly Lys Phe Leu Thr Leu Phe Tyr Thr Ile Val Thr
      225              230              235              240
Pro Ser Val Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys
      245              250              255
Glu Ala Met Lys Lys Val Leu Gly Lys Gly Ser Ala Glu Ile
      260              265              270

```

&lt;210&gt; 1680

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g597 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1680

```

Ile Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys
  1              5              10              15
Val Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys
      20              25              30
Ala His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala
      35              40              45
Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys
      50              55              60
Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr Ile
      65              70              75              80
Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg Val
      85              90              95
Leu Leu Ala Val Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala
      100              105              110
Tyr Ser

```

&lt;210&gt; 1681

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g598 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1681

```

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Val
1      5      10      15
Asp Ser Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
      20      25      30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
      35      40      45
Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
      50      55      60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65      70      75      80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
      85      90      95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
      100     105     110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
      115     120     125
Ser Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
      130     135     140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
145     150     155     160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
      165     170     175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Thr Phe Ile Tyr Arg
      180     185     190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
      195     200     205
Thr Ile Thr Pro
      210

```

&lt;210&gt; 1682

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g599 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1682

```

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
1      5      10      15
Asn Leu Val Ala Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
      20      25      30
Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Cys Met Leu
      35      40      45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
      50      55      60
Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
65      70      75      80
Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu

```

```

      85              90              95
Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
      100              105              110
Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys Val Ser
      115              120              125
Gln Xaa Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
      130              135              140
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Thr
      145              150              155              160
Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala
      165              170              175
Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
      180              185              190
Ala Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Gly Phe Tyr Thr
      195              200              205
Val Val Met Pro
      210

```

&lt;210&gt; 1683

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g600 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1683

```

Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1              5              10              15
Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
      20              25              30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
      35              40              45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
      50              55              60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65              70              75              80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
      85              90              95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
      100              105              110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
      115              120              125
Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
      130              135              140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
      145              150              155              160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165              170              175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Gly Leu Gly Val Tyr
      180              185              190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
      195              200              205
Met Tyr Thr Val Val Thr Pro
      210              215

```

&lt;210&gt; 1684

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g601 protein)



&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1684

```

Ile Cys Phe Pro Leu His Tyr Pro Ile Arg Met Arg Lys Arg Val Cys
 1           5           10           15
Ala Leu Met Ile Thr Gly Ser Trp Met Ile Gly Ser Ile Asn Ser Cys
      20           25           30
Ala His Thr Val Tyr Ala Leu Arg Ile Pro Tyr Cys Lys Ser Arg Ala
      35           40           45
Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys
      50           55           60
Thr Asp Thr Trp Val Tyr Glu Cys Thr Val Phe Leu Ser Thr Thr Ile
65           70           75           80
Phe Leu Val Phe Pro Phe Ile Cys Ile Ala Cys Ser Tyr Gly Arg Ile
      85           90           95
Leu Leu Ala Val Tyr His Met His Ser Ala Glu Gly Arg Lys Lys Ala
      100          105          110
Tyr Ser

```

&lt;210&gt; 1685

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g602 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1685

```

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1           5           10           15
His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
      20           25           30
Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
      35           40           45
Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg
      50           55           60
Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr
65           70           75           80
Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr
      85           90           95
Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys
      100          105          110
Glu Leu Leu Ala Val Val Arg Leu Ala Arg Val Asp Thr Ser Ser Asn
      115          120          125
Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe
      130          135          140
Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys
145          150          155          160
Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser
      165          170          175
His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr
      180          185          190
Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser
      195          200          205
Val Phe Tyr Ala Ile Leu Thr Pro
      210          215

```

&lt;210&gt; 1686

&lt;211&gt; 212

<212> PRT  
 <213> Unknown (H38g603 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(212)  
 <223> Xaa = Any Amino Acid

<400> 1686  
 Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu  
 1 5 10 15  
 Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr  
 20 25 30  
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe Val Leu  
 35 40 45  
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg  
 50 55 60  
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu  
 65 70 75 80  
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Val Leu Thr  
 85 90 95  
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys  
 100 105 110  
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val  
 115 120 125  
 Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe  
 130 135 140  
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys  
 145 150 155 160  
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His  
 165 170 175  
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg  
 180 185 190  
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr  
 195 200 205  
 Thr Ile Thr Pro  
 210

<210> 1687  
 <211> 114  
 <212> PRT  
 <213> Unknown (H38g604 protein)

<220>  
 <223> Synthetic construct

<400> 1687  
 Ile Cys Lys Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys  
 1 5 10 15  
 Ile Arg Leu Leu Ile Leu Ser Tyr Val Gly Gly Leu Leu His Ala Leu  
 20 25 30  
 Ile His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile  
 35 40 45  
 Val His His Ile Tyr Cys Asp Ile Ile Pro Leu Ser Lys Ile Ser Cys  
 50 55 60  
 Thr Asp Ser Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ser Gly Ser  
 65 70 75 80  
 Ile Gln Val Phe Ser Ile Val Thr Ile Leu Val Ser Tyr Thr Phe Val  
 85 90 95

Leu Phe Ala Ile Leu Lys Arg Lys Ser Asp Lys Gly Val Arg Lys Ala  
 100 105 110  
 Phe Ser

<210> 1688  
 <211> 111  
 <212> PRT  
 <213> Unknown (H38g605 protein)

<220>  
 <223> Synthetic construct

<400> 1688  
 Ile Cys Asn Pro Leu Arg Tyr Pro Ile Ile Met Ser Arg His Val Cys  
 1 5 10 15  
 Val Gln Met Ala Ala Ile Ser Trp Val Thr Gly Cys Leu Thr Ala Leu  
 20 25 30  
 Leu Val Thr Ser Cys Ala Leu Gln Ile Pro Leu Cys Gly Asn Val Ile  
 35 40 45  
 Asp His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Val  
 50 55 60  
 Ser Ser Leu Leu Val Asp Met Val Met Leu Val Val Ser Ile Leu Leu  
 65 70 75 80  
 Leu Pro Ile Pro Met Leu Leu Ile Cys Ile Ser Tyr Gly Phe Ile Leu  
 85 90 95  
 Ser Thr Ile Leu Arg Ile Gly Ser Thr Glu Gly Arg Asn Lys Ala  
 100 105 110

<210> 1689  
 <211> 223  
 <212> PRT  
 <213> Unknown (H38g606 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(223)  
 <223> Xaa = Any Amino Acid

<400> 1689  
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Ile Cys Gly Gly Met Glu Glu Ser Met Leu  
 35 40 45  
 Leu Ser Val Met Ala Tyr Gly Arg Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu  
 65 70 75 80  
 Leu Ser Ser Phe Cys Phe Val Ser Val Phe Leu Ser Leu Leu Asp Ser  
 85 90 95  
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Gly Phe Lys Asp Val  
 100 105 110  
 Asp Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Leu His Leu Ala  
 115 120 125  
 Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala  
 130 135 140  
 Val Phe Gly Phe Leu Pro Ile Leu Gly Thr Phe Phe Ser Tyr Cys Lys

145		150		155		160
Ile Val Ser Ser	Ile Leu Arg Val Ser	Ser Ser Gly Gly Lys Tyr Lys				
	165	170			175	
Ala Phe Ser Thr	Cys Gly Ser His Leu Pro Val Val Cys Xaa Phe Cys					
	180	185			190	
Gly Thr Gly Val	Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro					
	195	200			205	
Arg Lys Ser Ala Val	Pro Ser Val Met Tyr Pro Val Val Thr Ser					
	210	215			220	

&lt;210&gt; 1690

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g607 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1690

Phe Val Asp Ile	Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser	
1	5	10
Asn Ile Arg Thr	Gln Ser Lys Val Ile Thr Tyr Ala Asp Cys Ile Thr	
	20	25
Gln Met Tyr Phe	Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu	
	35	40
Thr Val Met Ala	Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His	
	50	55
Tyr Thr Val Ile	Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala	
65	70	75
Ser Trp Ile Met	Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val	
	85	90
Leu Pro Leu Leu	Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys	
	100	105
Glu Leu Asn Gln	Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn	
	115	120
Asp Met Val Met	Tyr Leu Ser Ala Val Leu Leu Gly Arg Gly Cys Phe	
	130	135
Thr Gly Ile Leu	Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala	
145	150	155
Ile Ser Ser Ala	Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser	
	165	170
His Leu Ser Val	Val Ser Leu Phe Tyr Cys Met Ser Leu Gly Val Tyr	
	180	185
Leu Ser Ala Ala	Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu	
	195	200
Met Tyr Thr Val	Val Thr Pro	
	210	215

&lt;210&gt; 1691

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g608 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1691

Met Ala Ile Arg	Asn His Ser Thr Leu His Lys Pro Met Tyr Phe Phe	
1	5	10
Leu Ala Asn Met	Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile	
	20	25
		30

Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly Gln  
 35 40 45  
 Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Asn Asp Arg  
 65 70 75 80  
 Tyr Met Ala Ile Cys Tyr Leu Leu His Asn Pro Val Ile Val Ser Gly  
 85 90 95  
 Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly  
 100 105 110  
 Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Asn Gly Gly  
 115 120 125  
 Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn  
 130 135 140  
 Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile Leu  
 145 150 155 160  
 Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr  
 165 170 175  
 Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly Arg  
 180 185 190  
 Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Phe Asn Val Val Ile Ile  
 195 200 205  
 Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser  
 210 215 220  
 Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val  
 225 230 235 240  
 Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys  
 245 250 255  
 Arg Ala Leu Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp  
 260 265 270  
 Pro Lys Lys Gly Ser Arg  
 275

&lt;210&gt; 1692

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g609 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1692

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu  
 1 5 10 15  
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met  
 20 25 30  
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met  
 35 40 45  
 Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val  
 65 70 75 80  
 Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr  
 85 90 95  
 Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr  
 100 105 110  
 Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met  
 130 135 140  
 Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val

145                      150                      155                      160  
 His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile  
                                  165                      170                      175  
 Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr  
                                  180                      185                      190  
 Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val  
                                  195                      200                      205  
 Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu  
                                  210                      215                      220  
 Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe  
 225                                   230                      235                      240  
 Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr  
                                  245                      250                      255  
 Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr  
                                  260                      265                      270  
 Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn  
                                  275                      280                      285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu  
                                  290                      295                      300  
 Lys Val Leu Arg Ser Lys Val Asp Ser Ser  
 305                                   310

<210> 1693

<211> 316

<212> PRT

<213> Unknown (H38g610 protein)

<220>

<223> Synthetic construct

<400> 1693

Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser  
 1                                      5                                      10                                      15  
 Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser  
                                  20                                      25                                      30  
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala  
                                  35                                      40                                      45  
 Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu  
                                  50                                      55                                      60  
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu  
 65                                      70                                      75                                      80  
 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser  
                                  85                                      90                                      95  
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu  
                                  100                                      105                                      110  
 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu  
                                  115                                      120                                      125  
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser  
                                  130                                      135                                      140  
 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser  
 145                                      150                                      155                                      160  
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val  
                                  165                                      170                                      175  
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr  
                                  180                                      185                                      190  
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro  
                                  195                                      200                                      205  
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu  
                                  210                                      215                                      220  
 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser  
 225                                      230                                      235                                      240

Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val  
 245 250 255  
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe  
 260 265 270  
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly  
 290 295 300  
 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala  
 305 310 315

<210> 1694

<211> 309

<212> PRT

<213> Unknown (H38g611 protein)

<220>

<223> Synthetic construct

<400> 1694

Met Lys Arg Glu Asn Phe Thr Leu Ile Thr Asp Phe Val Phe Gln Gly  
 1 5 10 15  
 Phe Ser Ser Phe His Glu Gln Gln Ile Thr Leu Phe Gly Val Phe Leu  
 20 25 30  
 Ala Leu Tyr Ile Leu Thr Leu Ala Gly Asn Ile Ile Ile Val Thr Ile  
 35 40 45  
 Ile Arg Ile Asp Leu His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Met Leu Ser Thr Ser Glu Thr Val Tyr Thr Leu Val Ile Leu Pro Arg  
 65 70 75 80  
 Met Leu Ser Ser Leu Val Gly Met Ser Gln Pro Met Ser Leu Ala Gly  
 85 90 95  
 Cys Ala Thr Gln Met Phe Phe Phe Val Thr Phe Gly Ile Thr Asn Cys  
 100 105 110  
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Met Val Ile Met Asn Lys Arg Leu Arg Ile Gln Leu  
 130 135 140  
 Val Leu Gly Ala Cys Ser Ile Gly Leu Ile Val Ala Ile Thr Gln Val  
 145 150 155 160  
 Thr Ser Val Phe Arg Leu Pro Phe Cys Ala Arg Lys Val Pro His Phe  
 165 170 175  
 Phe Cys Asp Ile Arg Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr  
 180 185 190  
 Val Asn Glu Ile Leu Thr Leu Ile Ile Ser Val Leu Val Leu Val Val  
 195 200 205  
 Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Ile  
 210 215 220  
 Leu Lys Ile Ala Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Thr Val Val Ile Val His Tyr Ser Cys Ala Ser Ile  
 245 250 255  
 Ala Tyr Leu Lys Pro Lys Ser Glu Asn Thr Arg Glu His Asp Gln Leu  
 260 265 270  
 Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val Val  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val  
 290 295 300  
 Gly Gly Lys Phe Ser  
 305

<210> 1695  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g612 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(216)  
 <223> Xaa = Any Amino Acid

<400> 1695  
 Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Ala Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Met Gln Ser His Arg Arg Ala Ile Ser His Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Phe Leu Phe Leu Cys Ala Cys Val Glu Gly Met Leu Leu  
 35 40 45  
 Thr Val Met Ala Tyr Asp Cys Phe Val Asp Ile Cys Arg Pro Leu His  
 50 55 60  
 Tyr Pro Val Ile Gly Asn Pro His Phe Cys Val Phe Phe Val Gly Val  
 65 70 75 80  
 Ser Phe Leu Leu Ser Leu Trp Asp Ser Gln Leu His Ser Trp Ile Val  
 85 90 95  
 Leu Gln Ile Thr Ile Phe Lys Asn Val Glu Ile Ser Asn Phe Val Cys  
 100 105 110  
 Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Gly Val Ile Asn  
 115 120 125  
 Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile  
 130 135 140  
 Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg  
 145 150 155 160  
 Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Gln Ala Val Val Cys Xaa Phe Tyr Arg Thr Gly Ile Gly Met Tyr  
 180 185 190  
 Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser  
 195 200 205  
 Leu Ile Tyr Ala Leu Val Thr Pro  
 210 215

<210> 1696  
 <211> 214  
 <212> PRT  
 <213> Unknown (H38g613 protein)

<220>  
 <223> Synthetic construct

<400> 1696  
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val  
 1 5 10 15  
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr  
 20 25 30  
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His  
 50 55 60  
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu  
 65 70 75 80



Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met  
                     85                    90                    95  
 Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys  
                     100                    105                    110  
 Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn  
                     115                    120                    125  
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu  
                     130                    135                    140  
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln  
 145                    150                    155                    160  
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser  
                     165                    170                    175  
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr  
                     180                    185                    190  
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val  
                     195                    200                    205  
 Met His Ala Val Val Thr  
                     210

<210> 1697

<211> 212

<212> PRT

<213> Unknown (H38g614 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1697

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu  
   1                    5                    10                    15  
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met  
                     20                    25                    30  
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu  
                     35                    40                    45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu  
                     50                    55                    60  
 Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr  
 65                    70                    75                    80  
 Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu  
                     85                    90                    95  
 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys  
                     100                    105                    110  
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys Val Ser  
                     115                    120                    125  
 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Ser Glu Ile Ser Ser Leu  
                     130                    135                    140  
 Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro Ser Thr  
 145                    150                    155                    160  
 Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala  
                     165                    170                    175  
 Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn  
                     180                    185                    190  
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr  
                     195                    200                    205  
 Val Val Ile Pro  
                     210

<210> 1698  
 <211> 212  
 <212> PRT  
 <213> Unknown (H38g615 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(212)  
 <223> Xaa = Any Amino Acid

<400> 1698  
 Leu Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Arg  
 1 5 10 15  
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met  
 20 25 30  
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Val Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu  
 50 55 60  
 Tyr Thr Val Ala Met Tyr Gln A Cys Ser Leu Leu Val Ala Thr  
 65 70 75 80  
 Ser Tyr Cys Trp Gly Ile V Leu Thr Leu Thr Xaa Phe Leu  
 85 90 95  
 Leu Glu Leu Ser Phe Arg Ile Ile Asn Asn Phe Val Cys  
 100 110  
 Glu His Ala Ala Ile Cys Ser Asp Pro Cys Val Ser  
 115 125  
 Gln Glu Ile Thr Phe Asn Glu Ile Ser Ser Leu  
 130 140  
 Thr Ser Tyr Ala Val Met Arg Thr Pro Ser Thr  
 145 155 160  
 Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala  
 165 170 175  
 Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn  
 180 185 190  
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr  
 195 200 205  
 Val Val Ile Pro  
 210

<210> 1699  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g616 protein)

<220>  
 <223> Synthetic construct

<400> 1699  
 Met Ser Ile Ser Asn Ile Thr Val Tyr Met Pro Ser Val Leu Thr Leu  
 1 5 10 15  
 Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro  
 20 25 30  
 Phe Cys Ala Ile Tyr Leu Ile Ala Met Ile Gly Asn Ser Leu Leu Leu  
 35 40 45  
 Ser Ile Ile Lys Ser Glu Arg Ser Leu His Glu Pro Leu Tyr Ile Phe  
 50 55 60  
 Leu Gly Met Leu Gly Ala Thr Asp Ile Ala Leu Ala Ser Ser Ile Met  
 65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Val Pro Glu Ile Tyr Phe  
 85 90 95  
 Asp Ser Cys Leu Leu Gln Met Trp Phe Ile His Thr Leu Gln Gly Ile  
 100 105 110  
 Glu Ser Gly Ile Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Tyr Pro Leu Arg His Ala Asn Ile Phe Thr His Gln Leu Val Ile  
 130 135 140  
 Gln Ile Gly Thr Met Val Val Leu Arg Ala Ala Ile Leu Val Ala Pro  
 145 150 155 160  
 Cys Leu Val Leu Ile Lys Cys Arg Phe Gln Phe Tyr His Thr Thr Val  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala  
 180 185 190  
 Ala Asn Val Gln Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Thr  
 195 200 205  
 Val Ala Gly Phe Asp Leu Thr Phe Ile Thr Leu Ser Tyr Ile Gln Ile  
 210 215 220  
 Phe Ile Thr Val Phe Arg Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala  
 225 230 235 240  
 Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu  
 245 250 255  
 Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ser His Ile Pro  
 260 265 270  
 Pro Tyr Ile His Ile Leu Phe Ser Ser Ile Tyr Leu Leu Val Pro Pro  
 275 280 285  
 Phe Leu Asn Pro Leu Val Tyr Gly Ala Lys Thr Thr Gln Ile Arg Ile  
 290 295 300  
 His Val Val Lys Met Phe Cys Ser  
 305 310

&lt;210&gt; 1700

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g617 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1700

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly  
 1 5 10 15  
 Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met  
 20 25 30  
 Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu  
 35 40 45  
 Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Ile Ile Leu Lys  
 65 70 75 80  
 Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly  
 85 90 95  
 Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met  
 130 135 140  
 Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met  
 145 150 155 160  
 Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His

```

      165      170      175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
      180      185      190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser S r Ile Leu Leu Leu Leu
      195      200      205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
      210      215      220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
      225      230      235      240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
      245      250      255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
      260      265      270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
      275      280      285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
      290      295      300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
      305      310      315

```

&lt;210&gt; 1701

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g618 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1701

```

Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
  1      5      10      15
Ser Phe Pro Glu Leu His His Leu Gln Gly Leu Leu Phe Val Ser Leu
      20      25      30
Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
      35      40      45
Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
      50      55      60
Ala Gln Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
      65      70      75      80
Lys Leu Leu Ala Gly Leu Pro Ala Glu Arg Arg Pro Ser Ile Ser Phe
      85      90      95
Ser Gly His Leu Thr Trp Leu Leu Leu Phe Leu Ser Leu Ser Ser
      100      105      110
Glu Cys Val Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val Ile
      115      120      125
Cys His Leu Leu His Tyr Leu Ser Pro Ser Trp Thr Pro Cys Ser Trp
      130      135      140
Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro Ala
      145      150      155      160
Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser Pro
      165      170      175
Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu Ser
      180      185      190
Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln Val
      195      200      205
Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His Ile
      210      215      220
Leu Ala Arg Ser Leu Arg Ile Pro Glu Arg Pro Ser Lys Leu Lys Ala
      225      230      235      240
Phe Pro Thr Tyr Ala Ser His Leu Gly Cys Gly Ser Ser Asn Leu Ile
      245      250      255

```

Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys Pro  
 260 265 270  
 Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala Lys  
 275 280 285  
 Leu Leu Gln Ala Leu Pro  
 290

<210> 1702  
 <211> 295  
 <212> PRT  
 <213> Unknown (H38g619 protein)

<220>  
 <223> Synthetic construct

<400> 1702  
 Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu  
 1 5 10 15  
 Ser Phe Pro Glu Leu Arg His Leu Gln Gly Leu Leu Phe Gly Leu Leu  
 20 25 30  
 Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly  
 35 40 45  
 Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu  
 50 55 60  
 Ala Lys Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro  
 65 70 75 80  
 Lys Leu Leu Ala Gly Leu Pro Gly Thr Ser Asp Asp His Leu Ile Ser  
 85 90 95  
 Phe Ser Gly His Leu Thr Trp Leu Leu Phe Leu Ser Leu Ser Ser  
 100 105 110  
 Ser Glu Cys Ile Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val  
 115 120 125  
 Ile Cys His Leu Leu His Tyr Pro Ala His His Gly Leu His Ala Ala  
 130 135 140  
 Arg Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro  
 145 150 155 160  
 Ala Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser  
 165 170 175  
 Pro Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu  
 180 185 190  
 Ser Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln  
 195 200 205  
 Val Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His  
 210 215 220  
 Ile Leu Ala Arg Ser Leu Arg Ile Pro Ala Lys Ala Gln Gln Leu Lys  
 225 230 235 240  
 Ala Phe Pro Thr Tyr Ala Ser His Leu Gly Trp Arg Pro Ser Asn Leu  
 245 250 255  
 Ile Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys  
 260 265 270  
 Pro Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala  
 275 280 285  
 Lys Leu Leu Gln Ala Leu Pro  
 290 295

<210> 1703  
 <211> 175  
 <212> PRT  
 <213> Unknown (H38g620 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(175)

<223> Xaa = Any Amino Acid

<400> 1703

Leu	Leu	Met	Ala	Ala	Asp	Asn	His	Thr	Arg	Val	Glu	Ala	Phe	Val	Leu
1				5					10					15	
Gln	Gly	Phe	Ser	Glu	Asp	Leu	Pro	Leu	Gln	Gly	Cys	Cys	Phe	Ala	Phe
			20					25					30		
Phe	Leu	Leu	Tyr	Leu	Met	Ala	Leu	Val	Gly	Asn	Ile	Leu	Met	Val	Met
		35					40					45			
Ala	Ile	Ser	Leu	Asn	Pro	Gly	Leu	His	Thr	Pro	Val	Tyr	Phe	Phe	Leu
	50					55					60				
Thr	Asn	Leu	Ala	Leu	Leu	Asp	Ile	Val	Cys	Thr	Ser	Met	Asp	Asn	Ser
65					70				75						80
Arg	Val	Val	Ala	Val	Leu	Tyr	Thr	Val	Val	Ser	Pro	Thr	Leu	Asn	Pro
			85					90						95	
Ser	Pro	Thr	Pro	Cys	Gly	Thr	Arg	Thr	Tyr	Gln	Xaa	His	Xaa	Gly	Glu
			100					105					110		
Cys	Phe	Leu	Ala	Ser	Gly	Lys	Arg	Lys	Gly	Ser	Phe	Xaa	Cys	Glu	Met
		115					120					125			
Phe	Gln	Val	Leu	Thr	Asn	Xaa	Phe	Gln	His	Met	Thr	Leu	Arg	Ile	Ser
		130				135					140				
Cys	Lys	Gln	Gln	Gly	Thr	Arg	Lys	Xaa	Leu	Met	Pro	His	Ile	Tyr	Lys
145					150					155					160
Xaa	Cys	Ala	Pro	Ala	Arg	Gly	Cys	His	His	Ser	Met	Trp	Asn	Ser	
				165				170						175	

<210> 1704

<211> 317

<212> PRT

<213> Unknown (H38g621 protein)

<220>

<223> Synthetic construct

<400> 1704

Met	Glu	Arg	Thr	Asn	Asp	Ser	Thr	Ser	Thr	Glu	Phe	Phe	Leu	Val	Gly
1				5					10					15	
Leu	Ser	Ala	His	Pro	Lys	Leu	Gln	Thr	Val	Phe	Phe	Val	Leu	Ile	Leu
			20					25					30		
Trp	Met	Tyr	Leu	Met	Ile	Leu	Leu	Gly	Asn	Gly	Val	Leu	Ile	Ser	Val
		35					40					45			
Ile	Ile	Phe	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Cys
	50					55					60				
Asn	Leu	Ser	Phe	Leu	Asp	Val	Cys	Tyr	Thr	Ser	Ser	Ser	Val	Pro	Leu
65					70				75						80
Ile	Leu	Ala	Ser	Phe	Leu	Ala	Val	Lys	Lys	Lys	Val	Ser	Phe	Ser	Gly
			85					90					95		
Cys	Met	Val	Gln	Met	Phe	Ile	Ser	Phe	Ala	Met	Gly	Ala	Thr	Glu	Cys
			100					105					110		
Met	Ile	Leu	Gly	Thr	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Tyr
		115					120					125			
Pro	Leu	Arg	Tyr	Pro	Val	Ile	Met	Ser	Lys	Gly	Ala	Tyr	Val	Ala	Met
	130					135					140				
Ala	Ala	Gly	Ser	Trp	Val	Thr	Gly	Leu	Val	Asp	Ser	Val	Val	Gln	Thr
145					150					155					160
Ala	Phe	Ala	Met	Gln	Leu	Pro	Phe	Cys	Ala	Asn	Asn	Val	Ile	Lys	His
				165				170						175	

Phe Val Cys Glu Ile Leu Ala Ile Leu Lys Leu Ala Cys Ala Asp Ile  
 180 185 190  
 Ser Ile Asn Val Ile Ser Met Thr Gly Ser Asn Leu Ile Val Leu Val  
 195 200 205  
 Ile Pro Leu Leu Val Ile Ser Ile Ser Tyr Ile Phe Ile Val Ala Thr  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Thr Glu Gly Lys His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe  
 245 250 255  
 Phe Met Tyr Ala Lys Pro Glu Ser Lys Ala Ser Val Asp Ser Gly Asn  
 260 265 270  
 Glu Asp Ile Ile Glu Ala Leu Ile Ser Leu Phe Tyr Gly Val Met Thr  
 275 280 285  
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 290 295 300  
 Ala Ala Val Lys Asn Ile Leu Cys Arg Lys Asn Phe Ser  
 305 310 315

&lt;210&gt; 1705

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g622 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1705

Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly  
 1 5 10 15  
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe  
 20 25 30  
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile  
 35 40 45  
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly  
 50 55 60  
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser  
 65 70 75 80  
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys  
 100 105 110  
 Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met  
 130 135 140  
 Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr  
 145 150 155 160  
 Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His  
 165 170 175  
 Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile  
 180 185 190  
 Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu  
 195 200 205  
 Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser  
 210 215 220  
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu  
 245 250 255  
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp

```

                260                265                270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
      275                280                285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290                295                300
Glu Ala Val Lys His Leu Pro Asn Arg Arg Phe Phe Ser Lys
305                310                315

```

<210> 1706  
 <211> 124  
 <212> PRT  
 <213> Unknown (H38g623 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(124)  
 <223> Xaa = Any Amino Acid

```

<400> 1706
Phe Leu Leu Xaa Ala Asn Tyr Ser Ala Glu Glu Arg Phe Leu Leu Leu
 1                5                10                15
Gly Phe Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val
      20                25                30
Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ser Ala Leu Val Leu
      35                40                45
Leu Ala Val Asp Pro Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Cys
      50                55                60
His Leu Ala Leu Val Asp Ala Gly Phe Thr Thr Ser Val Val Pro Pro
      65                70                75                80
Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu Tyr Val Pro Arg Ser His
      85                90                95
Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala Leu Gly Ser Ala Glu Cys
      100                105                110
Val His Leu Ala Val Met Ala Leu Gly Arg Ala Val
      115                120

```

<210> 1707  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g624 protein)

<220>  
 <223> Synthetic construct

```

<400> 1707
Met Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1                5                10                15
Gln Asp Pro Gly Val Gln Lys Ala Leu Phe Val Met Phe Leu Leu Thr
      20                25                30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Asp Ile Ile
      35                40                45
Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
      50                55                60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
      65                70                75                80
Val Gly Leu Phe Cys Asp Lys Lys Thr Ile Ser Phe Gln Gly Cys Met
      85                90                95
Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Val Phe Leu
      100                105                110

```



Leu Val Val Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Thr Ile Met Asn Arg Gln Val Cys Phe Leu Leu Leu Val  
 130 135 140  
 Val Ala Met Ile Gly Gly Phe Val His Ser Ala Phe Gln Ile Val Val  
 145 150 155 160  
 Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Val His Phe Ser Cys  
 165 170 175  
 Asp Met His Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Phe Ile  
 180 185 190  
 Gly Leu Thr Val Val Val Asn Ser Gly Ala Ile Cys Met Val Ile Phe  
 195 200 205  
 Asn Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Ser Ser Leu Lys Thr  
 210 215 220  
 Tyr Ser Gln Glu Lys Arg Gly Lys Ala Leu Ser Thr Cys Ser Ser Gly  
 225 230 235 240  
 Ser Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Ile Tyr Val  
 245 250 255  
 Arg Pro Val Ser Asn Phe Pro Thr Asp Lys Phe Met Thr Val Phe Tyr  
 260 265 270  
 Thr Ile Ile Thr His Met Leu Ser Pro Leu Ile Tyr Thr Leu Arg Asn  
 275 280 285  
 Ser Glu Met Arg Asn Ala Ile Glu Lys Leu Leu Gly Lys Lys Leu Thr  
 290 295 300  
 Ile Phe Ile Ile Gly Gly Val Ser Val Leu Met  
 305 310 315

&lt;210&gt; 1708

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g625 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1708

Arg Cys Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala  
 1 5 10 15  
 Leu Leu Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln  
 20 25 30  
 Met Phe Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile  
 35 40 45  
 Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe  
 50 55 60  
 Ser Gly Gly Arg Gln Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr  
 65 70 75 80  
 Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro  
 85 90 95  
 Ala Gln Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr  
 100 105 110  
 Thr Val Val Thr Pro  
 115

&lt;210&gt; 1709

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g626 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1709

```

Gly Leu Ser Asn Asn Val Thr Glu Phe Val Leu Leu Gly Asn Thr Gln
 1              5              10              15
Cys Pro Asp Val Gln Asn Ala Leu Phe Val Met Val Leu Leu Thr Tyr
      20              25              30
Val Val Ser Met Ala Gly Asn Leu Leu Ala Val Val Ala Ile Ile Ser
      35              40              45
Ser Pro Ser Phe Gly Ser Pro Met Tyr Phe Phe Leu Thr Cys Leu Leu
 50              55              60
Phe Ile Tyr Ala Ala Tyr Ser Asn Thr Ile Ser Pro Lys Leu Ile Ile
65              70              75              80
Gly Leu Leu His Asp Lys Lys Thr Ile Phe Phe Thr Ala Cys Met Gly
      85              90              95
Gln Leu Phe Ile Asp His Leu Phe Gly Gly Ala Glu Val Phe Leu Leu
      100              105              110
Val Gly Met Ser Tyr Asp Phe Tyr Val Ala Ile Ser Lys Pro Leu His
      115              120              125
Tyr Leu Thr Ile Met Asn Gln Gln Val Cys Ile Leu Leu Leu Val Val
      130              135              140
Ala Val Thr Gly Gly Phe Val Ser Cys Val Phe Gln Ile Val Val Val
145              150              155              160
Tyr Thr Leu Ser Phe Cys Gly Pro Asn Val Thr Asp His Phe Val Cys
      165              170              175
Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr Phe Ile
      180              185              190
Gly Leu Thr Val Val Ala Asn Gly Leu Ala Ile Cys Met Val Val Phe
      195              200              205
Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Asn Phe Lys Thr
      210              215              220
Tyr Ser Gln Glu Gly Arg Leu Lys Ala Leu Ser Ala Cys Ile Ser Tyr
225              230              235              240
Ile Thr Val Thr Val Leu Phe Leu Val Pro Cys Ile Phe Leu Phe Val
      245              250              255
Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Met Thr Val Phe Tyr
      260              265              270
Thr Val Ile Ile His Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275              280              285
Leu Glu Met Arg Ile Ala Val Lys Ser Asn Val Lys Lys Leu Trp His
      290              295              300
Xaa Lys Leu Asn Tyr Ser Xaa Asn Glu
305              310

```

&lt;210&gt; 1710

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g627 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1710

```

Met Arg Leu Ser Ser Asp Val Thr Ala Phe Val Leu Leu Gly Leu Thr
 1              5              10              15

```

Gln Asp Pro Asp Val Xaa Asn Ala Leu Phe Val Val His Leu Leu Thr  
 20 25 30  
 Tyr Ile Met Thr Met Val Gly Asn Leu Pro Ile Val Val Thr Ile Ile  
 35 40 45  
 Ala Thr Pro Thr Leu Gly Ser Pro Val Tyr Phe Phe Ile Val Cys Leu  
 50 55 60  
 Ser Phe Ile Asp Val Val Tyr Ser Thr Thr Ile Pro Pro Lys Leu Ile  
 65 70 75 80  
 Val Ser Tyr Leu His Asp Lys Lys Thr Ile Ser Phe Arg Ala Cys Met  
 85 90 95  
 Gly Gln Pro Phe Ile Asp His Leu Val Gly Gly Ala Glu Ala Phe Ile  
 100 105 110  
 Leu Leu Val Met Ala Tyr Asn Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Phe Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val  
 130 135 140  
 Val Ala Val Thr Ala Gly Phe Val His Ser Val Phe Gln Ile Leu Val  
 145 150 155 160  
 Ala Tyr Ser Leu Leu Phe Cys Gly Pro Asn Ile Ile Asp His Phe Phe  
 165 170 175  
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala His Thr Asp Thr Tyr Phe  
 180 185 190  
 Ile Gly Leu Thr Val Val Ala Asn Gly Gly Gly Ile Cys Met Val Leu  
 195 200 205  
 Phe Ile Leu Leu Leu Ile Ser Cys Gly Val Ile Leu Ile Ser Leu Lys  
 210 215 220  
 Thr Tyr Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser  
 225 230 235 240  
 His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr  
 245 250 255  
 Val Arg Pro Val Ser Asn Phe Pro Ile Asn Lys Phe Ile Thr Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Xaa Glu Met Lys Asn Ala Ile Gly Asn Leu Trp Cys Lys Tyr Xaa  
 290 295 300  
 Leu Xaa Ile Glu Xaa Glu Gly Thr Phe Ser Cys Arg Tyr Arg Val Met  
 305 310 315 320  
 Gln Val Lys

&lt;210&gt; 1711

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g628 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(235)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1711

Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Ile Asp Leu Cys Tyr  
 1 5 10 15  
 Ser Phe Val Phe Thr Pro Lys Met Leu Met Ser Phe Ile Ser Glu Arg  
 20 25 30  
 Asn Ile Ile Ser Phe Pro Gly Cys Ile Thr Gln Leu Phe Phe Phe Cys  
 35 40 45  
 Phe Phe Val His Ser Glu Cys Tyr Val Leu Thr Ala Met Ala Tyr Asp

50	55	60
Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Met Val Thr Thr Ser		
65	70	75
Pro Gln Ile Cys Ser Leu Leu Met Leu Gly Ser Tyr Val Met Gly Phe		80
	85	90
Ala Gly Ala Met Val His Thr Glu Cys Met Met Lys Leu Ile Phe Cys		95
	100	105
Asp Ser Asn Val Ile Asn His Asn Met Cys Asp Ile Phe Pro Leu Leu		110
	115	120
Gln Leu Ser Cys Ser Ser Thr Xaa Ala Asn Glu Leu Val Met Ser Val		125
	130	135
Ile Val Gly Thr Val Val Ile Val Ser Ser Leu Ile Ile Leu Ile Ser		140
145	150	155
Tyr Ala Leu Ile Leu Phe Asn Ile Leu His Met Ser Ser Ala Glu Gly		160
	165	170
Trp Phe Lys Ala Ile Gly Thr Cys Gly Ser His Ile Ile Thr Val Gly		175
	180	185
Leu Phe Tyr Glu Phe Gly Leu Ile Thr His Val Lys Leu Ser Ser Asp		190
	195	200
Trp Tyr Met Gly Gln Gly Lys Phe Leu Ser Val Phe Tyr Thr Asn Val		205
	210	215
Val Pro Met Leu Asn Pro Phe Ile Tyr Cys Leu		220
225	230	235

&lt;210&gt; 1712

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g629 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(308)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1712

Met Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser		
1	5	10
Gln Tyr Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Ile		15
	20	25
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Ile Val Val Ser Ile Ile		30
	35	40
Ala Ser Pro Phe Leu Gly Ser Pro Val Tyr Phe Phe Leu Ala Cys Leu		45
	50	55
Ser Phe Ile Asp Ala Val Tyr Ser Thr Thr Ile Ser Pro Val Leu Ile		60
65	70	75
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met		80
	85	90
Gly Gln Leu Phe Ile Glu His Leu Phe Gly Asp Thr Asp Val Phe Leu		95
	100	105
Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Lys Pro Leu		110
	115	120
Arg Tyr Leu Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val		125
	130	135
Val Ala Val Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Leu Val		140
145	150	155
Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Tyr His Phe Phe		160
	165	170
Cys Asn Ile Tyr Pro Leu Leu Asp Leu Glu Cys Thr Asp Thr Tyr Phe		175
	180	185
		190

Val Gly Leu Ala Val Val Phe Asn Gly Gly Ala Ile Cys Met Val Ile  
 195 200 205  
 Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu Lys  
 210 215 220  
 Thr Tyr Ser Pro Glu Gly Arg His Lys Ala Pro Phe Ile Cys Ser Ser  
 225 230 235 240  
 His Phe Ile Met Val Ile Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr  
 245 250 255  
 Val Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Leu Thr Val Phe  
 260 265 270  
 Tyr Ser Val Ile Thr Pro Lys Leu Asn Pro Phe Ile Tyr Met Leu Arg  
 275 280 285  
 Asn Ser Glu Met Arg Asn Ala Ile Glu Asn Leu Leu Gly Tyr Gln Ser  
 290 295 300  
 Gly Lys Thr Gly  
 305

&lt;210&gt; 1713

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g630 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(230)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1713

Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser Leu Pro Asp Ile Gly Phe  
 1 5 10 15  
 Thr Ser Ser Met Val Pro Lys Met Ile Val Asp Ile Xaa Ser His Ser  
 20 25 30  
 Arg Leu Ile Ser Xaa Ala Gly Cys Leu Thr Pro Met Ser Leu Phe Ala  
 35 40 45  
 Ile Phe Gly Gly Met Glu Glu Asn Met Leu Leu Ser Val Ile Ala Tyr  
 50 55 60  
 Asp Pro Phe Val Ala Ile Cys His Pro Leu Tyr His Ser Ala Ile Met  
 65 70 75 80  
 Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Ser Phe Phe Ser Gln  
 85 90 95  
 Ser Leu Leu Asp Ala Gln Val His Asn Leu Ile Ala Leu Gln Met Thr  
 100 105 110  
 Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln  
 115 120 125  
 Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met  
 130 135 140  
 Tyr Ser Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu  
 145 150 155 160  
 Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Arg Arg Val Ser Ser Ser  
 165 170 175  
 Gly Gly Lys Tyr Lys Ala Cys Ser Thr Cys Gly Ser His Leu Ser Val  
 180 185 190  
 Val Cys Xaa Phe Tyr Gly Thr Gly Phe Trp Gly Tyr Leu Ser Ser Asp  
 195 200 205  
 Val Ser Ser Ser Pro Gly Lys Ala Ala Val Ala Ser Val Met Tyr Thr  
 210 215 220  
 Val Val Thr Pro Met Leu  
 225 230

<210> 1714  
 <211> 227  
 <212> PRT  
 <213> Unknown (H38g632 protein)

<220>  
 <223> Synthetic construct

<400> 1714  
 Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu  
 1 5 10 15  
 Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala  
 20 25 30  
 Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu  
 35 40 45  
 Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu  
 50 55 60  
 His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala  
 65 70 75 80  
 Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp  
 85 90 95  
 Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val Asn His Phe Phe  
 100 105 110  
 Cys Asp Ser Pro Pro Val Leu Lys Leu Val Cys Ala Asp Thr Ala Leu  
 115 120 125  
 Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro  
 130 135 140  
 Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu  
 145 150 155 160  
 Lys Ile Pro Ser Ala Lys Gly Lys His Lys Ala Phe Ser Thr Cys Ser  
 165 170 175  
 Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr  
 180 185 190  
 Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu  
 195 200 205  
 Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Phe His Leu  
 210 215 220  
 Leu Ser Trp  
 225

<210> 1715  
 <211> 192  
 <212> PRT  
 <213> Unknown (H38g633 protein)

<220>  
 <223> Synthetic construct

<400> 1715  
 Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile  
 1 5 10 15  
 Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu  
 20 25 30  
 Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu  
 35 40 45  
 His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asp Ile  
 50 55 60  
 Ala Tyr Ala Cys Asn Thr Val Pro Arg Met Leu Val Asn Leu Leu His  
 65 70 75 80  
 Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu  
 85 90 95

Phe Ser Thr Phe Ala Val Thr Glu Cys Leu Leu Leu Val Val Met Ser  
                   100                  105                  110  
 Tyr Asp Leu Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Phe Ile Ile  
                   115                  120                  125  
 Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile Thr Ser Trp Thr Cys  
                   130                  135                  140  
 Gly Ser Leu Leu Ala Met Val His Val Ser Leu Ile Leu Arg Leu Pro  
                   145                  150                  155                  160  
 Phe Cys Gly Pro Arg Glu Ile Asn His Phe Leu Cys Glu Ile Leu Ala  
                   165                  170                  175  
 Val Leu Arg Leu Gly Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile  
                   180                  185                  190

<210> 1716

<211> 308

<212> PRT

<213> Unknown (H38g634 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1716

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
   1                  5                  10                  15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe  
                   20                  25                  30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
                   35                  40                  45  
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro  
   65                  70                  75                  80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
                   85                  90                  95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
                   100                  105                  110  
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile  
                   115                  120                  125  
 Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala  
                   130                  135                  140  
 Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln  
   145                  150                  155                  160  
 Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu  
                   165                  170                  175  
 Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys  
                   180                  185                  190  
 Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile  
                   195                  200                  205  
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile  
                   210                  215                  220  
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala  
   225                  230                  235                  240  
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly  
                   245                  250                  255  
 Arg Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg  
                   260                  265                  270  
 Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Ser Met Leu

275 280 285  
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu  
 290 295 300  
 Arg Arg Pro Gln  
 305

<210> 1717  
 <211> 238  
 <212> PRT  
 <213> Unknown (H38g635 protein)

<220>  
 <223> Synthetic construct

<400> 1717  
 Met Tyr Leu Phe Leu Arg Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr  
 1 5 10 15  
 Ser Thr Ile Val Pro Lys Met Ile Val Asp Ile Gln Ser His Ser Arg  
 20 25 30  
 Val Ile Ser Tyr Ala Gly Arg Leu Thr Gln Met Ser Leu Phe Ala Ile  
 35 40 45  
 Phe Gly Gly Met Glu Asp Asn Met Leu Leu Ser Val Met Ala Tyr Asp  
 50 55 60  
 Arg Phe Val Ala Ile Cys His Pro Leu Tyr His Ser Ala Ile Met Asn  
 65 70 75 80  
 Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu Ser Phe Phe Phe Phe Leu  
 85 90 95  
 Ser Leu Leu Asp Thr Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr  
 100 105 110  
 Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln  
 115 120 125  
 Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Val  
 130 135 140  
 Tyr Phe Pro Ala Val Ile Phe Val Phe Leu Pro Ile Ser Gly Thr Leu  
 145 150 155 160  
 Phe Ser Leu Lys Leu Phe Val Ser Ser Ile Leu Arg Val Ser Ser Ser  
 165 170 175  
 Gly Gly Lys Tyr Lys Thr Phe Ser Thr Cys Gly Ser His Leu Ser Val  
 180 185 190  
 Ile Cys Leu Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp  
 195 200 205  
 Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val Met Tyr Lys  
 210 215 220  
 Met Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Arg  
 225 230 235

<210> 1718  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g636 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(321)  
 <223> Xaa = Any Amino Acid

<400> 1718  
 Phe Lys Arg Ser Ile Thr Phe Thr Pro Thr Thr Phe Thr Leu Val Gly  
 1 5 10 15



```

Ile Pro Gly Leu Glu Ala Glu His Tyr Trp Ile Ser Ile Pro Phe Cys
      20      25      30
Leu Ile Tyr Thr Ile Ile Phe Pro Gly Asn Gly Ile Ile Leu His Ile
      35      40      45
Ile Arg Ile Asp Ser Ser Leu His Gln Pro Met Tyr Tyr Phe Leu Ala
      50      55      60
Met Pro Ala Phe Val Glu Leu Gly Val Ser Ala Ser Thr Met Pro Thr
      65      70      75      80
Val Leu Ser Ile Phe Leu Phe Gly Ile Asn Asp Val Ser Phe Gly Gly
      85      90      95
Cys Leu Leu Gln Met Phe Ser Met His Ser Phe Thr Leu Met Glu Ser
      100      105      110
Gly Val Leu Leu Ala Met Ser Val Asp Arg Phe Val Ala Ile Tyr Ser
      115      120      125
Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ile Ala Cys Ile Ser Gly Met
      130      135      140
Gly Ala Ala Ile Ala Leu Arg Ser Val Met Leu Met Leu Pro Leu Leu
      145      150      155      160
Phe Leu Leu Arg Arg Leu Pro Phe Cys Gly His Asn Thr Leu Thr His
      165      170      175
Ser Tyr Cys Leu His Ser Asp Leu Ile Lys Leu Pro Cys Gly Asp Thr
      180      185      190
Arg Pro Asn Ser Ile Leu Ala Leu Phe Val Ile Thr Phe Thr Phe Gly
      195      200      205
Leu Asp Leu Leu Phe Ile Val Val Ser Tyr Val Leu Ile Leu His Thr
      210      215      220
Val Leu Glu Ile Ala Ser Arg Ser Arg Ala Trp Gln Ala Leu Asn Thr
      225      230      235      240
Cys Val Ser His Ile Cys Ala Val Leu Val Tyr Tyr Val Pro Met Ile
      245      250      255
Ser Leu Ser Xaa Val His Arg Phe Gly Arg His Leu Pro Pro Leu Phe
      260      265      270
Gln Thr Val Thr Ala Asn Ala Tyr Leu Phe Phe Pro Pro Val Val Asn
      275      280      285
Pro Ile Val Tyr Ser Ile Lys Ile Lys Glu Ile Arg Asn Ser Val Val
      290      295      300
Leu Thr Leu Ser Arg Lys Arg Gly Glu Phe Xaa Trp Arg Pro Lys Ile
      305      310      315      320
Pro

```

&lt;210&gt; 1719

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g637 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(291)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1719

```

Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe Leu
      1      5      10      15
Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      20      25      30
Met Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu Ser
      35      40      45
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Gln

```

50	55	60
Met Thr Val Asp Ile Gln Ser Arg Ser Arg Val Ile Ser Tyr Ala Gly		
65	70	75
Cys Leu Thr Gln Lys Ser Leu Phe Ala Ile Phe Gly Gly Thr Glu Glu		80
	85	90
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys		95
	100	105
His Pro Leu Tyr His Ser Ala Ile Met Asn Leu Cys Phe Cys Gly Phe		110
	115	120
Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu		125
	130	135
Tyr Asn Leu Ile Ala Leu Leu Met Thr Cys Phe Lys Glu Val Asp Ile		140
145	150	155
Pro Asn Phe Phe Cys Asp Leu Ser Gln Leu Pro His Leu Ala Cys Cys		160
	165	170
Asp Thr Phe Ile Asn Asn Ile Ile Met Tyr Phe Pro Thr Ala Ile Phe		175
	180	185
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val		190
	195	200
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe		205
210	215	220
Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Arg		225
225	230	235
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys		240
	245	250
Gly Ala Val Ala Ala Val Met Tyr Thr Val Val Thr Ser Met Leu Asn		255
	260	265
Pro Phe Ile Tyr Ser Leu Gly Asn Arg Asp Ile Lys Ser Val Leu Arg		270
	275	280
Arg Pro Gln		285
290		

&lt;210&gt; 1720

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g638 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1720

Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Thr Val Ile Ala		
1	5	10
Gly Leu Val Ile Gly Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala Ala		15
	20	25
Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val Glu Asn Phe Leu Leu		30
	35	40
Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val Cys Lys Pro Leu His		45
50	55	60
Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala Cys Leu Ala Ile Ile		65
65	70	75
Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile His Ile Gly Glu Thr		80
	85	90
Leu Ser Leu Phe Leu Tyr Gly Pro Asn Glu Val His Cys Phe Phe Cys		95
	100	105
Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys Asp Arg His Val Asn		110
	115	120
Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn Ile Phe Ser Ala Ile		125
	130	135
Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Lys		140
145	150	155
		160

Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu Ser Thr Cys Ala Ser  
                                   165                                  170                                  175  
 His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr  
                                   180                                  185                                  190  
 Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Leu Ala Ser  
                                   195                                  200                                  205  
 Val Phe Tyr Thr Met Ile Ile Pro  
                                   210                                  215

&lt;210&gt; 1721

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g639 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1721

Phe Val Asp Ile Cys Phe Ser Cys Thr Thr Val Pro Lys Met Leu Ala  
   1                                  5                                  10                                  15  
 Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr  
                                   20                                  25                                  30  
 Gln Met Tyr Phe Val Phe Met Phe Val Asp Thr Asp Asn Phe Leu Leu  
                                   35                                  40                                  45  
 Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His  
                                   50                                  55                                  60  
 Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly  
   65                                  70                                  75                                  80  
 Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met  
                                   85                                  90                                  95  
 Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys  
                                   100                                  105                                  110  
 Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn  
                                   115                                  120                                  125  
 Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe  
                                   130                                  135                                  140  
 Leu Cys Asn Leu Ala Ser Tyr Met His Ile Thr Cys Thr Gly Leu Lys  
   145                                  150                                  155                                  160  
 Gly Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser  
                                   165                                  170                                  175  
 His Leu Ala Val Gly Leu Leu Phe Tyr Ser Thr Ile Thr Ala Val Tyr  
                                   180                                  185                                  190  
 Phe Asn Pro Leu Ser Ser His Ser Ala Ala Lys Asp Thr Met Ala Thr  
                                   195                                  200                                  205  
 Val Leu Tyr Thr Val Val Thr Pro  
                                   210                                  215

&lt;210&gt; 1722

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g640 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1722

Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His Cys  
   1                                  5                                  10                                  15  
 Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser Thr  
                                   20                                  25                                  30  
 Ile His Thr Gly Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn Val

```

      35      40      45
Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser Cys
   50      55      60
Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala Phe
65      70      75      80
Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe Ile
      85      90      95
Ile Ala Ser Ile Leu Arg Ile Arg Ser Thr Glu Gly Arg Ser Lys Ala
      100      105      110
Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Gly Phe Phe Gly
      115      120      125
Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp
      130      135      140
Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Ile Val Val
145      150      155

```

&lt;210&gt; 1723

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g641 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1723

```

Met Lys Thr Leu Cys Ser Phe Leu Gln Ile Ser Arg Asn Met His Gln
 1      5      10      15
Glu Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Leu Ser Asn
      20      25      30
Gln Ala Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Ser Met Tyr
      35      40      45
Val Val Thr Val Val Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu
      50      55      60
Asp Ile Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Tyr Leu Ser
65      70      75      80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
      85      90      95
Asn Ile Gln Thr Asn Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
      100      105      110
Gln Met Tyr Phe Ser Ile Val Phe Val Val Thr Asp Asn Leu Leu Leu
      115      120      125
Gly Thr Met Ala Phe Asp His Phe Val Ala Ile Cys His Pro Leu Asn
      130      135      140
Tyr Thr Thr Phe Met Arg Ala Arg Phe Gly Thr Leu Leu Thr Val Ile
145      150      155      160
Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu
      165      170      175
Ile Gln Leu Leu Phe Cys Asp His Asn Thr Leu Pro His Phe Phe Cys
      180      185      190
Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Met Ile Asn
      195      200      205
Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe
      210      215      220
Val Leu Ile Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Gly
225      230      235      240
Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      245      250      255
His Leu Thr Ile Ala Leu Leu Phe Tyr Gly Thr Thr Val Gly Val Tyr
      260      265      270
Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala
      275      280      285

```

Val Leu Phe Thr Val Val Thr Pro Met Met Asn Pro Phe Ile Tyr Ser  
 290 295 300  
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg  
 305 310 315 320  
 Lys Ile Ser Ser Leu  
 325

<210> 1724

<211> 315

<212> PRT

<213> Unknown (H38g642 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1724

Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe Ser  
 1 5 10 15  
 Gln Asp Pro Gly Met Gln Lys Glu Leu Phe Val Met Phe Leu Phe Thr  
 20 25 30  
 Tyr Val Val Thr Val Leu Gly Asn Gln Leu Ile Val Val Thr Ile Ile  
 35 40 45  
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu  
 50 55 60  
 Ser Phe Ile Asp Ala Ala Tyr Phe Thr Val Ile Ser Pro Lys Leu Ile  
 65 70 75 80  
 Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Gln Thr Phe Met  
 85 90 95  
 Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Ala Phe Leu  
 100 105 110  
 Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Thr Leu  
 115 120 125  
 His Tyr Leu Thr Ile Met Thr Arg Gln Val Cys Ile Leu Ala Leu Leu  
 130 135 140  
 Val Ala Ala Thr Gly Gly Phe Val His Ser Val Phe Gln Ile Val Val  
 145 150 155 160  
 Val Tyr Ser Leu Pro Phe Cys Gly Ala Asn Val Ile Asp His Phe Ser  
 165 170 175  
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Xaa Thr Asp Thr Tyr Phe  
 180 185 190  
 Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Leu Cys Met Val Ile  
 195 200 205  
 Phe Thr Leu Leu Ile Ile Ser Tyr Arg Val Ile Leu Asn Ser Leu Lys  
 210 215 220  
 Thr Tyr Thr Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser  
 225 230 235 240  
 His Ile Thr Val Ile Val Leu Phe Phe Ile Pro Cys Ile Ser Ile Tyr  
 245 250 255  
 Val Arg Pro Val Ser Asn Phe Ser Ile Asp Thr Phe Met Thr Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Tyr Thr Phe Arg  
 275 280 285  
 Asn Ser Glu Met Arg Asn Val Ile Glu Lys Leu Leu Val Lys Lys Val  
 290 295 300  
 Thr Ile Phe Arg Ile Thr Gly Ser Ile Leu Met  
 305 310 315

<210> 1725  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g643 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(314)  
 <223> Xaa = Any Amino Acid

<400> 1725  
 Met Arg Gln Asn Lys Asn Asn Thr Glu Phe Val Leu Leu Gly Phe Ser  
 1 5 10 15  
 Gln Asp Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Thr  
 20 25 30  
 Xaa Leu Val Thr Thr Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile  
 35 40 45  
 Ala Ser Pro Ser Leu Gly Ser Pro Val Tyr Phe Xaa Leu Ala Cys Leu  
 50 55 60  
 Ser Cys Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile  
 65 70 75 80  
 Val Glu Leu Leu Ile Asp Lys Lys Thr Ile Ser Phe Arg Ala Cys Met  
 85 90 95  
 Gly Gln Leu Phe Ile Glu His Leu Phe Gly Gly Thr Glu Ile Phe Ile  
 100 105 110  
 Leu Met Met Met Ala Cys Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val  
 130 135 140  
 Leu Ala Val Thr Gly Gly Phe Val His Ser Met Phe Gln Thr Val Val  
 145 150 155 160  
 Val Tyr Asn Leu Pro Phe Ser Gly Pro Asn Val Ile Asp Ile Asp His  
 165 170 175  
 Phe Val Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Phe Thr Asp Thr  
 180 185 190  
 Tyr Phe Ile Gly Leu Thr Val Val Val Asn Gly Gly Ala Met Cys Met  
 195 200 205  
 Val Ile Phe Thr Ile Leu Leu Ile Ser Tyr Gly Ile Ile Leu Asn Ser  
 210 215 220  
 Leu Lys Thr Tyr Ser Gln Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Ser Pro His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe  
 245 250 255  
 Ile Tyr Val Arg Pro Val Ser Thr Phe Pro Ile Asp Lys Phe Met Thr  
 260 265 270  
 Val Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Ser Glu Met Arg Asn Ser Ile Glu Asn Leu Leu Cys Lys  
 290 295 300  
 Lys Ala Ile Cys Ser Xaa Asn Lys Ser Val  
 305 310

<210> 1726  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g644 protein)

<220>  
 <223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1726

Glu	Xaa	Met	Arg	Gln	Asn	Asn	Ser	Ser	Thr	Glu	Phe	Val	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Gln	Asp	Pro	Asp	Val	Gln	Asn	Ala	Leu	Phe	Val	Met	Phe	Leu
			20					25					30		
Leu	Thr	Tyr	Ile	Val	Thr	Met	Val	Gly	Asn	Leu	Leu	Ile	Val	Val	Thr
		35					40					45			
Ile	Ile	Ala	Ser	Pro	Ser	Leu	Gly	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
His	Leu	Ser	Phe	Ile	Asp	Ala	Val	Tyr	Ser	Thr	Thr	Ile	Ser	Pro	Val
65					70					75					80
Leu	Ile	Val	Asp	Leu	Leu	Cys	Asp	Lys	Lys	Thr	Ile	Ser	Phe	Xaa	Ala
			85						90					95	
Cys	Met	Gly	Gln	Leu	Phe	Ile	Asp	His	Leu	Phe	Gly	Gly	Ser	Glu	Val
			100					105					110		
Phe	Leu	Leu	Val	Val	Met	Ala	Cys	Asp	Arg	Cys	Val	Ala	Ile	Cys	Lys
	115						120					125			
Pro	Leu	His	Tyr	Leu	Thr	Ile	Met	Asn	Arg	Gln	Val	Cys	Ile	Leu	Leu
	130					135					140				
Leu	Val	Leu	Ala	Val	Thr	Gly	Gly	Phe	Val	His	Pro	Val	Phe	Gln	Val
145					150					155					160
Val	Val	Val	Tyr	Ser	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His
			165						170					175	
Phe	Phe	Cys	Asp	Ile	Tyr	Pro	Leu	Leu	Glu	Leu	Ala	Cys	Thr	Asp	Thr
			180					185					190		
Tyr	Phe	Ile	Gly	Leu	Thr	Val	Val	Phe	Asn	Gly	Gly	Ala	Met	Arg	Met
	195						200					205			
Val	Ile	Leu	Thr	Leu	Leu	Leu	Val	Phe	Tyr	Gly	Val	Ile	Leu	Asn	Ser
	210					215					220				
Leu	Lys	Thr	Tyr	Ser	Gln	Gly	Arg	His	Lys	Ala	Leu	Ser	Thr	Cys	
225					230				235					240	
Ser	Ser	His	Val	Thr	Val	Val	Ile	Leu	Phe	Phe	Ala	Ser	Cys	Ile	Phe
			245						250					255	
Ile	Tyr	Val	Arg	Pro	Val	Ser	Asn	Phe	Pro	Val	Asp	Lys	Phe	Met	Thr
		260						265					270		
Val	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Cys	Met
		275					280					285			
Leu	Arg	Asn	Ser	Glu	Met	Arg	Asn	Ala	Ile	Glu	Lys	Leu	Leu	Cys	Lys
	290					295					300				
Met	Asn	Cys	Ser	Xaa	Asn	Lys	Ser	Val	Pro	Ser					
305					310					315					

&lt;210&gt; 1727

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g645 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1727

Met Gly Leu Ser Asn Asn Val Thr Glu Leu Phe Leu Leu Gly Leu Thr

```

      1      5      10      15
Gln Asp Leu Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Thr
      20      25      30
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
      35      40      45
Ala Thr Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
      50      55      60
Ser Phe Ile Asp Ala Val Tyr Ser Thr Thr Ile Tyr Pro Lys Leu Val
      65      70      75      80
Val Asp Xaa Leu His Asn Xaa Lys Thr Ile Leu Phe Pro Thr Cys Met
      85      90      95
Gly Gln Pro Leu Thr Asp His Leu Phe Gly Gly Val Glu Val Phe Phe
      100      105      110
Leu Leu Val Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Phe Thr Ile Met Asn Arg Gln Val Phe Ile Leu Leu Leu Val
      130      135      140
Val Ala Val Thr Gly Gly Phe Val Arg Ser Val Phe Gln Ile Val Val
      145      150      155      160
Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe
      165      170      175
Cys Asn Met Tyr Pro Leu Met Glu Met Ala Xaa Thr Asp Thr Tyr Phe
      180      185      190
Ile Gly Leu Thr Val Val Phe Lys Val Glu Ala Ile Cys Val Val Ile
      195      200      205
Phe Thr Leu Leu Leu Ile Ser Ser Gly Val Ile Leu Ile Ser Leu Lys
      210      215      220
Thr Tyr Ser Gln Glu Gly Arg His Lys Ala Leu Phe Thr Cys Ser Ser
      225      230      235      240
Arg Ile Thr Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245      250      255
Val Arg Pro Val Phe Asn Phe Pro Ile Asp Lys Phe Ile Ile Val Phe
      260      265      270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Met Leu Arg
      275      280      285
Asn Ser Xaa Thr Arg Asn Ala Ile Glu Asn Pro Xaa Cys Lys Lys Leu
      290      295      300
Thr Val Asp Arg Ile Arg Val Tyr Ile
      305      310

```

&lt;210&gt; 1728

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g646 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1728

```

Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
      1      5      10      15
Gln Asp Pro Asp Met Gln Asn Thr Leu Phe Val Met Phe Leu Leu Thr
      20      25      30
Tyr Ile Val Thr Val Val Gly Asn Leu Leu Val Ala Val Thr Ile Ile
      35      40      45
Val Ser Pro Ser Leu Ser Ser Pro Met Xaa Phe Phe Leu Ala Cys Leu
      50      55      60

```



Ser Leu Ile Asp Ala Val Leu Ser Thr Thr Ile Ser Pro Ile Leu Ile  
 65 70 75 80  
 Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met  
 85 90 95  
 Gly Gln Leu Phe Thr Asp His Leu Phe Gly Gly Thr Glu Ile Phe Leu  
 100 105 110  
 Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Thr Ile Met Asn Arg Gln Val Ser Ile Leu Leu Leu Val  
 130 135 140  
 Val Ala Met Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Ala Val  
 145 150 155 160  
 Leu Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe  
 165 170 175  
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Ser  
 180 185 190  
 Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Met Cys Met Val Ile  
 195 200 205  
 Phe Ala Leu Leu Leu Ile Ser Tyr Gly Val Ser Leu Asn Ser Leu Lys  
 210 215 220  
 Thr Tyr Ser Gln Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Ser Ser  
 225 230 235 240  
 His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr  
 245 250 255  
 Val Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Val Thr Val Phe  
 260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Phe Leu Tyr Thr Leu Arg  
 275 280 285  
 Asn Ser Glu Met Ile Asn Ala Ile Lys His Leu Leu Cys Lys Lys Leu  
 290 295 300  
 Thr Ile Val Arg Ile Arg Val Ser Leu Leu Met  
 305 310 315

&lt;210&gt; 1729

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g647 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1729

Met Gly Ser Ser Asn Asn Val Thr Glu Phe Val Leu Leu Ala Leu Thr  
 1 5 10 15  
 Gln Ala Pro Asp Val Gln Lys Val Leu Phe Val Met Phe Leu Phe Thr  
 20 25 30  
 Tyr Ile Val Thr Met Val Gly Asn Leu Leu Thr Val Val Thr Ile Phe  
 35 40 45  
 Ala Ser Pro Ser Leu Gly Ser Pro Val Xaa Leu Phe Leu Ala Cys Leu  
 50 55 60  
 Ser Leu Met Asp Ala Val Tyr Ser Thr Ser Phe Ser Pro Lys Leu Met  
 65 70 75 80  
 Ile Asp Leu Leu Cys Asp Lys Lys Thr Val Ser Phe Pro Ala Cys Met  
 85 90 95  
 Gly Gln Leu Phe Ala Asp His Leu Phe Gly Gly Val Glu Val Phe Leu  
 100 105 110  
 Phe Val Gly Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu

```

      115      120      125
His Tyr Leu Ile Ile Val Asn Arg Leu Val Cys Ile Leu Leu Leu Val
  130      135      140
Val Ala Val Thr Gly Gly Phe Xaa His Ser Met Phe Leu Phe Phe Xaa
145      150      155      160
Ile Tyr Leu Phe Phe Tyr Val Asn Ser Met Phe Gln Ile Val Val Val
      165      170      175
Tyr Ser Leu Pro Phe Cys Gly Ser Asn Val Ile Asp His Ile Val Cys
      180      185      190
Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Ala Asp Thr Tyr Phe Ile
      195      200      205
Gly Leu Thr Val Ile Ala Asn Gly Gly Ala Ile Cys Met Val Ile Phe
      210      215      220
Cys Leu Leu Leu Thr Ser Tyr Gly Val Ile Leu Asn Phe Leu Lys Thr
225      230      235      240
Tyr Ser Gln Glu Gly Arg His Arg Thr Leu Ser Thr Cys Ser Ser His
      245      250      255
Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr Val
      260      265      270
Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Ile Thr Glu Phe Tyr
      275      280      285
Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Gln Pro Leu Arg Asn
      290      295      300
Xaa Glu Met Arg Ile Thr Met Lys Lys Leu Trp Cys Xaa Thr Xaa Thr
305      310      315      320
Ile Val

```

&lt;210&gt; 1730

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g648 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1730

```

Met Lys Asn Lys Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
  1      5      10      15
Gln Asn Pro Glu Gly Gln Lys Val Leu Phe Val Thr Phe Leu Leu Ile
      20      25      30
Tyr Met Val Thr Ile Met Gly Asn Leu Leu Ile Ile Val Thr Ile Met
      35      40      45
Ala Ser Gln Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu
      50      55      60
Ser Phe Ile Asp Thr Val Tyr Ser Thr Ala Phe Ala Pro Lys Met Ile
      65      70      75      80
Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Gln Gly Cys Met
      85      90      95
Ala Gln Leu Phe Met Asp His Leu Phe Ala Gly Ala Glu Val Ile Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys Pro Leu
      115      120      125
His Glu Leu Ile Thr Met Asn Arg Arg Val Cys Val Leu Met Leu Leu
      130      135      140
Ala Ala Trp Ile Gly Gly Phe Leu His Ser Leu Val Gln Phe Leu Phe
145      150      155      160
Ile Tyr Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Asn Phe Leu
      165      170      175
Cys Asp Leu Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asn Thr Tyr Val
      180      185      190

```

Thr Gly Leu Ser Met Ile Ala Asn Gly Gly Ala Ile Cys Ala Val Thr  
 195 200 205  
 Phe Phe Thr Ile Leu Leu Ser Tyr Gly Val Ile Leu His Ser Leu Lys  
 210 215 220  
 Thr Gln Ser Leu Glu Gly Lys Arg Lys Ala Phe Tyr Thr Cys Ala Ser  
 225 230 235 240  
 His Val Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr  
 245 250 255  
 Ala Arg Pro Asn Ser Thr Phe Pro Ile Asp Lys Ser Met Thr Val Val  
 260 265 270  
 Leu Thr Phe Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Lys  
 275 280 285  
 Asn Ala Glu Met Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Val  
 290 295 300  
 Ser Leu Ala Gly Lys Trp  
 305 310

&lt;210&gt; 1731

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g649 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1731

Met Val Gly Asn Leu Leu Ile Trp Val Thr Thr Ile Gly Ser Pro Ser  
 1 5 10 15  
 Leu Gly Ser Leu Met Tyr Phe Phe Leu Ala Tyr Leu Ser Leu Met Asp  
 20 25 30  
 Ala Ile Tyr Ser Thr Ala Met Ser Pro Lys Leu Met Ile Asp Leu Leu  
 35 40 45  
 Cys Asp Lys Ile Ala Ile Ser Leu Ser Ala Cys Met Gly Gln Leu Phe  
 50 55 60  
 Ile Glu His Leu Leu Gly Gly Ala Glu Val Phe Leu Leu Val Val Met  
 65 70 75 80  
 Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro Leu His Tyr Leu Asn  
 85 90 95  
 Ile Met Asn Arg Leu Val Cys Ile Leu Leu Leu Val Val Ala Met Ile  
 100 105 110  
 Gly Gly Phe Val His Ser Val Val Gln Ile Val Phe Leu Tyr Ser Leu  
 115 120 125  
 Pro Ile Cys Gly Pro Asn Val Ile Asp His Ser Val Cys Asp Met Tyr  
 130 135 140  
 Pro Leu Leu Glu Leu Leu Cys Leu Asp Thr Tyr Phe Ile Gly Leu Thr  
 145 150 155 160  
 Val Val Ala Asn Gly Gly Ile Ile Cys Met Val Ile Phe Thr Phe Leu  
 165 170 175  
 Leu Ile Ser Cys Gly Val Ile Leu Asn Phe Leu Lys Thr Tyr Ser Gln  
 180 185 190  
 Glu Glu Arg His Lys Ala Leu Pro Thr Cys Ile Ser His Ile Ile Val  
 195 200 205  
 Val Ala Leu Val Phe Val Pro Cys Ile Phe Met Tyr Val Arg Pro Val  
 210 215 220  
 Ser Asn Phe Pro Phe Asp Lys Leu Met Thr Val Phe Tyr Ser Ile Ile  
 225 230 235 240  
 Thr Leu Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Gln Ser Glu Met  
 245 250 255  
 Lys Asn Ala Met Lys Asn Leu Trp Cys Glu Lys Leu Ser Ile Val Arg  
 260 265 270  
 Lys Arg Val

275

<210> 1732  
 <211> 218  
 <212> PRT  
 <213> Unknown (H38g650 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(218)  
 <223> Xaa = Any Amino Acid

<400> 1732  
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Leu Ile Ser Xaa Ala Gly Cys Leu Thr  
 20 25 30  
 Pro Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu  
 35 40 45  
 Leu Ser Val Ile Ala Tyr Asp Pro Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 65 70 75 80  
 Leu Ser Phe Phe Ser Gln Ser Leu Leu Asp Ala Gln Val His Asn Leu  
 85 90 95  
 Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe  
 100 105 110  
 Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe  
 115 120 125  
 Thr Asn Asn Ile Ile Met Tyr Ser Pro Ala Ala Ile Phe Gly Phe Leu  
 130 135 140  
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile  
 145 150 155 160  
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Leu Ser Thr Cys  
 165 170 175  
 Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly  
 180 185 190  
 Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val  
 195 200 205  
 Ala Ser Val Met Tyr Thr Val Val Thr Pro  
 210 215

<210> 1733  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g651 protein)

<220>  
 <223> Synthetic construct

<400> 1733  
 Ser Met Ala Leu Met Leu Ile Cys Thr Thr Gly Pro Lys Met Ala Phe  
 1 5 10 15  
 Asn Tyr Leu Ser Gly Ser Lys Ser His Phe Tyr Gly Cys Cys Ala Thr  
 20 25 30  
 Gln Ile Phe Phe Tyr Thr Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile Cys His Pro Leu Arg  
 50 55 60

Tyr Thr Asn Leu Met Ser Pro Lys Ile Cys Gly Leu Met Thr Ala Phe  
 65 70 75 80  
 Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Val Val Ala Thr  
 85 90 95  
 Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys  
 100 105 110  
 Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Ser Asp Thr Ser Ile Phe  
 115 120 125  
 Glu Lys Ile Leu Phe Ile Cys Cys Ile Val Met Ile Val Phe Pro Val  
 130 135 140  
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His  
 145 150 155 160  
 Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser  
 165 170 175  
 His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr  
 180 185 190  
 Ile Arg Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys Met Val Ser  
 195 200 205  
 Val Phe Tyr Thr Ile Leu Thr Pro  
 210 215

&lt;210&gt; 1734

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g652 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1734

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu  
 1 5 10 15  
 Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr  
 20 25 30  
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe Val Leu  
 35 40 45  
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg  
 50 55 60  
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu  
 65 70 75 80  
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr  
 85 90 95  
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Glu His Tyr Phe Cys  
 100 105 110  
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val  
 115 120 125  
 Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe  
 130 135 140  
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys  
 145 150 155 160  
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His  
 165 170 175  
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg  
 180 185 190  
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr  
 195 200 205  
 Thr Ile Thr Pro

210

<210> 1735  
 <211> 223  
 <212> PRT  
 <213> Unknown (H38g653 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(223)  
 <223> Xaa = Any Amino Acid

<400> 1735  
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Ile Phe Xaa Gly Arg Glu Glu Ser Met Leu  
 35 40 45  
 Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Pro  
 50 55 60  
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Val Cys  
 65 70 75 80  
 Cys Pro Cys Phe Phe Phe Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser  
 85 90 95  
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val  
 100 105 110  
 Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala  
 115 120 125  
 Cys Cys Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala  
 130 135 140  
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys  
 145 150 155 160  
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Gly Gly Arg Tyr Lys  
 165 170 175  
 Ala Leu Ser Thr Cys Gly Ser His Val Ser Val Val Cys Xaa Val Tyr  
 180 185 190  
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro  
 195 200 205  
 Arg Lys Gly Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro  
 210 215 220

<210> 1736  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g654 protein)

<220>  
 <223> Synthetic construct

<400> 1736  
 Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val  
 1 5 10 15  
 Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala  
 20 25 30  
 Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu  
 35 40 45  
 Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His  
 50 55 60

Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala  
 65 70 75 80  
 Ser Arg Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr  
 85 90 95  
 Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys  
 100 105 110  
 Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn  
 115 120 125  
 Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu  
 130 135 140  
 Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg  
 145 150 155 160  
 Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser  
 165 170 175  
 His Leu Ile Val Val Ser Leu Phe Asn Ser Thr Ala Val Ser Val Tyr  
 180 185 190  
 Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser  
 195 200 205  
 Leu Phe Tyr Gly Ile Ile Ala Pro  
 210 215

&lt;210&gt; 1737

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g655 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(218)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1737

Leu Pro Asp Ile Gly Phe Thr Ser Thr Ile Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Asp Ser Met Leu  
 35 40 45  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu  
 65 70 75 80  
 Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln Leu His Asn Leu  
 85 90 95  
 Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe  
 100 105 110  
 Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe  
 115 120 125  
 Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu  
 130 135 140  
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Ser Ser Ile  
 145 150 155 160  
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Tyr  
 165 170 175  
 Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr Gly Thr Gly Val Gly  
 180 185 190  
 Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val  
 195 200 205  
 Ala Ser Val Met Tyr Thr Val Val Thr Pro

210

215

<210> 1738  
 <211> 221  
 <212> PRT  
 <213> Unknown (H38g656 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(221)  
 <223> Xaa = Any Amino Acid

<400> 1738  
 Phe Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Pro Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Ile Phe Gly Asp Thr Glu Glu Asn Met Phe  
 35 40 45  
 Leu Ser Val Val Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Ser  
 65 70 75 80  
 Leu Ser Leu Val Phe Phe Phe Phe Phe Ser Leu Leu Asp Ser Gln Leu  
 85 90 95  
 His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile  
 100 105 110  
 Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys Cys  
 115 120 125  
 Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala Ile Phe  
 130 135 140  
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Cys Tyr Lys Ile Val  
 145 150 155 160  
 Ser Phe Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe  
 165 170 175  
 Ser Ala Cys Gly Ser His Leu Ser Val Val Tyr Xaa Phe Tyr Gly Thr  
 180 185 190  
 Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys  
 195 200 205  
 Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro  
 210 215 220

<210> 1739  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g657 protein)

<220>  
 <223> Synthetic construct

<400> 1739  
 Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly  
 1 5 10 15  
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser  
 20 25 30  
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu  
 35 40 45  
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala Ile Cys Gln Pro Leu Thr  
 50 55 60



```

Tyr Ser Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
65      70      75      80
Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Ala Met
      85      90      95
Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu Val Asn His Phe Tyr Cys
      100     105     110
Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys Ser Ser Thr Gln Leu Asn
      115     120     125
Glu Leu Leu Leu Phe Val Ala Ala Phe Met Ala Val Ala Pro Leu
      130     135     140
Val Phe Ile Ser Val Pro Tyr Ala His Val Val Ala Ala Val Leu Gln
145      150     155     160
Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
      165     170     175
His Leu Thr Val Val Gly Ile Phe Tyr Gly Thr Gly Val Phe Ser Tyr
      180     185     190
Met Arg Leu Gly Ser Val Glu Ser Ser Asp Lys Asp Lys Gly Val Gly
      195     200     205
Val Phe Met Thr Val Ile Asn Pro
      210     215

```

&lt;210&gt; 1740

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g658 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1740

```

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
1      5      10      15
Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
      20      25      30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
      35      40      45
Thr Val Met Ala Phe Asp Arg Cys Ala Ala Ile Cys Gln Pro Leu Arg
      50      55      60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65      70      75      80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
      85      90      95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
      100     105     110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
      115     120     125
Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
      130     135     140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
145      150     155     160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
      165     170     175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
      180     185     190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
      195     200     205
Thr Ile Thr Pro

```

210

<210> 1741  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g659 protein)

<220>  
 <223> Synthetic construct

<400> 1741  
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln  
 1 5 10 15  
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp Cys Leu Thr  
 20 25 30  
 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu  
 35 40 45  
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
 50 55 60  
 Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu  
 65 70 75 80  
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met  
 85 90 95  
 Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys  
 100 105 110  
 Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr Arg Val Asn  
 115 120 125  
 Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe  
 130 135 140  
 Leu Leu Ile Leu Gly Ser Tyr Ala Arg Val Val Ser Ser Ile Leu Lys  
 145 150 155 160  
 Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr  
 180 185 190  
 Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala  
 195 200 205  
 Met Met Tyr Thr Val Val Thr Pro  
 210 215

<210> 1742  
 <211> 146  
 <212> PRT  
 <213> Unknown (H38g660 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(146)  
 <223> Xaa = Any Amino Acid

<400> 1742  
 Thr Leu Gln Asn Ile Thr Ser Thr Ser Ile Ile Phe Leu Leu Thr Gly  
 1 5 10 15  
 Val Pro Gly Leu Glu Ala Phe His Thr Trp Ile Ser Ile Pro Phe Cys  
 20 25 30  
 Phe Leu Ser Val Thr Ala Leu Leu Gly Asn Ser Leu Ile Leu Phe Ala  
 35 40 45  
 Thr Ile Thr Gln Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60

Met Leu Ser Ala Thr Asp Leu Gly Leu Ser Ile Ser Thr Leu Val Thr  
 65 70 75 80  
 Met Leu Ser Ile Phe Trp Phe Asn Val Arg Glu Ile Ser Phe Asn Ala  
 85 90 95  
 Cys Leu Ser His Met Phe Phe Ile Lys Phe Phe Thr Val Met Glu Ser  
 100 105 110  
 Ser Val Leu Leu Ala Met Ala Phe Asp Arg Leu Val Pro Ser Leu Ser  
 115 120 125  
 Pro Xaa Tyr Ala Met Ile Xaa Leu Thr Gln Ile Ala Lys Met Ser Ala  
 130 135 140  
 Val Tyr  
 145

<210> 1743

<211> 334

<212> PRT

<213> Unknown (H38g661 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1743

Ala Gly Val Glu Asn Asp Asn Thr Ser Ser Phe Glu Gly Phe Ile Leu  
 1 5 10 15  
 Val Gly Phe Ser Asp Arg Pro His Leu Glu Leu Ile Val Phe Val Val  
 20 25 30  
 Val Leu Ile Phe Tyr Leu Leu Thr Leu Leu Gly Asn Met Thr Ile Val  
 35 40 45  
 Leu Leu Ser Ala Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ala Asn Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Gly Ser Ile  
 65 70 75 80  
 Pro Gln Met Leu Tyr Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr  
 85 90 95  
 Val Gly Cys Ala Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Gly Val  
 100 105 110  
 Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Val  
 115 120 125  
 Cys Lys Pro Leu His Tyr Thr Ile Ile Met His Pro Arg Leu Cys Gly  
 130 135 140  
 Gln Leu Ala Ser Val Ala Trp Leu Ser Gly Phe Gly Asn Ser Leu Ile  
 145 150 155 160  
 Met Ala Pro Gln Thr Leu Met Leu Pro Arg Cys Gly His Arg Arg Val  
 165 170 175  
 Asp His Phe Leu Cys Glu Met Pro Ala Leu Ile Gly Met Ala Cys Val  
 180 185 190  
 Asp Thr Met Met Leu Glu Ala Leu Ala Phe Ala Leu Ala Ile Phe Ile  
 195 200 205  
 Ile Leu Ala Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Val Gly  
 210 215 220  
 Gly Thr Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe  
 225 230 235 240  
 Asn Thr Cys Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr  
 245 250 255  
 Ile Ile Tyr Met Tyr Leu Gln Pro Ala Asn Thr Tyr Ser Gln Asp Gln  
 260 265 270  
 Gly Lys Phe Leu Thr Leu Phe Tyr Thr Ile Val Thr Pro Ser Val Asn

275	280	285
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Met Lys		
290	295	300
Lys Val Leu Gly Lys Gly Ser Ala Glu Ile Xaa Xaa Gly Val Ile Lys		
305	310	315
Leu Trp Asp Cys Ile Leu Thr His Leu Leu Tyr Met Leu Leu		
325	330	

&lt;210&gt; 1744

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g662 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(275)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1744

Leu Tyr Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Tyr		
1	5	10
Phe Leu Thr Met Leu Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr		
20	25	30
Met Pro Thr Val Met Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser		
35	40	45
Ser Val Gly Cys Phe Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val		
50	55	60
Val Glu Ser Gly Ser Leu Ala Met Ala Tyr Asp Arg Leu Ile Ala		
65	70	75
Ile Arg Asn Pro Leu Arg Tyr Ala Ser Ile Ser Thr Asn Thr Arg Val		
85	90	95
Ile Ala Leu Gly Val Gly Leu Phe Leu Arg Gly Leu Val Ser Ile Leu		
100	105	110
Pro Val Ile Leu Arg Leu Phe Pro Phe Pro Tyr Gly Lys Ser His Val		
115	120	125
Ile Thr Arg Ala Phe Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys		
130	135	140
Ala Asp Ile Thr Ser Asn Lys Leu Tyr Pro Val Ile Leu Ile Ser Leu		
145	150	155
Thr Ile Ser Leu Asn Ser Leu Ile Thr Pro Ser Ser Tyr Ile Leu Ile		
165	170	175
Leu Asn Thr Val Ile Gly Ile Ala Ser Gly Glu Glu Lys Thr Lys Ala		
180	185	190
Leu Asn Thr Cys Ile Ser His Ile Ser Cys Val Leu Ile Ser Tyr Val		
195	200	205
Thr Val Met Gly Leu Thr Phe Ile Tyr Lys Phe Gly Lys Asn Val Pro		
210	215	220
Lys Val Val His Ile Ile Ile Ser Tyr Ile Tyr Phe Leu Phe Pro Pro		
225	230	235
Leu Met Asn Pro Val Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr		
245	250	255
Gly Ile Ile Arg Leu Leu Ser Lys His Arg Phe Ser Arg Xaa Thr Arg		
260	265	270
Ile Trp Lys		
275		

&lt;210&gt; 1745

&lt;211&gt; 219

&lt;212&gt; PRT

<213> Unknown (H38g663 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amino Acid

<400> 1745

```

Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met Glu Glu Asn Met Leu
          35           40           45
Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr Cys Ser Ala Ile Phe Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
          65           70           75           80
Leu Ser Phe Phe Phe Phe Phe Leu Ser Leu Ser Asp Ser Gln Leu His
          85           90           95
Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro
          100          105          110
Asn Phe Phe Trp Glu Pro Ser Gln Leu Ser His Leu Ala Cys Cys Asp
          115          120          125
Thr Phe Thr Arg Asn Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
          130          135          140
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Phe Ser
          145          150          155          160
Ile Leu Arg Val Ser Ser Ser Gly Gly Lys His Lys Ala Phe Ser Thr
          165          170          175
Arg Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Ile
          180          185          190
Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Ala Ala
          195          200          205
Val Ala Ser Val Met Tyr Thr Val Ala Ile Pro
          210          215

```

<210> 1746

<211> 218

<212> PRT

<213> Unknown (H38g664 protein)

<220>

<223> Synthetic construct

<400> 1746

```

Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro Lys Met Val Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Thr Leu Leu
          35           40           45
Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu
          65           70           75           80
Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu His Asn Met
          85           90           95
Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu Ile Pro Asn Phe

```

<220>  
<223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(216)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1748

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
      20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
      35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
      50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
      65           70           75           80
Leu Ser Phe Phe Phe Ser Phe Ser Gln Leu His Asn Leu Ile Ala Leu
      85           90           95
Lys Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp
      100          105          110
Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Lys
      115          120          125
Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser
      130          135          140
Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile Leu Arg Val
      145          150          155          160
Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His
      165          170          175
Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly Gly Tyr Leu
      180          185          190
Ser Ser Asp Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val Ala Ser
      195          200          205
Val Met Tyr Thr Val Val Thr Pro
      210          215

```

&lt;210&gt; 1749

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g667 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1749

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
      20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
      35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
      50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
      65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
      85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
      100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
      115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro

```

130	135	140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu		
145	150	155
Gly Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser		160
	165	170
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met		175
	180	185
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu		190
	195	200
Ser Leu Phe Tyr Ser Leu Phe Asn Pro		205
210	215	

&lt;210&gt; 1750

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g668 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1750

Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Thr Val Ile Ala		
1	5	10
Gly Leu Val Ile Gly Asp Glu Val Ile Ser Tyr Ser Ala Cys Ala Ala		15
	20	25
Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val Glu Asn Phe Leu Leu		30
	35	40
Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val Cys Lys Pro Leu His		45
	50	55
Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala Cys Leu Ala Ile Ile		60
65	70	75
Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile His Ile Gly Glu Thr		80
	85	90
Leu Ser Leu Phe Leu Asn Gly Pro Asn Glu Val His Cys Ile Phe Cys		95
	100	105
Asp Val Pro Val Met Ala Leu Ser Cys Cys Asp Arg His Val Asn		110
	115	120
Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn Ile Phe Ser Ala Ile		125
	130	135
Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Glu		140
145	150	155
Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu Ser Asn Cys Ala Ser		160
	165	170
His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr		175
	180	185
Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Leu Ala Ser		190
	195	200
Val Phe Tyr Thr Met Ile Ile Pro		205
210	215	

&lt;210&gt; 1751

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g669 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1751

Met Ala Ala Glu Asn Ser Ser Phe Val Thr Gln Phe Ile Leu Ala Gly		
1	5	10
		15



Leu Thr Asp Gln Pro Gly Val Gln Ile Pro Leu Phe Phe Leu Phe Leu  
 20 25 30  
 Gly Phe Tyr Val Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Ser Glu Ser  
 100 105 110  
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu  
 130 135 140  
 Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr  
 145 150 155 160  
 Ala Cys Met Met Gly Val Thr Phe Cys Ala Asn Asn Leu Val Asn His  
 165 170 175  
 Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Cys Ala Cys Thr Ser Thr  
 180 185 190  
 Tyr Val Asn Glu Leu Val Val Phe Val Val Val Gly Ile Asp Ile Gly  
 195 200 205  
 Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser  
 210 215 220  
 Ile Phe His Ile Asp Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala  
 245 250 255  
 Phe Met Tyr Leu Lys Pro Phe Ser Leu Leu Ala Met Asn Gln Gly Lys  
 260 265 270  
 Val Ser Ser Leu Phe Tyr Thr Thr Val Val Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Lys Lys Ile  
 290 295 300  
 Leu Asn Lys Asn Ala Phe Ser  
 305 310

&lt;210&gt; 1752

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g670 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1752

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly  
 1 5 10 15  
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys  
 65 70 75 80  
 Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys  
 85 90 95  
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr

```

      100      105      110
Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
      115      120      125
Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met
      130      135      140
Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly
145      150      155      160
Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr
      165      170      175
Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His
      180      185      190
Val Ser Glu Leu Val Phe Phe Ile Val Val Gly Val Ile Thr Met Leu
      195      200      205
Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile
      210      215      220
Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Trp
225      230      235      240
Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe Gly Ser Gly Thr Phe
      245      250      255
Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Asn His Gly Arg Phe
      260      265      270
Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Ser Ile
      275      280      285
Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala Leu Gly Lys Thr Leu
      290      295      300
Lys Arg Val Leu Phe
305

```

&lt;210&gt; 1753

&lt;211&gt; 297

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g671 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(297)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1753

```

Met Lys Xaa Met Ala Val Glu Asn Asn Ser Ser Val Thr Glu Phe Ile
 1      5      10      15
Leu Val Arg Leu Thr Asn Ser Arg Cys Pro Ser Val Leu Phe Leu Met
      20      25      30
Trp Ser Leu Trp Gly Glu Phe Glu His Asn Phe Met Ser Leu Asn Ser
      35      40      45
His Leu His Thr Pro Thr His Phe Phe Leu Phe Thr Leu Ser Phe Ile
      50      55      60
Asp Val Cys Tyr Ser Phe Val Cys Thr Thr Lys Ile Pro Met Gly Phe
65      70      75      80
Ile Ser Glu Arg Asn Ile Ile Ser Phe Val Gly Trp Pro Thr Xaa Leu
      85      90      95
Tyr Phe Phe Cys Ile Phe Val Lys Glu Pro Lys Asn Gly Val Ile Val
      100      105      110
Gly Ile Met Phe Ser Ala Lys Met Leu Val Cys Arg Glu Ile Met Asp
      115      120      125
Xaa Ser Leu Met Xaa Asn Xaa Lys Met His Met Ala Leu Glu Arg Ser
      130      135      140
Asp Phe Arg Met Gly Xaa Thr Gly Ser Ala Thr Lys Lys His Leu Ile
145      150      155      160

```

<210> 1754  
<211> 313  
<212> PRT  
<213> Unknown (H38g672 protein)  
  
<220>  
<223> Synthetic construct

973

[illegible]

<210> 1755

**<211> 357**

<212> PRT

<213> Unknown (H38g673 protein)

**<220>**

<223> Synthetic construct

**<400> 1755**

Met 1	Asn	Trp	Val	Asn 5	Lys	Ser	Val	Pro	Gln 10	Glu	Phe	Ile	Leu 15	Leu	Val
Phe	Ser	Asp	Gln 20	Pro	Trp	Leu	Glu	Ile 25	Pro	Pro	Phe	Val 30	Met	Phe	Leu
Phe	Ser	Tyr	Ile 35	Leu	Thr	Ile	Phe 40	Gly	Asn	Leu	Thr	Ile 45	Ile	Leu	Val
Ser	His 50	Val	Asp	Phe	Lys	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Ser
Asn 65	Leu	Ser	Leu	Leu	Asp 70	Leu	Cys	Tyr	Thr	Thr 75	Ser	Thr	Val	Pro	Gln
Met	Leu	Val	Asn 85	Ile	Cys	Asn	Thr	Arg 90	Lys	Val	Ile	Ser	Tyr 95	Gly	Gly
Cys	Val	Ala	Gln 100	Leu	Phe	Ile	Phe 105	Leu	Ala	Leu	Gly	Ser	Thr 110	Glu	Cys
Leu	Leu	Leu	Ala 115	Val	Met	Cys	Phe 120	Asp	Arg	Phe	Val	Ala 125	Ile	Cys	Arg
Pro	Leu	His	Tyr 130	Ser	Ile	Ile 135	Met	His	Gln	Arg	Leu 140	Cys	Phe	Gln	Leu
Ala 145	Ala	Ala	Ser	Trp	Ile 150	Ser	Gly	Phe	Ser	Asn 155	Ser	Val	Leu	Gln	Ser
Thr	Trp	Thr	Leu 165	Lys	Met	Pro	Leu	Cys 170	Gly	His	Lys	Glu	Val 175	Asp	His
Phe	Phe	Cys	Glu 180	Val	Pro	Ala	Leu 185	Leu	Lys	Leu	Ser	Cys	Val 190	Asp	Thr
Thr	Ala	Asn 195	Glu	Ala	Glu	Leu 200	Phe	Ile	Ser	Val	Leu 205	Phe	Leu	Leu	
Ile 210	Pro	Val	Thr	Leu	Ile 215	Leu	Ile	Ser	Tyr	Ala 220	Phe	Ile	Val	Gln	Ala
Val 225	Leu	Arg	Ile	Gln	Ser 230	Ala	Glu	Gly	Gln	Arg 235	Lys	Ala	Phe	Gly	Thr
Cys	Gly	Ser	His 245	Leu	Ile	Val	Val	Ser 250	Leu	Phe	Tyr	Gly	Thr 255	Ala	Ile
Ser	Met	Tyr	Leu 260	Gln	Pro	Pro	Ser	Pro 265	Ser	Ser	Lys	Asp	Arg 270	Gly	Lys
Met	Val	Ser 275	Leu	Phe	Cys	Gly	Ile 280	Ile	Ala	Pro	Met	Leu 285	Asn	Pro	Leu
Ile	Tyr 290	Thr	Leu	Arg	Asn 295	Lys	Glu	Val	Lys	Glu 300	Ala	Phe	Lys	Arg	Leu
Val 305	Ala	Lys	Ser	Leu	Leu 310	Asn	Gln	Glu	Ile	Arg 315	Asn	Met	Gln	Met	Ile
Ser	Phe	Ala	Lys 325	Asp	Thr	Val	Leu	Thr 330	Tyr	Leu	Thr	Asn	Phe 335	Ser	Ala
Ser	Cys	Pro	Ile 340	Phe	Val	Ile	Thr	Ile 345	Glu	Asn	Tyr	Cys	Asn 350	Leu	Pro

Gln Arg Lys Phe Pro  
355

<210> 1756

<211> 331

<212> PRT

<213> Unknown (H38g674 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1756

```

Met Ala Pro Gly Asn Gly Phe Phe Met Thr Lys Ile Ile Leu Leu Glu
 1           5           10           15
Leu Thr Asp Gln Pro Asp Leu Gln Leu Pro Leu Phe Phe Leu Phe Leu
      20           25           30
Val Tyr Gly His Cys Val Gly Lys Phe Gly Leu Val Thr Leu Val Val
      35           40           45
Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu
      50           55           60
Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Gln Met Leu
      65           70           75           80
Met Asn Phe Ile Thr Gln Lys Asp Ile Ile Ser His Met Gly Cys Met
      85           90           95
Ser Gln Leu Phe Phe Phe Ala Leu Phe Phe Phe Gly Ile Ser Glu Cys
      100          105          110
Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Ala Cys His His Asp His
      115          120          125
His Val Ala Ile Cys Asn Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro
      130          135          140
Lys Val Tyr Ser His Leu Met Leu Gly Leu Tyr Leu Leu Ala Phe Ser
      145          150          155          160
Ser Ala Met Ala His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp
      165          170          175
Ala Asn Thr Ile His Pro Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln
      180          185          190
Leu Ser Cys Thr Gly Thr Tyr Ile Asn Glu Leu Val Val Ser Thr Ala
      195          200          205
Ala Val Ile Ile Ser Thr Val Thr Ile Phe Ile Ser Cys Gly Cys Ser
      210          215          220
Ser Tyr Ile Ile Leu His Ile Asn Ser Lys Glu Gly Arg Ser Lys Ala
      225          230          235          240
Leu Asn Thr Cys Ser Ser Asn Leu Ile Ala Val Ser Leu Met Phe Gly
      245          250          255
Ser Cys Ala Phe Met Cys Leu Lys Pro Ser Ser Ala Gly Ser Met Asp
      260          265          270
Glu Gly Lys Ile Ser Ser Val Phe Tyr Thr Asn Thr Ala Pro Leu Met
      275          280          285
Asn Pro Leu Ile Tyr Ser Leu Met Asn Lys Met Phe Asn Phe Leu Xaa
      290          295          300
Glu Lys Asn Pro Ser Arg Lys Lys Phe Xaa Leu Glu Ile Val Ser Phe
      305          310          315          320
Cys Ala Cys Ile Phe Arg Thr Gly Ser Phe Cys
      325          330

```

<210> 1757

<211> 332

<212> PRT  
 <213> Unknown (H38g675 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(332)  
 <223> Xaa = Any Amino Acid

<400> 1757

Met	Ala	Pro	Gly	Asn	Gly	Ser	Leu	Met	Asn	Glu	Phe	Ile	Leu	Val	Gly
1				5					10					15	
Leu	Thr	Asp	Xaa	Pro	Asp	Leu	Xaa	Leu	Pro	Leu	Phe	Phe	Met	Phe	Leu
			20					25					30		
Val	Met	Tyr	Val	Val	Thr	Val	Ile	Arg	Asn	Phe	Val	Leu	Val	Ile	Leu
		35					40					45			
Thr	Met	Arg	Asn	Ser	Arg	Leu	His	Thr	Pro	Lys	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
Lys	Leu	Phe	Phe	Thr	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Phe	Ile	Leu	Gln
65					70					75				80	
Leu	Pro	Arg	Lys	Cys	Ile	Ser	Glu	Glu	Asn	Val	Ile	Ser	Tyr	Met	Val
				85					90					95	
Cys	Met	Ile	Xaa	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Xaa
			100					105					110		
Phe	Ile	Ser	Glu	Cys	Tyr	Met	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Cys	Cys
			115				120						125		
Val	Ala	Ile	Cys	Tyr	Pro	Leu	Leu	Tyr	His	Ile	Ala	Met	Ser	Pro	Lys
	130					135					140				
Val	Cys	Phe	Ser	Leu	Met	Leu	Gly	Ser	Tyr	Phe	Leu	Ser	Phe	Ser	Gly
145					150					155				160	
Ala	Met	Ala	His	Thr	Gly	Cys	Met	Leu	Arg	Leu	Thr	Cys	Asp	Ala	Asn
			165					170						175	
Thr	Ile	Asn	His	Tyr	Phe	Arg	Asp	Ile	Leu	Pro	Val	Phe	Gln	Leu	Ser
			180					185					190		
Cys	Thr	Ser	Thr	Tyr	Ile	Asn	Glu	Leu	Val	Val	Phe	Ile	Val	Ala	Gly
		195				200						205			
Ile	Asn	Thr	Ile	Val	Pro	Thr	Val	Thr	Val	Phe	Ile	Ser	Tyr	Gly	Asp
	210					215					220				
Ile	Leu	Ser	Arg	Ile	Leu	His	Ile	Ser	Ser	Asn	Glu	Gly	Arg	Ser	Lys
225					230					235				240	
Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Ile	Ile	Ala	Val	Ser	Leu	Phe	Phe
			245						250					255	
Gly	Leu	Ser	Ala	Phe	Met	Tyr	Leu	Lys	Pro	Ser	Ser	Ala	Gly	Ser	Met
			260					265					270		
Asp	Glu	Gly	Lys	Phe	Ser	Ser	Val	Phe	Tyr	Met	Asn	Gly	Leu	Pro	Met
		275					280					285			
Met	Ser	Ser	Leu	Ile	Tyr	Ser	Leu	Arg	Arg	Lys	Asp	Val	Lys	Phe	Ala
	290					295					300				
Met	Gly	Lys	Ser	Leu	Ser	Arg	Arg	Met	Phe	Leu	Pro	Xaa	Thr	Thr	Phe
305					310					315				320	
Leu	Cys	Val	Cys	Ser	Tyr	Arg	Met	Gly	Ile	Leu	Cys				
			325					330							

<210> 1758  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g676 protein)

<220>  
 <223> Synthetic construct

&lt;400&gt; 1758

```

Met Asp Ser Leu Asn Gln Thr Arg Val Thr Glu Phe Val Phe Leu Gly
 1          5          10          15
Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala Phe Ser
          20          25          30
Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile Ala
          35          40          45
Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val Pro Lys
65          70          75          80
Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe Asp Asn
          85          90          95
Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala Glu Ile
          100          105          110
Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Thr
          115          120          125
Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile Gln Leu
          130          135          140
Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly Gln Thr
145          150          155          160
Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile Asp Ser
          165          170          175
Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile Ser Leu
          195          200          205
Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu Val Ser
          210          215          220
Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys Ile Phe
          245          250          255
Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val Val Ser
          260          265          270
Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Thr
          275          280          285
Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg Gln Arg
          290          295          300
Gln Val Phe Phe Thr Lys Ser Tyr Thr
305          310

```

&lt;210&gt; 1759

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g677 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1759

```

Met Ala Pro Gly Asn Ile Ser Thr Val Ala Glu Leu Ile Leu Val Gly
 1          5          10          15
Leu Lys Asp Gln Thr Asp Leu Gln Pro Pro Leu Phe Phe Leu Phe Leu
          20          25          30
Val Met Gly Val Val Ala Gly Xaa Gly Asn Leu Gly Leu Val Thr Leu

```

```
<210> 1760
<211> 322
<212> PRT
<213> Unknown (H38g678 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(322)
<223> Xaa = Any Amino Acid
```

```

<400> 1760
Met Ser Val Val Glu Ala Asn Asn Ile Ser Gly Pro Val Ser Glu Phe
  1             5             10             15
Ile Leu Leu Gly Phe Pro Cys Arg Cys Arg Glu Thr Lys Ile Leu Leu
      20             25             30
Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Met Gly Asn Thr
    35             40             45
Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met
    50             55             60
Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Ile Ser
  65             70             75             80

```



```

Ser Asp Val Pro Asn Met Leu Ala Asn Leu Ile Ser His Ile Lys Ser
      85                      90                      95
Ile Ser Tyr Ala Gly Cys Leu Leu Gln Phe Phe Tyr Phe Ser Met Cys
      100                    105                    110
Ala Ala Glu Gly Tyr Phe Leu Ser Val Met Ser Phe Asp Arg Phe Leu
      115                    120                    125
Thr Ile Cys Arg Pro Leu His Tyr Pro Thr Val Met Thr His His Leu
      130                    135                    140
Cys Val Xaa Leu Val Ala Phe Cys Arg Ala Gly Gly Phe Leu Ser Ile
      145                    150                    155                    160
Leu Met Pro Ala Val Leu Met Ser Arg Val Pro Phe Cys Gly Pro Asn
      165                    170                    175
Ile Thr Asp His Phe Phe Cys Asn Leu Gly Pro Leu Leu Ala Leu Ser
      180                    185                    190
Cys Ala Pro Val Pro Lys Thr Thr Leu Thr Cys Ala Thr Val Ser Ser
      195                    200                    205
Leu Ile Ile Phe Ile Thr Phe Leu Tyr Ile Leu Gly Ser His Ile Leu
      210                    215                    220
Val Leu Arg Ala Val Leu Trp Val Pro Ala Gly Ser Gly Arg Asn Lys
      225                    230                    235                    240
Ala Phe Ser Thr Cys Ala Ser His Phe Leu Val Val Ser Phe Phe Tyr
      245                    250                    255
Gly Ser Val Met Val Met Tyr Val Ser Pro Gly Ser Arg Ser Arg Pro
      260                    265                    270
Gly Thr Gln Lys Phe Val Thr Leu Phe Tyr Cys Thr Ala Thr Pro Phe
      275                    280                    285
Phe Asn Pro Leu Thr Tyr Ser Leu Trp Asn Lys Asp Met Thr Asp Ala
      290                    295                    300
Leu Lys Lys Val Leu Gly Val Pro Ser Lys Glu Ile Tyr Trp Asn Thr
      305                    310                    315                    320
Leu Lys

```

&lt;210&gt; 1761

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g679 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1761

```

Met Glu Glu Ala Ile Leu Leu Asn Gln Thr Ser Leu Val Thr Tyr Phe
  1                      5                      10                      15
Arg Leu Arg Gly Leu Ser Val Asn His Lys Ala Arg Ile Ala Met Phe
      20                    25                    30
Ser Met Phe Leu Ile Phe Tyr Val Leu Thr Leu Ile Gly Asn Val Leu
      35                    40                    45
Ile Val Ile Thr Ile Ile Tyr Asp His Arg Leu His Thr Pro Met Tyr
      50                    55                    60
Phe Phe Leu Ser Asn Leu Ser Phe Ile Asp Val Cys His Ser Thr Val
      65                    70                    75                    80
Thr Val Pro Lys Met Leu Arg Asp Val Trp Ser Glu Glu Lys Leu Ile
      85                    90                    95
Ser Ph Asp Ala Cys Val Thr Gln Met Phe Phe Leu His Leu Phe Ala
      100                    105                    110
Cys Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val

```

115	120	125
Ala Ile Cys Lys Pro Leu Gln Tyr Met Ile Val Met Asn Trp Lys Val		
130	135	140
Cys Val Leu Leu Ala Val Ala Leu Trp Thr Gly Gly Thr Ile His Ser		
145	150	155
Ile Ala Leu Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro Asp		
165	170	175
Glu Ile Asp Asn Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala		
180	185	190
Cys Ile Asp Thr Pro Tyr Val Leu Glu Ile Leu Ile Val Ser Asn Ser		
195	200	205
Gly Leu Ile Ser Val Val Cys Phe Val Val Leu Val Val Ser Tyr Ala		
210	215	220
Val Ile Leu Val Ser Leu Arg Gln Gln Ile Ser Lys Gly Lys Trp Lys		
225	230	235
Ala Leu Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu		
245	250	255
Gly His Cys Ile Phe Ile Tyr Ser Arg Pro Ser Thr Ser Leu Pro Glu		
260	265	270
Asp Lys Ala Val Ser Val Phe Phe Thr Ala Val Thr Pro Leu Leu Asn		
275	280	285
Pro Ile Ile Tyr Thr Leu Arg Asn Glu Glu Met Lys Ser Ala Leu Asn		
290	295	300
Lys Leu Val Gly Arg Lys Glu Arg Lys Glu Glu Lys Xaa Lys Cys Pro		
305	310	315
Thr Ser Leu Gly Tyr Val Val Leu Gln Ile Lys Glu Ala Pro Cys		
325	330	335

&lt;210&gt; 1762

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g680 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(161)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1762

Thr Gly Thr Gly Xaa Trp Leu Cys His Ala Met Ile Leu Thr Pro Leu		
1	5	10
Thr Phe Gln Leu Pro Tyr Cys Gly Leu Thr Arg Trp Asp Tyr Tyr Phe		
20	25	30
Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu		
35	40	45
Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys		
50	55	60
Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser		
65	70	75
Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser		
85	90	95
Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile		
100	105	110
Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile		
115	120	125
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu		
130	135	140
Arg Asn Lys Asp Val Lys Ser Asp Gln Pro Xaa Gly Met Tyr Phe Pro		
145	150	155
		160

Arg

<210> 1763  
 <211> 134  
 <212> PRT  
 <213> Unknown (H38g681 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(134)  
 <223> Xaa = Any Amino Acid

<400> 1763  
 Leu Leu Phe Leu Met Phe Phe Ile Thr Ser Leu Gly His Lys Phe His  
 1 5 10 15  
 Leu Ile Ser Phe Pro Phe Ser Gln Gln Thr Thr Xaa Gln Lys Tyr Phe  
 20 25 30  
 Ile Ile Phe Glu Val Xaa Leu Cys Xaa Xaa His Thr Leu Thr Ala Leu  
 35 40 45  
 Ile Tyr Cys Xaa Met Ser Leu Phe Xaa Gly Ile Asp Leu Phe Val Gly  
 50 55 60  
 Tyr Asn Pro Cys Ser Pro Arg Val Leu Phe Leu Phe Leu Gly Arg Gly  
 65 70 75 80  
 Pro Ser Gly Phe Ser Leu Glu Ser Leu Ser Phe Tyr Arg Thr Ser Phe  
 85 90 95  
 Thr Trp Gln His Leu His Leu Lys Phe Tyr Cys Pro Ser Xaa Gly Xaa  
 100 105 110  
 Leu Leu Lys Ser Phe Leu Ser Ala Ile Trp Leu Leu Phe Ser Thr Tyr  
 115 120 125  
 Phe Leu Arg Val Leu Ser  
 130

<210> 1764  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g682 protein)

<220>  
 <223> Synthetic construct

<400> 1764  
 Met Ala Thr Ser Asn His Ser Ser Gly Ala Glu Phe Ile Leu Ala Gly  
 1 5 10 15  
 Leu Thr Gln Arg Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Phe Leu  
 35 40 45  
 Ile Ala Leu Ser Ser Gln Leu Tyr Pro Pro Val Tyr Tyr Phe Leu Ser  
 50 55 60  
 His Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Val Pro Glu Glu Asn Ile Ile Ser Phe Leu Glu  
 85 90 95  
 Cys Ile Thr Gln Leu Tyr Phe Phe Leu Ile Phe Val Ile Ala Glu Gly  
 100 105 110  
 Tyr Leu Leu Thr Ala Met Glu Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu Leu Tyr Asn Ile Val Met Ser His Arg Val Cys Ser Ile Met

```

      130              135              140
Met Ala Val Val Tyr Ser Leu Gly Phe Leu Trp Ala Thr Val His Thr
145              150              155              160
Thr Arg Met Ser Val Leu Ser Phe Cys Arg Ser His Thr Val Ser His
      165              170              175
Tyr Phe Cys Asp Ile Leu Pro Leu Leu Thr Leu Ser Cys Ser Ser Thr
      180              185              190
His Ile Asn Glu Ile Leu Leu Phe Ile Ile Gly Gly Val Asn Thr Leu
      195              200              205
Ala Thr Thr Leu Ala Val Leu Ile Ser Tyr Ala Phe Ile Phe Ser Ser
      210              215              220
Ile Leu Gly Ile His Ser Thr Glu Gly Gln Ser Lys Ala Phe Gly Thr
225              230              235              240
Cys Ser Ser His Leu Leu Ala Val Gly Ile Phe Phe Gly Ser Ile Thr
      245              250              255
Phe Met Tyr Phe Lys Pro Pro Ser Ser Thr Thr Met Glu Lys Glu Lys
      260              265              270
Val Ser Ser Val Phe Tyr Ile Thr Ile Ile Pro Met Leu Asn Pro Leu
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Lys Lys Met
      290              295              300
Thr Arg Gly Arg Gln Ser Ser
305              310

```

&lt;210&gt; 1765

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g683 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1765

```

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val
 1              5              10              15
Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met
      20              25              30
Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile
      35              40              45
Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe
      50              55              60
Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile
65              70              75              80
Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser
      85              90              95
Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala
      100              105              110
Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala
      115              120              125
Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys
      130              135              140
Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala
145              150              155              160
Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu
      165              170              175
Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys
      180              185              190

```

Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala  
 195 200 205  
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val  
 210 215 220  
 Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly  
 245 250 255  
 Thr Leu Ile Ala Thr Tyr Leu Val Pro Ser Ala Asn Ser Ser Gln Leu  
 260 265 270  
 Leu Cys Lys Gly Ser Ser Leu Leu Tyr Ile Ile Leu Thr Pro Met Phe  
 275 280 285  
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Glu Ala Leu  
 290 295 300  
 Lys Lys Cys Leu Arg Lys Lys Ser Gly Val Cys Leu  
 305 310 315

&lt;210&gt; 1766

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g684 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1766

Pro Val Arg Thr Leu Glu Thr Thr Asn Ile Thr Gly Phe Val Asn Glu  
 1 5 10 15  
 Phe Ile Leu Leu Gly Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu  
 20 25 30  
 Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr  
 35 40 45  
 Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met  
 50 55 60  
 Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser  
 65 70 75 80  
 Ser Asp Val Pro Ile Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser  
 85 90 95  
 Ile Ser Cys Ala Gly Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys  
 100 105 110  
 Ala Ala Glu Cys Leu Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro  
 115 120 125  
 Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Leu Met Thr His His Val  
 130 135 140  
 Cys Ala His Phe Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu  
 145 150 155 160  
 Leu Thr Pro Leu Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn  
 165 170 175  
 Thr Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser  
 180 185 190  
 Cys Ala Pro Ile Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala  
 195 200 205  
 Leu Ile Ile Phe Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys  
 210 215 220  
 Val Leu Ser Thr Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His  
 260 265 270  
 Gly Ile Lys Lys Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe

275	280	285
Phe Asn Pro Leu Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala		
290	295	300
Leu Lys Lys Phe Leu Arg Asn Arg His Thr Val		
305	310	315

&lt;210&gt; 1767

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g685 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1767

Leu Ile Ala Thr Gly Asn Trp Thr Arg Ile Ser Lys Phe Ile Leu Met		
1	5	10
Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu Phe Leu Thr		
20	25	30
Phe Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Cys Leu Ile Ile		
35	40	45
Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met Tyr Phe Phe		
50	55	60
Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Ala		
65	70	75
Pro Asn Met Leu Trp Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe		
85	90	95
Leu Gly Cys Ala Thr Xaa Met Tyr Phe Val Phe Phe Phe Gly Val Ala		
100	105	110
Glu Cys Leu Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile		
115	120	125
Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg Thr Leu Ala		
130	135	140
Lys Leu Ala Ala Thr Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val		
145	150	155
Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val		
165	170	175
Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala		
180	185	190
Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val		
195	200	205
Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr His Ile Ala		
210	215	220
Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe		
225	230	235
Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser		
245	250	255
Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly		
260	265	270
Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn		
275	280	285
Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser		
290	295	300
Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu		
305	310	315

&lt;210&gt; 1768

<211> 324  
 <212> PRT  
 <213> Unknown (H38g686 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 1768  
 Met Ala Val Glu Asn Asp Ser Ser Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Gln Pro Glu Ile Xaa Leu Pro Leu Phe Phe Leu Phe Leu  
 20 25 30  
 Val Asn Tyr Met Thr Thr Met Val Gly Asn Leu Ser Leu Ile Asn Leu  
 35 40 45  
 Ile Cys Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Phe Val Phe Thr Pro Lys  
 65 70 75 80  
 Met Leu Met Ser Phe Ile Ser Glu Arg Asn Ile Ile Ser Phe Pro Gly  
 85 90 95  
 Cys Val Thr Gln Leu Phe Phe Phe Cys Phe Phe Val His Ser Glu Cys  
 100 105 110  
 Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Met Val Thr Thr Ser Pro Gln Ile Cys Ser Leu Leu  
 130 135 140  
 Met Leu Gly Ser Tyr Val Met Gly Phe Ala Gly Ala Met Val His Thr  
 145 150 155 160  
 Glu Cys Met Met Lys Leu Ile Phe Cys Asp Ser Asn Val Ile Asn His  
 165 170 175  
 Tyr Met Cys Asp Ile Phe Pro Leu Leu Gln Leu Ser Cys Ser Ser Thr  
 180 185 190  
 Xaa Ala Asn Glu Leu Val Met Ser Val Ile Val Gly Thr Val Val Ile  
 195 200 205  
 Val Ser Ser Leu Ile Ile Leu Ile Ser Tyr Ala Leu Ile Leu Phe Asn  
 210 215 220  
 Ile Leu His Met Ser Ser Ala Glu Gly Trp Phe Lys Ala Ile Gly Thr  
 225 230 235 240  
 Cys Gly Ser His Ile Ile Thr Val Gly Leu Phe Tyr Glu Phe Gly Leu  
 245 250 255  
 Ile Thr His Val Lys Leu Ser Ser Asp Trp Tyr Met Gly Gln Gly Lys  
 260 265 270  
 Phe Leu Ser Val Phe Tyr Thr Asn Glu Val Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Glu Thr  
 290 295 300  
 Leu Asn Lys Ile Thr Asn Xaa Val Glu Pro Met Val Leu Pro Xaa Pro  
 305 310 315 320  
 Leu Ser Asn Cys

<210> 1769  
 <211> 331  
 <212> PRT  
 <213> Unknown (H38g687 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1769

```

Met Arg Xaa Ile Asn Gln Thr Gln Val Ile Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
 20           25           30
Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu
 35           40           45
Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50           55           60
Asn Leu Ser Leu Ala Asp Leu Tyr Phe Ser Thr Asn Ile Leu Pro Gln
 65           70           75           80
Ala Leu Val His Leu Leu Ser Ile Asn Asn Leu Ile Ala Phe Thr Leu
 85           90           95
Ser Leu Thr Gln Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
100           105           110
Ala Leu Ile Ala Val Met Ser Tyr Asn Pro Tyr Val Ala Ile Cys Asn
115           120           125
Pro Leu His Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu
130           135           140
Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
145           150           155           160
Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
165           170           175
Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr
180           185           190
His Ala Ser Glu Met Ala Ile Tyr Leu Thr Gly Val Val Ile Leu Leu
195           200           205
Ile Pro Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr
210           215           220
Val Val Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr
225           230           235           240
Cys Gly Ser His Leu Met Val Val Ile Leu Leu Asn Gly Ser Ala Ile
245           250           255
Leu Thr Cys Met Thr Pro Lys Ser Ser Lys Gln Gln Xaa Lys Ser Val
260           265           270
Ser Val Phe Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Leu Ile Tyr
275           280           285
Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Val Ala Thr
290           295           300
Arg Asn Phe Pro Xaa Arg Leu Gly Ile His Thr Asp Ser Glu Leu Arg
305           310           315           320
Glu Pro Phe Gly Phe Leu Leu Pro Lys Thr Cys
325           330

```

<210> 1770

<211> 183

<212> PRT

<213> Unknown (H38g688 protein)

<220>

<223> Synthetic construct

<400> 1770

```

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1           5           10           15

```



Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys  
                   20                  25                  30  
 Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr  
                   35                  40                  45  
 Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu  
                   50                  55                  60  
 Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met  
                   65                  70                  75                  80  
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met  
                   85                  90                  95  
 Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile  
                   100                  105                  110  
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
                   115                  120                  125  
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile  
                   130                  135                  140  
 Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu  
                   145                  150                  155                  160  
 Thr Ile Ser Val Pro Phe Cys Gly Pro Asn Asp Ile Asp His Tyr Ser  
                   165                  170                  175  
 Arg Asp Val Tyr Pro Leu Leu  
                   180

&lt;210&gt; 1771

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g689 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(224)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1771

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ser Val  
   1                  5                  10                  15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
                   20                  25                  30  
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Arg His Ala  
                   35                  40                  45  
 Pro Glu Val Met Ala Tyr Asp Leu Phe Val Ala Ile Cys His Leu Leu  
                   50                  55                  60  
 Tyr Arg Ser Ala Ile Leu Asn Pro Phe Val Arg Gly Phe Leu Asp Leu  
                   65                  70                  75                  80  
 Leu Ser Leu Leu Leu Val Phe Phe Phe Phe Leu Ile Ser Leu Leu Asp  
                   85                  90                  95  
 Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp  
                   100                  105                  110  
 Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu  
                   115                  120                  125  
 Ala Cys Cys Asp Thr Phe Thr Arg Asn Asn Asn Met Tyr Phe Pro Ala  
                   130                  135                  140  
 Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Cys  
                   145                  150                  155                  160  
 Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr  
                   165                  170                  175  
 Lys Pro Ser Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe  
                   180                  185                  190  
 Tyr Gly Ala Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Phe

195 200 205  
 Pro Arg Lys Gly Ala Val Ala Ser Val Thr Tyr Tyr Thr Val Val Thr  
 210 215 220

<210> 1772  
 <211> 215  
 <212> PRT  
 <213> Unknown (H38g690 protein)

<220>  
 <223> Synthetic construct

<400> 1772  
 Met Asp Val Arg Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe Asn  
 1 5 10 15  
 Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Ala Thr Gln  
 20 25 30  
 Ile Phe Phe Cys Val Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu Ala  
 35 40 45  
 Val Met Ser Tyr Asp Cys Tyr Ile Ala Ile Cys His Pro Leu Arg Tyr  
 50 55 60  
 Thr Asn Leu Met Arg Pro Lys Ile Cys Arg Leu Met Thr Ala Phe Ser  
 65 70 75 80  
 Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Tyr Ala Val Ala Thr Phe  
 85 90 95  
 Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys Glu  
 100 105 110  
 Leu Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe Glu  
 115 120 125  
 Lys Val Ile Phe Ile Cys Ser Ile Val Met Leu Val Phe Pro Val Ala  
 130 135 140  
 Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala Val Ile His Met  
 145 150 155 160  
 Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser His  
 165 170 175  
 Leu Met Val Val Gly Met Phe Tyr Gly Ala Gly Leu Phe Met Tyr Ile  
 180 185 190  
 Gln Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys Leu Val Ser Val  
 195 200 205  
 Phe Tyr Thr Ile Leu Thr Pro  
 210 215

<210> 1773  
 <211> 127  
 <212> PRT  
 <213> Unknown (H38g691 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(127)  
 <223> Xaa = Any Amino Acid

<400> 1773  
 Asn Leu Leu Pro Val Trp Thr Pro Gly Ser Arg Val Pro Ser Xaa Ser  
 1 5 10 15  
 Gln Ile Ser Val Ser Glu Lys Gln Gly Met Ser Phe Pro Lys Lys Leu  
 20 25 30  
 Phe Gln Asn His Lys Leu Phe Leu Leu Phe Ala Gly Met Asn Val Phe  
 35 40 45

Leu Gln Thr Val Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro  
 50 55 60  
 Leu His Tyr Arg Val Ile Met Asn Pro Gly Ile Phe Gly Leu Trp Val  
 65 70 75 80  
 Leu Val Ser Trp Ser Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Arg  
 85 90 95  
 Met Val Leu Gln Leu Ser Phe Cys Thr Asn Leu Glu Ile Pro His Ile  
 100 105 110  
 Phe Phe Cys Glu Leu Asn Gln Leu Ile Leu Leu Ala Cys Ser Asn  
 115 120 125

&lt;210&gt; 1774

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g692 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(216)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1774

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu  
 1 5 10 15  
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Ile Met  
 20 25 30  
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu  
 50 55 60  
 Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr  
 65 70 75 80  
 Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu  
 85 90 95  
 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys  
 100 105 110  
 Glu His Ala Ala Val Val Ala Val Ser Trp Ser Asp Pro Cys Val Ser  
 115 120 125  
 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Gly Leu  
 130 135 140  
 Val Ile Ile Leu Thr Pro Tyr Ala Phe Ile Phe Ile Thr Val Met Lys  
 145 150 155 160  
 Thr Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser  
 165 170 175  
 His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr  
 180 185 190  
 Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser  
 195 200 205  
 Val Leu Tyr Thr Val Val Ile Pro  
 210 215

&lt;210&gt; 1775

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g693 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(215)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1775

```

Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Met Gln Ser His Ser Arg Ile Ile Ser His Ala Gly Cys Leu Thr
          20           25           30
Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp Asp Met Leu Leu
          35           40           45
Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys His Pro Leu His
          50           55           60
Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu Val Leu Met
65           70           75           80
Ser Ile Phe Leu Ser Leu Leu Asp Ser Xaa Leu His Asn Ser Val Leu
          85           90           95
Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn Phe Phe Cys
          100          105          110
Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Phe Ile Ser Asn
          115          120          125
Ile Phe Ile Arg Leu Asp Ser Thr Ile Phe Gly Phe Leu Pro Ile Ser
          130          135          140
Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
145          150          155          160
Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His
          165          170          175
Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu
          180          185          190
Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val Ala Ser Val
          195          200          205
Leu Tyr Ala Met Val Thr Pro
          210          215

```

&lt;210&gt; 1776

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g694 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(217)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1776

```

Leu Pro Asp Ile Gly Phe Thr Pro Thr Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly Cys Leu Thr Val
          20           25           30
Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Thr Leu Leu Leu
          35           40           45
Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys His Pro Leu Tyr
          50           55           60
His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu
65           70           75           80
Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu His Asn Met Ile
          85           90           95
Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
          100          105          110

```

```

Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
    115                120                125
Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro
    130                135                140
Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Glu Ile Val Ser Ser Ile Leu
    145                150                155                160
Arg Val Ser Ser Xaa Gly Gly Lys Tyr Lys Ala Phe Ala Thr Cys Gly
    165                170                175
Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly
    180                185                190
Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val Ala
    195                200                205
Ser Val Met Tyr Ala Val Val Thr Pro
    210                215

```

&lt;210&gt; 1777

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g695 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(230)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1777

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala Lys Met Ile Val
 1          5          10          15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
    20          25          30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Ser Met Leu
    35          40          45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
    50          55          60
Tyr Arg Ser Ala Ile Leu Ser Arg Asp Ser Val Pro Ser Xaa Ile Cys
    65          70          75          80
Cys Leu Cys Phe Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Phe
    85          90          95
Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
    100         105         110
Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Leu Trp Glu Pro Ser
    115         120         125
Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
    130         135         140
Met Tyr Phe Pro Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Pro
    145         150         155         160
Phe Leu Leu Gln Trp Ser Lys Ile Val Ser Ser Thr Leu Arg Val Ser
    165         170         175
Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
    180         185         190
Ser Val Val Cys Xaa Phe Cys Gly Thr Gly Val Gly Gly Tyr Leu Gly
    195         200         205
Ser Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met
    210         215         220
Tyr Thr Val Val Thr Pro
    225         230

```

&lt;210&gt; 1778

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g696 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1778

```

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
 1           5           10           15
Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu
          20           25           30
Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
          35           40           45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
          50           55           60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
65           70           75           80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
          85           90           95
Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
          100          105          110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
          130          135          140
Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
145           150           155           160
Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
          165          170          175
Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
          180          185          190
Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
          195          200          205
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
          210          215          220
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225           230           235           240
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
          245          250          255
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
          260          265          270
Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
          290          295          300
Ile Lys Ile Gln Arg Arg Asn Ile Phe
305           310

```

&lt;210&gt; 1779

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g697 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1779

```

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
 1           5           10           15
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
          20           25           30

```

Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu  
           35                  40                  45  
 Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
           50                  55                  60  
 Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65                  70                  75                  80  
 Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu  
                   85                  90                  95  
 Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly  
                   100                  105                  110  
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser  
           115                  120                  125  
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu  
           130                  135                  140  
 Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr  
 145                  150                  155                  160  
 Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His  
                   165                  170                  175  
 Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr  
           180                  185                  190  
 His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu  
           195                  200                  205  
 Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser  
           210                  215                  220  
 Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr  
 225                  230                  235                  240  
 Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr  
                   245                  250                  255  
 Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys  
           260                  265                  270  
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu  
           275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val  
           290                  295                  300  
 Leu Val Gly Lys  
 305

&lt;210&gt; 1780

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g698 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1780

Met Ala Pro Gly Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Ala Gly  
           1                  5                  10                  15  
 Leu Thr His Gln Pro Asp Leu Gln Ser Pro Leu Phe Phe Leu Phe Leu  
                   20                  25                  30  
 Val Ile Tyr Val Val Thr Leu Leu Gly Asn Leu Gly Leu Val Thr Leu  
           35                  40                  45  
 Ile Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
           50                  55                  60  
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys  
 65                  70                  75                  80  
 Met Leu Met Asn Phe Ile Ser Glu Lys Asn Ile Ile Ser Phe Lys Gly

```
<210> 1781
<211> 314
<212> PRT
<213> Unknown (H38a699 protein)
```

<400>	1781															
Met	Lys	Pro	Gly	Asn	Glu	Thr	Gln	Ile	Ser	Gln	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Leu	Ser	Glu	Glu	Pro	Glu	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu	
			20					25					30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Thr	Ile	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
Asn	Leu	Ser	Phe	Ala	Asp	Ile	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro	Lys	
65					70					75					80	
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Ser	Arg	Val	Ile	Thr	Tyr	Ala	Asp	
				85					90					95		
Cys	Ile	Thr	Gln	Met	Cys	Phe	Phe	Ile	Leu	Phe	Val	Val	Leu	Asp	Ser	
			100					105					110			
Leu	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	
			115				120					125				
Pro	Leu	His	Tyr	Thr	Val	Ile	Met	Asn	Ser	Trp	Leu	Cys	Gly	Leu	Leu	
						135					140					
Val	Leu	Val	Ser	Trp	Ile	Val	Ser	Ile	Leu	Tyr	Ser	Leu	Leu	Gln	Ser	
145					150					155					160	



```

Ile Met Ala Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His
      165      170      175
Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr
      180      185      190
Phe Ile Asn Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly
      195      200      205
Gly Cys Leu Ala Gly Ile Leu Tyr Thr Tyr Phe Lys Ile Leu Cys Cys
      210      215      220
Ile Cys Ser Ile Ser Ser Ala Gln Gly Met Asn Lys Ala Leu Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala
      260      265      270
Ala Ala Ser Val Met Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Arg Ala Leu Asn Arg Phe
      290      295      300
Phe Arg Glu Gln Lys Gln Glu Gly His Phe
      305      310

```

&lt;210&gt; 1782

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g700 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1782

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser
  20      25      30
Leu Ser Leu Ser Leu Asn Leu Val Thr Val Leu Arg Asn Leu Leu Ser
  35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
  50      55      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Leu Thr Ser Ala Thr
  65      70      75      80
Val Pro Lys Val Ile Leu Asp Met Gln Ser His Ser Arg Val Ile Ser
  85      90      95
His Val Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
  100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Gly Cys Phe Val Ala
  115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
  130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Asn Leu Leu Asp Ser Gln
  145      150      155      160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
  165      170      175
Ile Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys
  180      185      190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
  195      200      205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile

```

210	215	220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala		
225	230	235
Phe Ser Thr Tyr Gly Ser His Leu Gly Val Val Cys Trp Phe Tyr Gly		240
	245	250
Thr Val Ile Gly Met Tyr Leu Ala Ser Ala Val Ser Pro Pro Pro Arg		255
	260	265
Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu		270
	275	280
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu		285
	290	295
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser		300
305	310	315
Phe Phe Leu Cys		320

&lt;210&gt; 1783

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g701 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(339)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1783

Pro Ile Glu Gln Gly Asn Tyr Thr Arg Val Lys Glu Phe Phe Phe Gln		
1	5	10
Gly Leu Thr Gln Ser Gln Glu Leu Ser Leu Val Leu Phe Leu Phe Leu		15
	20	25
Phe Phe Val Tyr Ser Ala Thr Val Leu Gly Asn Leu Leu Ile Met Val		30
	35	40
Val Val Thr Cys Glu Ser Arg Leu His Thr Pro Thr Tyr Phe Leu Leu		45
	50	55
Cys Asn Leu Ser Val Leu Val Ile Cys Phe Ser Ser Ile Thr Ala Arg		60
65	70	75
Lys Val Leu Ile Asp Leu Ser Ser Arg Lys Thr Ile Ser Phe Asn Gly		80
	85	90
Cys Met Thr Gln Met Phe Phe Phe His Leu Leu Gly Gly Thr Asp Val		95
	100	105
Phe Ser Leu Phe Val Met Ala Phe Asp Gln Tyr Met Ala Ile Phe Lys		110
	115	120
Pro Leu His Cys Val Thr Ile Val Ser Arg Gly Gln Cys Ile Pro Tyr		125
	130	135
Ile Val Ser Arg Gly Arg Glu Xaa Gly Ala Gly Leu Ile Met Ala Ser		140
145	150	155
Trp Val Gly Gly Phe Val His Ser Ile Val Gln Val Phe Leu Leu Leu		160
	165	170
Pro Leu Pro Phe Cys Gly His His Met Ile Asp Gly Phe Tyr Cys Asp		175
	180	185
Val Pro Gln Val Leu Lys Leu Ala Cys Thr His Thr Phe Ala Leu Glu		190
	195	200
Val Leu Met Ile Ser Asn Asn Gly Leu Ile Ser Met Leu Trp Phe Ile		205
	210	215
Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met Leu Arg Ser His		220
225	230	235
Thr Glu Glu Gly Arg Arg Lys Ala Ile Ala Thr Cys Thr Ser His Ile		240
	245	250
		255

Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val His Ala Gln  
                   260                  265                  270  
 Pro Phe Thr Ala Leu Pro Thr Asp Arg Ala Val Ser Ile Thr Phe Thr  
                   275                  280                  285  
 Val Ile Ile Pro Val Leu Asn Pro Met Ile Tyr Thr Leu Arg Asn Gln  
                   290                  295                  300  
 Glu Met Lys Ser Ala Leu Arg Arg Arg Lys Lys Arg Pro Ser Gly Lys  
 305                  310                  315                  320  
 Gly Xaa Met Leu Arg Ser Pro Asp Trp Lys Ile Arg Thr Glu Lys Tyr  
                   325                  330                  335  
 Phe Phe Ile

<210> 1784

<211> 335

<212> PRT

<213> Unknown (H38g702 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1784

Ser Thr Tyr Pro Gln Asn Leu Thr Asp Val Ser Leu Phe Leu Leu Leu  
 1                  5                  10                  15  
 Gly Ser Ser Glu Asp Pro Glu Gln Gln Pro Val Leu Ala Gly Leu Phe  
                   20                  25                  30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
                   35                  40                  45  
 Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu  
 50                  55                  60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ser Met Val Pro  
 65                  70                  75                  80  
 Lys Met Ile Val Asp Ile Xaa Ser His Ser Arg Leu Ile Ser Xaa Ala  
                   85                  90                  95  
 Gly Cys Leu Thr Pro Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
                   100                  105                  110  
 Glu Asn Met Leu Leu Ser Val Ile Ala Tyr Asp Pro Phe Val Ala Ile  
                   115                  120                  125  
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly  
 130                  135                  140  
 Phe Leu Val Leu Leu Ser Phe Phe Ser Gln Ser Leu Leu Asp Ala Gln  
 145                  150                  155                  160  
 Val His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu  
                   165                  170                  175  
 Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys  
                   180                  185                  190  
 Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Ser Pro Ala Ala Ile  
                   195                  200                  205  
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile  
                   210                  215                  220  
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala  
 225                  230                  235                  240  
 Cys Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly  
                   245                  250                  255  
 Thr Gly Phe Trp Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Gly  
                   260                  265                  270  
 Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Pro

275	280	285
Asn Pro Phe Ile Tyr Ser	Leu Arg Asn Arg Asp Ile	Lys Ser Val Leu
290	295	300
Arg Arg Pro His Gly Ser Thr Val	Xaa Cys Gln Tyr Leu Leu Ile	Cys
305	310	315
Ser Met Pro Phe Val Val Trp Val	Lys Lys Gly Ser Lys Val	Lys
325	330	335

&lt;210&gt; 1785

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g703 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1785

Met Lys Asn Cys Thr Arg Val Lys Glu Phe Ile Phe Leu Gly Leu Thr	
1 5 10 15	
Gln Asn Gly Asp Thr Arg Leu Val Leu Phe Leu Phe Leu Leu Val	
20 25 30	
Tyr Met Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr Val Thr	
35 40 45	
Cys Glu Ser Cys Leu His Met Pro Met Tyr Phe Leu Leu His Asn Leu	
50 55 60	
Ser Ile Ala Asp Ile Cys Phe Tyr Ser Ile Thr Glu Pro Lys Val Leu	
65 70 75 80	
Val Asp Leu Leu Ser Glu Arg Lys Thr Ile Ser Phe Asn Gly Cys Phe	
85 90 95	
Thr Gln Met Phe Leu Phe His Leu Ile Gly Gly Val Asp Ala Phe Ser	
100 105 110	
Leu Ser Val Met Ala Leu Asp Gln Tyr Val Ala Ile Ser Lys Ser Leu	
115 120 125	
His Tyr Ala Thr Ile Met Ser Arg Asp Arg Cys Ile Gly Leu Thr Val	
130 135 140	
Ala Ala Trp Leu Gly Gly Phe Val His Ser Ile Val Gln Ile Thr Leu	
145 150 155 160	
Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr Phe Tyr	
165 170 175	
Cys Asp Val Pro Gln Val Leu Lys Leu Ala His Thr Asp Ile Phe Ile	
180 185 190	
Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Leu Thr Thr Leu Trp	
195 200 205	
Phe Phe Leu Leu Leu Val Ser Tyr Met Val Ile Leu Ser Leu Leu Lys	
210 215 220	
Ser Gln Ala Gly Xaa Gly Arg Arg Lys Val Ile Ser Thr Cys Thr Ser	
225 230 235 240	
His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val Tyr	
245 250 255	
Ala Arg Pro Phe Thr Ala Leu Pro Thr Asp Lys Ala Ile Ser Val Thr	
260 265 270	
Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg	
275 280 285	
Asn His Glu Met Lys Ser Thr Met Lys Arg Arg Arg Leu Xaa Pro Ser	
290 295 300	
Asp Arg Lys Xaa Thr Ser Ala Ser Leu Leu Leu	
305 310 315	

<210> 1786  
 <211> 321  
 <212> PRT  
 <213> Unknown (H38g704 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(321)  
 <223> Xaa = Any Amino Acid

<400> 1786  
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Lys Val Leu Leu Gly  
 1 5 10 15  
 Ser Leu Xaa Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser  
 20 25 30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Val Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Ser Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro  
 65 70 75 80  
 Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Val  
 85 90 95  
 Ser Cys Leu Thr Gln Ile Ser Phe Leu Val Leu Phe Ala Cys Met Glu  
 100 105 110  
 Asp Met Leu Thr Val Met Ala Tyr Asp Arg Val Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Arg Val Phe Leu  
 130 135 140  
 Val Leu Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser  
 145 150 155 160  
 Trp Ile Val Leu Gln Phe Thr Leu Phe Lys Asn Val Glu Asn Ser Ser  
 165 170 175  
 Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser  
 180 185 190  
 Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Tyr Gly Ser Gln Leu Ala Ala Leu Cys Xaa Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ala Leu Pro Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu Asn Phe Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu  
 290 295 300  
 Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu  
 305 310 315 320  
 Cys

<210> 1787  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g705 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1787

```

Lys Gln Gln Glu Asn Gly Thr Cys Leu Val Thr Glu Phe Leu Met Met
 1           5           10           15
Gly Phe Ser Asn Leu Pro His Leu Arg Asn Thr Leu Phe Thr Leu Phe
          20           25           30
Phe Leu Thr Tyr Leu Val Thr Leu Gly Gly Asn Val Thr Ile Ile Thr
          35           40           45
Ile Thr His Ala Asp Arg Ser Arg His Thr Pro Met Tyr His Phe Leu
          50           55           60
Val Val Leu Ser Leu Ser Glu Thr Val Leu Tyr Thr Leu Val Thr Ile
65           70           75           80
Pro Ser Met Leu Ala His Leu Leu Met Glu Thr Arg Pro Ile Ser Ile
          85           90           95
Pro Gly Cys Gln Ala Gln Met Phe Phe Phe Leu Gly Leu Gly Cys Ser
          100          105          110
His Cys Phe Leu Leu Thr Leu Met Gly Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ser Met Val Met Arg Pro Thr Val Cys Leu
          130          135          140
Cys Leu Gly Ala Leu Val Phe Cys Ser Gly Phe Ser Val Ala Leu Ile
145          150          155          160
Glu Thr Ser Met Ile Phe Ser Ser Pro Phe Cys Gly Gly Asp His Val
          165          170          175
Glu His Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ser Cys Ala
          180          185          190
Lys Ser Ala Ser Lys Ala Leu Gly Ile Phe Phe Leu Ser Val Leu Val
          195          200          205
Val Leu Met Ser Phe Val Pro Ile Leu Phe Ser Tyr Ala Phe Ile Val
          210          215          220
Ala Ala Ile Val Arg Ile Ser Leu Ala Ala Gly Arg Arg Lys Ala Phe
225          230          235          240
Ser Thr Cys Val Ala His Val Thr Val Val Val His Phe Asp Cys
          245          250          255
Ala Ser Ile Ile Tyr Leu Arg Pro Glu Ser Gly Ala Asn Pro Asp Gln
          260          265          270
Asp Arg Leu Val Ala Val Phe Tyr Thr Val Val Met Pro Leu Leu Asn
          275          280          285
Pro Val Val Cys Thr Leu Trp Asn Lys Glu Val Arg Val Ala Leu Arg
          290          295          300
Arg Thr Leu Ala Trp Ser Arg Gly Val Phe Lys Xaa Glu Ser
305          310          315

```

&lt;210&gt; 1788

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g706 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1788

```

Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu Lys Leu Ala
 1           5           10           15

```

Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe Ala Ala Arg  
                   20                  25                  30  
 Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala Ser Tyr Gly  
           35                  40                  45  
 Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly Gly Arg Arg  
           50                  55                  60  
 Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val Cys Leu Phe  
 65                  70                  75                  80  
 Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln Arg Tyr Asn  
                   85                  90                  95  
 Gln His Gly Asn Arg Phe Val Ser Leu Phe Tyr Thr Val Val Thr Pro  
                   100                  105                  110

&lt;210&gt; 1789

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g707 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1789

Met Asp Gln Arg Asn Tyr Thr Arg Val Lys Glu Phe Thr Phe Leu Gly  
 1                  5                  10                  15  
 Ile Thr Gln Ser Arg Glu Leu Ser Gln Val Leu Phe Thr Phe Leu Phe  
           20                  25                  30  
 Leu Val Tyr Met Thr Thr Leu Met Gly Asn Phe Leu Ile Met Val Thr  
           35                  40                  45  
 Val Thr Cys Glu Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
           50                  55                  60  
 Asn Leu Ser Ile Leu Asp Ile Cys Phe Ser Ser Ile Thr Ala Pro Lys  
 65                  70                  75                  80  
 Val Leu Ile Asp Leu Leu Ser Glu Thr Lys Thr Ile Ser Phe Ser Gly  
                   85                  90                  95  
 Cys Val Thr Gln Met Phe Phe Phe His Leu Leu Gly Gly Ala Asp Val  
           100                  105                  110  
 Phe Ser Leu Ser Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Ser Lys  
           115                  120                  125  
 Pro Leu His Tyr Met Thr Ile Met Ser Arg Gly Arg Cys Thr Gly Leu  
           130                  135                  140  
 Ile Val Gly Phe Leu Gly Gly Gly Leu Val His Ser Ile Ala Gln Ile  
 145                  150                  155                  160  
 Ser Leu Leu Leu Pro Leu Pro Val Cys Gly Pro Asn Val Leu Asp Thr  
                   165                  170                  175  
 Phe Tyr Cys Asp Val Pro Gln Val Leu Lys Leu Ala Cys Thr Asp Thr  
           180                  185                  190  
 Phe Thr Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Val Ser Trp  
           195                  200                  205  
 Phe Val Phe Phe Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met  
           210                  215                  220  
 Leu Arg Ser His Thr Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys  
 225                  230                  235                  240  
 Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr  
                   245                  250                  255  
 Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Thr Asp Thr Ala Ile Ser  
           260                  265                  270  
 Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Ile Ile Tyr Thr  
           275                  280                  285  
 Leu Arg Asn Gln Glu Met Lys Leu Ala Met Arg Lys Leu Lys Arg Arg  
           290                  295                  300  
 Leu Gly Gln Ser Glu Arg Ile Leu Ile

305

310

&lt;210&gt; 1790

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g708 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1790

```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
 1          5          10          15
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
 20        25        30
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
 35        40        45
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50        55        60
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Phe Ile Phe Gly
 65        70        75        80
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
 85        90        95
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
100       105       110
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
115       120       125
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
130       135       140
Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145       150       155       160
Leu Leu

```

&lt;210&gt; 1791

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g709 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1791

```

Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe Thr
 1          5          10          15
Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu
 20        25        30
Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala
 35        40        45
Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp Arg
 50        55        60
Ala Ala Ala Val Cys Arg Pro Leu Arg Tyr Ala Gly Leu Val Ser Pro
 65        70        75        80
Arg Leu Cys Arg Thr Leu Ala Ser Ala Ser Trp Leu Ser Gly Leu Thr
 85        90        95
Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys Ala
100       105       110
Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu Lys
115       120       125
Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe Ala
130       135       140

```



Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala Ser  
 145 150 155 160  
 Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly Gly  
 165 170 175  
 Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val Cys  
 180 185 190  
 Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln Arg  
 195 200 205  
 Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val  
 210 215 220  
 Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys Val  
 225 230 235 240  
 Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln Ala  
 245 250 255  
 Gly Gln

&lt;210&gt; 1792

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g710 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1792

Met Gln Arg Ala Asn His Ser Thr Val Thr Gln Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Ser Val Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr  
 35 40 45  
 Val Trp Ser Glu Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Cys  
 50 55 60  
 Ala Leu Ser Val Ser Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg  
 65 70 75 80  
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala  
 85 90 95  
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser  
 100 105 110  
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Gly Cys Ala Cys Leu  
 130 135 140  
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr  
 145 150 155 160  
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His  
 165 170 175  
 Phe Ala Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp  
 180 185 190  
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu  
 195 200 205  
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala  
 210 215 220  
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Val Val Val His Tyr Gly Phe Ala  
 245 250 255  
 Ser Val Ile Tyr Leu Lys Pro Lys Ser Pro Gln Ser Leu Glu Gly Asp  
 260 265 270  
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro

	275		280		285
Ile	Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys				
	290		295		300
Thr	Phe Phe Ser Lys Leu Tyr Pro Glu Lys Asn Val				
305		310		315	

<210> 1793  
 <211> 225  
 <212> PRT  
 <213> Unknown (H38g711 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(225)  
 <223> Xaa = Any Amino Acid

<400> 1793

Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro	Lys	Met	Ile	Val
1				5					10					15	
Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Leu	Ser	Tyr	Ala	Gly	Cys	Leu	Ile
		20						25					30		
Arg	Cys	Leu	Ser	Leu	Pro	Leu	Leu	Glu	Ala	Trp	Lys	Arg	Gly	Met	Leu
		35				40					45				
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu
	50					55				60					
Tyr	Arg	Ser	Ala	Ile	Leu	Asn	Pro	Xaa	Phe	Cys	Gly	Phe	Leu	Asp	Leu
65				70					75					80	
Leu	Ser	Phe	Phe	Phe	Leu	Phe	Val	Cys	Phe	Val	Phe	Leu	Ser	Leu	Leu
			85					90						95	
Asp	Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Ser	Lys
		100						105					110		
Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Pro	His
	115						120					125			
Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr	Arg	Asn	Ile	Asn	Met	Tyr	Phe	Pro
	130					135					140				
Ala	Ala	Val	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Phe	Tyr	Ser	Tyr
145					150					155					160
Cys	Lys	Ile	Leu	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys
			165						170					175	
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa
		180					185						190		
Phe	Tyr	Gly	Thr	Gly	Val	Gly	Gly	Tyr	Leu	Gly	Ser	Asp	Val	Ser	Ser
	195					200						205			
Ser	Pro	Arg	Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr
	210					215						220			

Pro  
 225

<210> 1794  
 <211> 218  
 <212> PRT  
 <213> Unknown (H38g712 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(218)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1794

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Ser Met Leu
          35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Cys His Ser Ala Ile Thr Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
65           70           75           80
Leu Ser Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln Leu His Asn Leu
          85           90           95
Ile Ala Leu Gln Arg Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
          100          105          110
Phe Cys Asp Pro Ser Gln Phe Pro Arg Leu Ala Cys Cys Gly Thr Phe
          115          120          125
Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
          130          135          140
Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Phe Ser Ile
          145          150          155          160
Leu Arg Val Ser Ser Ser Gly Gly Lys His Lys Ala Phe Ser Thr Arg
          165          170          175
Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly
          180          185          190
Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val
          195          200          205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
          210          215

```

&lt;210&gt; 1795

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g713 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1795

```

Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met Ala
 1           5           10           15
Gly Phe Leu Ile Glu Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala Ala
          20           25           30
Gln Met Tyr Ile Phe Val Ala Phe Ala Thr Val Glu Asn Tyr Leu Leu
          35           40           45
Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu His
          50           55           60
Tyr Thr Thr Thr Met Thr Thr Thr Val Cys Ala Arg Leu Ala Ile Gly
65           70           75           80
Ser Tyr Leu Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asp Thr
          85           90           95
Phe Ser Leu Ser Phe Cys Lys Ser Asn Glu Val His His Phe Phe Cys
          100          105          110
Asp Ile Pro Ala Val Met Val Leu Ser Cys Ser Asp Arg His Ile Ser
          115          120          125
Glu Leu Val Leu Ile Tyr Val Val Ser Phe Asn Ile Phe Ile Ala Leu
          130          135          140
Leu Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Ile Thr Ile Leu Lys
          145          150          155          160
Met His Ser Ala Ser Val Tyr Gln Lys Pro Leu Ser Thr Cys Ala Ser

```

165 170 175  
 His Phe Ile Ala Val Gly Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr  
 180 185 190  
 Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala Pro  
 195 200 205  
 Val Phe Tyr Thr Met Val Ile Pro  
 210 215

&lt;210&gt; 1796

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g714 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1796

Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met Leu Thr  
 1 5 10 15  
 Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys Ile Met  
 20 25 30  
 Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu Ile Leu  
 35 40 45  
 Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro Leu Arg  
 50 55 60  
 Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala Val Ala  
 65 70 75 80  
 Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Leu Val Leu Ile  
 85 90 95  
 Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Cys Glu  
 100 105 110  
 Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln  
 115 120 125  
 Val Val Ile Phe Ala Ala Cys Val Phe Ile Leu Val Gly Pro Leu Cys  
 130 135 140  
 Leu Val Leu Val Ser Tyr Leu Arg Ile Leu Ala Ala Ile Leu Arg Ile  
 145 150 155 160  
 Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His  
 165 170 175  
 Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met  
 180 185 190  
 Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu  
 195 200 205  
 Phe Tyr Ser Leu Phe Asn Pro  
 210 215

&lt;210&gt; 1797

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g715 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1797

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg  
 1 5 10 15  
 Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile  
 20 25 30  
 Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser  
 35 40 45

```

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
 50                      55                      60
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
65                      70                      75                      80
Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
                      85                      90                      95
Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
                      100                      105                      110
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
                      115                      120                      125
Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
130                      135                      140
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
145                      150                      155                      160
Leu Leu

```

&lt;210&gt; 1798

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g716 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(224)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1798

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1                      5                      10                      15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
                      20                      25                      30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
                      35                      40                      45
Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Pro
50                      55                      60
Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Gln Asp Leu
65                      70                      75                      80
Leu Ser Leu Tyr Phe Phe Leu Phe Phe Ser Phe Phe Leu Arg Leu Leu
                      85                      90                      95
Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys
                      100                      105                      110
Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser Gln Leu Ser His
115                      120                      125
Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Met Tyr Phe Pro Ala
130                      135                      140
Ala Ile Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Tyr Cys
145                      150                      155                      160
Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr
                      165                      170                      175
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
180                      185                      190
Tyr Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser
195                      200                      205
Leu Arg Lys Ala Ala Val Ala Ser Val Met Tyr Lys Met Val Thr Pro
210                      215                      220

```

&lt;210&gt; 1799

&lt;211&gt; 218

<212> PRT  
 <213> Unknown (H38g717 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(218)  
 <223> Xaa = Any Amino Acid

<400> 1799  
 Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met Glu Glu Ser Met Leu  
 35 40 45  
 Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 65 70 75 80  
 Cys Phe Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu  
 85 90 95  
 Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu Ile Pro Asn Phe  
 100 105 110  
 Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe  
 115 120 125  
 Thr Ile Asn Ile Val Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu  
 130 135 140  
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile  
 145 150 155 160  
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys  
 165 170 175  
 Gly Ser His Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly  
 180 185 190  
 Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val  
 195 200 205  
 Ala Ser Val Met Tyr Thr Val Val Thr Pro  
 210 215

<210> 1800  
 <211> 295  
 <212> PRT  
 <213> Unknown (H38g718 protein)

<220>  
 <223> Synthetic construct

<400> 1800  
 Leu Ile Phe Phe Leu Ile Tyr Pro Leu Ile Leu Val Gly Asn Asp Gln  
 1 5 10 15  
 Ile Leu Val Val Val Met Ala Glu Ala Ser Leu His Lys Pro Val Tyr  
 20 25 30  
 Phe Phe Leu Ile Asn Leu Ser Ala Leu Asp Ile Leu Ser Thr Thr Val  
 35 40 45  
 Thr Val Pro Lys Thr Leu Pro Leu Phe Leu Leu Gly Asp His Phe Leu  
 50 55 60  
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Leu Phe His Ser Phe Ser  
 65 70 75 80  
 Cys Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val  
 85 90 95

```

Ala Ile Cys His Pro Leu Gln Tyr Pro Val Leu Met Asn Pro Gln Thr
      100      105      110
Asn Ala Val Leu Ala Thr Gly Ala Trp Leu Thr Ala Leu Leu Pro
      115      120      125
Ile Pro Ala Val Val Gln Thr Ser Gln Met Ala Phe Asp Ser Ile Ala
      130      135      140
Asp Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser
      145      150      155      160
Cys Ser Asp Thr Ser Pro Gln Thr Phe Met Gly Phe Cys Ile Ala Met
      165      170      175
Val Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Ala His
      180      185      190
Ile Leu Thr Ser Val Leu Arg Ile Asn Ser Gln Glu Gly Arg Ser Lys
      195      200      205
Ala Phe Ser Thr Cys Ser Ser His Leu Pro Val Val Gly Thr Tyr Tyr
      210      215      220
Ser Ser Ile Ala Ile Ala Tyr Val Ala Tyr Ser Ala Asp Leu Pro Leu
      225      230      235      240
Asp Phe His Val Met Gly Asn Val Val His Ala Leu Leu Leu Pro Leu
      245      250      255
Leu Leu Leu Leu Pro Leu Pro Leu Leu Pro Leu Pro Leu Arg Leu Pro
      260      265      270
Leu Leu Leu Leu Leu Arg Ser Pro Ser Ser Ser Ser Ser Pro Ser
      275      280      285
Pro Ser Ser Ser Phe Phe Phe
      290      295

```

&lt;210&gt; 1801

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g719 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1801

```

Met Glu Met Glu Asn Cys Thr Arg Val Lys Glu Phe Ile Phe Leu Gly
  1      5      10      15
Leu Thr Gln Asn Arg Glu Val Ser Leu Val Leu Phe Leu Phe Leu Leu
      20      25      30
Leu Val Tyr Val Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr
      35      40      45
Val Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu His
      50      55      60
Asn Leu Ser Ile Ala Asp Ile Cys Phe Ser Ser Ile Thr Val Pro Lys
      65      70      75      80
Val Leu Val Asp Leu Leu Ser Glu Arg Lys Thr Ile Ser Phe Asn His
      85      90      95
Cys Phe Thr Gln Met Phe Leu Phe His Leu Ile Gly Gly Val Asp Val
      100      105      110
Phe Ser Leu Ser Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser Lys
      115      120      125
Pro Leu His Tyr Ala Thr Ile Met Ser Arg Asp Gln Cys Ile Gly Leu
      130      135      140
Thr Val Ala Ala Trp Leu Gly Gly Phe Val His Ser Ile Val Gln Ile
      145      150      155      160
Ser Leu Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr
      165      170      175
Phe Tyr Cys Asp Val His Arg Val Leu Lys Leu Ala His Thr Asp Ile
      180      185      190
Phe Ile Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Leu Thr Thr

```

195	200	205
Leu Trp Phe Phe Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Ser Leu		
210	215	220
Pro Lys Ser Gln Ala Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys		
225	230	235
Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr		
245	250	255
Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Met Asp Lys Ala Ile Ser		
260	265	270
Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr		
275	280	285
Leu Arg Asn His Glu Met Lys Ser Ala Met Arg Arg Leu Lys Arg Arg		
290	295	300
Leu Val Pro Ser Asp Arg Lys		
305	310	

&lt;210&gt; 1802

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g720 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1802

Thr Met Gln Gln Asn Asn Ser Val Pro Glu Phe Ile Leu Leu Gly Leu		
1	5	10
Thr Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile		
20	25	30
Phe Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile		
35	40	45
Lys Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr		
50	55	60
Leu Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu		
65	70	75
Ile Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys		
85	90	95
Met Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe		
100	105	110
Val Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro		
115	120	125
Leu Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile		
130	135	140
Val Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile		
145	150	155
Leu Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr		
165	170	175
Cys Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr		
180	185	190
Met Ile Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser		
195	200	205
Ser Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu		
210	215	220
Arg Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr		
225	230	235
Ser His Ile Ile Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile		
245	250	255
Tyr Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val		
260	265	270
Phe Tyr Thr Ile Gly Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu		
275	280	285



Arg Asn Ala Glu Val Lys Asn Ala Met Arg Lys  
290 295

<210> 1803  
<211> 314  
<212> PRT  
<213> Unknown (H38g721 protein)

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(314)  
<223> Xaa = Any Amino Acid

<400> 1803  
Met Glu Leu Gly Asn Val Thr Arg Val Lys Glu Phe Ile Phe Leu Gly  
1 5 10 15  
Leu Thr Gln Ser Gln Asp Gln Ser Leu Val Leu Phe Leu Phe Leu Cys  
20 25 30  
Leu Val Tyr Met Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr  
35 40 45  
Val Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
50 55 60  
Asn Leu Ala Ile Leu Asp Ile Cys Phe Ser Ser Thr Thr Ala Pro Lys  
65 70 75 80  
Val Leu Leu Asp Leu Leu Ser Lys Lys Lys Thr Ile Ser Tyr Thr Ser  
85 90 95  
Cys Met Thr Gln Ile Phe Leu Phe His Leu Leu Gly Gly Ala Asp Ile  
100 105 110  
Phe Ser Leu Ser Val Met Ala Phe Asp Cys Tyr Met Ala Ile Ser Lys  
115 120 125  
Pro Leu His Tyr Val Thr Ile Met Ser Arg Gly Gln Cys Thr Ala Leu  
130 135 140  
Ile Ser Ala Ser Trp Met Gly Gly Phe Val His Ser Ile Val Gln Ile  
145 150 155 160  
Ser Leu Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr  
165 170 175  
Phe Tyr Cys Asp Val Pro Gln Val Leu Lys Leu Thr Cys Thr Asp Thr  
180 185 190  
Phe Ala Leu Glu Phe Leu Met Ile Ser Asn Asn Gly Leu Val Thr Thr  
195 200 205  
Leu Trp Phe Ile Phe Leu Leu Val Ser Tyr Thr Val Ile Leu Met Thr  
210 215 220  
Leu Arg Ser Gln Ala Gly Gly Gly Arg Arg Lys Ala Ile Ser Thr Cys  
225 230 235 240  
Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr  
245 250 255  
Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Thr Glu Lys Ala Ile Ser  
260 265 270  
Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr  
275 280 285  
Leu Arg Asn Gln Glu Met Lys Ser Ala Met Arg Arg Leu Lys Arg Arg  
290 295 300  
Leu Val Pro Ser Glu Arg Glu Xaa Lys Thr  
305 310

<210> 1804  
<211> 314  
<212> PRT  
<213> Unknown (H38g722 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1804

```

Met Leu Gly Leu Asn His Thr Ser Met Ser Glu Phe Ile Leu Val Gly
 1           5           10           15
Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu
      20           25           30
Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
      35           40           45
Val Trp Ser Glu Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Cys
      50           55           60
Val Leu Ser Val Ser Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
      65           70           75           80
Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
      85           90           95
Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
      100          105          110
Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Gly Cys Ala Cys Leu
      130          135          140
Val Gly Cys Ser Trp Ala Gly Gly Ser Val Met Gly Met Val Val Thr
      145          150          155          160
Ser Ala Ile Phe Gln Leu Thr Phe Cys Gly Ser His Glu Ile Gln His
      165          170          175
Phe Leu Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asn Asn
      180          185          190
Val Pro Ala Val Ala Leu Gly Val Gly Leu Val Cys Ile Met Ala Leu
      195          200          205
Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
      210          215          220
Asp Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
      225          230          235          240
Thr Cys Ala Ser His Leu Ile Val Val Ile Val His Tyr Gly Phe Ala
      245          250          255
Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro His Ser Gln Glu Gly Asp
      260          265          270
Thr Leu Met Ala Thr Thr Tyr Ala Val Leu Thr Pro Phe Leu Ser Pro
      275          280          285
Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Arg
      290          295          300
Thr Phe Leu Ser Thr Leu Tyr Ser Ser Gly
      305          310

```

&lt;210&gt; 1805

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g723 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1805

```

Met Pro Gly Gln Asn Tyr Arg Thr Ile Ser Glu Phe Ile Leu Ser Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln Gln Leu Leu Pro Val Leu Phe Leu Leu Tyr
      20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
      35           40           45

```

Thr Val Trp Ile Glu Arg Arg Leu His Thr Pro Met Tyr Leu Phe Leu  
 50 55 60  
 Cys Ala Leu Ser Ile Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro  
 65 70 75 80  
 Arg Met Leu Ala Asp Leu Leu Phe Thr His Arg Ser Ile Thr Phe Val  
 85 90 95  
 Ala Cys Ala Ile Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His  
 100 105 110  
 Ser Phe Leu Leu Met Val Met Gly Tyr Asp His Tyr Val Thr Ile Cys  
 115 120 125  
 His Pro Leu His Tyr Asn Met Leu Met Ser Pro Arg Gly Cys Ala His  
 130 135 140  
 Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val  
 145 150 155 160  
 Thr Met Met Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His  
 165 170 175  
 His Phe Leu Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Gly Ser  
 180 185 190  
 Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala  
 195 200 205  
 Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Phe Val Phe Ile Val  
 210 215 220  
 Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe  
 225 230 235 240  
 Ser Thr Cys Val Ser His Leu Thr Val Val Val Met His Tyr Ser Phe  
 245 250 255  
 Ala Ser Leu Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser  
 260 265 270  
 Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser  
 275 280 285  
 Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn  
 290 295 300  
 Lys Asn Phe Cys Arg Arg Phe Cys Pro Leu Ser Ser  
 305 310 315

&lt;210&gt; 1806

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g724 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(161)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1806

Gly Trp Lys Ser Ser Thr Phe Asn Ile Ser Cys Thr Lys Phe Phe Leu  
 1 5 10 15  
 Val Gly Phe Pro Gly Leu Arg Glu Trp Trp Pro Leu Leu Val Leu Pro  
 20 25 30  
 Leu Val Phe Leu Phe Val Thr Ile Ile Ser Ala Asn Ala Leu Val Ile  
 35 40 45  
 His Thr Val Val Ala Arg Gln Asn Leu His Gln Pro Thr Cys Met Leu  
 50 55 60  
 Ile Thr Val Leu Leu Ala Val Asn Ile Arg Ala Ala Thr Ala Val Met  
 65 70 75 80  
 Pro Lys Met Leu Glu Gly Phe Val Tyr Tyr Ala Asn Pro Ile Ser Leu  
 85 90 95  
 His Gly Arg Leu Ala Xaa Val Phe Phe Ile Tyr Phe Thr Leu Leu Leu

```

      100      105      110
Asp Tyr Asn Phe Leu Trp Pro Trp Pro Trp Thr Gly Tyr Phe Ala Ile
      115      120      125
Cys His Pro Leu Cys Phe Ser Asp Leu Met Thr Ser Gln Leu Leu Gly
      130      135      140
Leu Leu Ala Ile Leu Ala Phe Glu Gln Ser Pro Gly Ser Asp Pro Ala
145      150      155      160
Pro

```

<210> 1807  
 <211> 198  
 <212> PRT  
 <213> Unknown (H38g725 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(198)  
 <223> Xaa = Any Amino Acid

```

<400> 1807
Val Ala Ile Cys His Pro Leu Cys Phe Gln Thr Glu Xaa Leu Pro Ser
  1          5          10          15
Trp Leu Gly Leu Leu Ala Ile Leu Ala Leu Thr Gln Ser Trp Gly Val
      20      25      30
Thr Val Pro Leu Val Val Leu Thr Ala Lys Ala Asp Phe Cys Arg Thr
      35      40      45
Ala Val Ile Arg His Phe Thr Cys Glu Cys Ile Ala Leu Leu Ser Ile
  50          55          60
Ala Cys Gly Asp Leu Thr Phe Asn Asn Trp Leu Gly Leu Ala Met Cys
65          70          75          80
Leu Val Thr Val Ile Ser Asp Met Ala Leu Leu Gly Thr Ser Tyr Thr
      85          90          95
His Ile Ile Tyr Ala Ala Phe Arg Ile Ser Ser Trp Gly Ala Gln Ala
      100      105      110
Lys Ala Leu His Thr Cys Gly Ser His Leu Leu Val Ile Leu Ser Ile
      115      120      125
Tyr Val Ser Gly Leu Ser Thr Ser Ile Thr Phe Xaa Val Ala Lys Thr
      130      135      140
Val Ser Gln Asn Val Gln Asn Leu Leu Ser Ala Ile Tyr Leu Leu Leu
145          150          155          160
Pro Gly Ala Leu Asn Pro Val Ile Tyr Gly Val Arg Thr Arg Glu Ile
      165      170      175
Gln Gln His Val Glu Lys Met Leu Cys Glu Lys Glu Thr Ala Gln Lys
      180      185      190
Ala Gly Glu Lys Pro Lys
      195

```

<210> 1808  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g726 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(315)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1808

Phe Ser Gln Asn Leu Leu Ile Ser Gly Ser Gly Ser Phe Val Leu Leu  
 1 5 10 15  
 Gly Met Pro Gly Leu Glu Ala Leu His Ala Trp Leu Ser Val Pro Val  
 20 25 30  
 Cys Leu Leu Tyr Met Ala Ala Leu Val Gly Asn Ala Leu Leu Val Gly  
 35 40 45  
 Leu Val Val Ala Asp Lys Ala Leu Trp Ala Pro Met Tyr Gln Leu Leu  
 50 55 60  
 Trp Leu Leu Ala Ala Ala Asp Phe Val Leu Ala Thr Ser Thr Val Pro  
 65 70 75 80  
 Lys Ala Leu Ala Val Leu Trp Gly Leu Ser Ser Glu Ile Ser Phe Gly  
 85 90 95  
 Gly Cys Leu Ala Gln Leu Phe Val Ala His Ser Val Asn His Cys His  
 100 105 110  
 Ile Ala Glu Ser Ser Val Leu Leu Ser Thr Ala Val Asp Cys Gln Pro  
 115 120 125  
 Leu Arg Tyr Gly Ala Leu Leu Ala Gln Phe Val Val Gly Leu Val Ala  
 130 135 140  
 Leu Thr Thr Met Thr Arg Asp Val Cys Val Met Tyr Thr Leu Xaa Phe  
 145 150 155 160  
 Leu Phe Lys Lys Leu Pro Tyr Cys Gly Gln Trp Ala Leu Pro His Thr  
 165 170 175  
 Tyr Cys Glu His Met Gly Val Ala Cys Leu Ala Cys Gly Asp Thr Cys  
 180 185 190  
 Pro Ile Ile Arg Tyr Gly Leu Ala Thr Thr Leu Leu Ser Pro Ala Leu  
 195 200 205  
 Asp Leu Gly Leu Ile Gly Ala Ser Tyr Ala Leu Ile Phe Arg Ala Val  
 210 215 220  
 Cys Arg Leu Pro Ser His Val Ala Cys His Lys Ala Leu Gly Asn Cys  
 225 230 235 240  
 Gly Thr Tyr Ala Ser Ile Ile Gly Leu Phe Tyr Thr Pro Ala Leu Phe  
 245 250 255  
 Ser Phe Leu Ala His Cys Phe Gly Cys His Thr Val Pro Asn His Ile  
 260 265 270  
 His Ile Leu Leu Ala Asn Leu Tyr Ala Val Val Phe Pro Ala Phe Asn  
 275 280 285  
 Pro Val Val Tyr Gly Val Gln Thr Gln Gln Ser Ser Glu Ala Gln Glu  
 290 295 300  
 Leu Ala Ser Thr Phe Leu Gly Arg Ser Ser Glu  
 305 310 315

&lt;210&gt; 1809

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g727 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1809

Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu  
 20 25 30  
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val  
 35 40 45  
 Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val Pro His

```

65              70              75              80
Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
              85              90              95
Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
              100             105             110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
              115             120             125
Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
              130             135             140
Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
145             150             155             160
Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
              165             170             175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
              180             185             190
Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
              195             200             205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
              210             215             220
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225             230             235             240
Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
              245             250             255
Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
              260             265             270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn Ser Leu
              275             280             285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Phe Lys Arg Leu
              290             295             300
Met Pro Arg Ile Phe Phe Cys Lys Lys
305              310

```

&lt;210&gt; 1810

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g728 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1810

```

Gly Thr Leu Asn Leu Ser Ser Phe Asn Pro Gly Leu Phe Ile Leu Leu
1          5          10          15
Gly Ile Pro Gly Leu Glu Trp Phe Cys Ile Trp Met Gly Ile Leu Ser
          20          25          30
Phe Thr Ser Tyr Leu Val Ser Leu Ala Gly Asn Val Ile Leu Leu Tyr
          35          40          45
Leu Ile Thr Val Glu His Asn Leu His Lys Pro Met Phe Ser Phe Leu
          50          55          60
Ser Ile Pro Ala Ser Ala Asn Leu Ile Leu Cys Ile Thr Tyr Phe Pro
65          70          75          80
Lys Thr Phe Gly Ile Phe Xaa Leu Lys Ala Gln Lys Ile Ile Phe Pro
          85          90          95
Gly Cys Phe Thr Arg Phe Phe Phe Phe Gly Leu Leu His Phe Ser Phe
          100          105          110
Phe Leu Asp Leu Ala Ile Leu Leu Gly Leu Ala Phe Asp His Tyr Met
          115          120          125

```

```

Thr Ile Gly Phe Leu Leu Arg Tyr Thr Ser Gly Leu Thr Pro Arg Thr
130          135          140
Leu Gly Lys Ile Val Val Ser Ile Asp Xaa Arg Phe Asn Asn Ile Leu
145          150          155          160
Pro Ile Asp Phe Leu Gly Lys His Leu Pro Phe Cys Arg Thr His Ile
165          170          175
Asn Ser Asn Thr Tyr Cys Glu His Ile Gly Val Ala Leu Leu Ser Tyr
180          185          190
Ala Asp Ile Ser Ile Asn Ile Trp Tyr Asp Phe Thr Ile Leu Val Met
195          200          205
Thr Ile Ile Ser Asp Leu Ile Leu Thr Asp Ile Ser Tyr Thr Leu Thr
210          215          220
Leu His Ala Val Phe His Leu Pro Ser Ser Asp Ala Leu Leu Lys Ala
225          230          235          240
Leu Ser Thr Cys Gly Ser His Val Ser Val Ile Leu Met Leu Tyr Thr
245          250          255
Pro Thr Met Leu Ser Ala Leu Thr His His Phe Gly Gln Ser Ile Ser
260          265          270
Cys Thr Phe Tyr Ile Met Phe Val Gly Leu Tyr Arg Ala Ile Pro Pro
275          280          285
Val Leu Asn Ser Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gly Asn
290          295          300
Lys Val Ile Leu Leu Phe Phe Leu Lys Gly Met Gln Xaa Tyr Glu Asp
305          310          315          320
Glu Asn Met

```

&lt;210&gt; 1811

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g729 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT.

&lt;222&gt; (1)...(337)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1811

```

Met Lys Lys Asn Ala Ser Phe Glu Asp Phe Phe Ile Leu Leu Gly Phe
1      5      10      15
Ser Asn Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile
20     25     30
Phe Tyr Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser
35     40     45
Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
50     55     60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu
65     70     75     80
Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys
85     90     95
Thr Val Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val
100    105    110
Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro
115    120    125
Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala
130    135    140
Ala Ala Ser Trp Val Ser Gly Phe Thr Thr Ser Ala Leu His Ser Ser
145    150    155    160
Phe Thr Phe Trp Ile Pro Leu Cys Arg His Arg Leu Val Asp His Phe

```

```

                165                170                175
Phe Cys Glu Ala Pro Ala Leu Leu Arg Leu Ser Cys Val Asp Thr Xaa
                180                185                190
Ala Asn Glu Leu Thr Leu Met Val Met Ser Ser Ile Phe Val Leu Ile
                195                200                205
Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile Ala Arg Ala Val
                210                215                220
Leu Ser Met Gln Ser Thr Thr Gly Leu Gln Lys Val Leu Arg Thr Cys
225                230                235                240
Gly Ala His Leu Met Val Val Ser Leu Phe Phe Ile Pro Val Met Cys
                245                250                255
Met Tyr Leu Gln Pro Pro Ser Glu Asn Ser Gln Asp Gln Gly Lys Phe
                260                265                270
Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro Leu Ile
                275                280                285
Tyr Thr Phe Arg Asn Lys Asp Val Arg Gly Ala Val Lys Arg Leu Met
                290                295                300
Gly Trp Glu Trp Gly Met Xaa Gln Gly Asn His Val Xaa Leu Leu Phe
305                310                315                320
Phe Leu Gly Ser Phe His Phe Glu Arg Leu Phe Pro Cys Phe Phe Val
                325                330                335
Ile

```

<210> 1812  
 <211> 319  
 <212> PRT  
 <213> Unknown (H38g730 protein)

<220>  
 <223> Synthetic construct  
  
 <221> VARIANT  
 <222> (1)...(319)  
 <223> Xaa = Any Amino Acid

```

<400> 1812
Met Ala Met Tyr Asn Met Ser Asp His Gly Thr Gly Leu Phe Ile Leu
 1                5                10                15
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Val Trp Ile Ser Ile Pro
                20                25                30
Phe Cys Leu Ile Tyr Leu Met Ala Val Val Ala Lys Ser Ile Leu Leu
                35                40                45
Tyr Leu Ile Val Val Glu His Ser Leu His Ala Pro Met Phe Phe Phe
 50                55                60
Leu Ser Met Leu Ala Ile Thr Asp Leu Ile Leu Ser Thr Thr Cys Val
65                70                75                80
Pro Lys Thr Leu Ser Ile Phe Trp Phe Gly Pro Gln Ile Ser Phe Pro
                85                90                95
Gly Cys Leu Thr Gln Leu Phe Phe Leu His Tyr Ser Phe Val Leu Asp
                100                105                110
Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Cys
                115                120                125
Ser Pro Leu Arg Tyr Thr Thr Ile Leu Thr Pro Lys Thr Ile Val Lys
130                135                140
Ile Ala Val Gly Ile Cys Phe Arg Ser Phe Cys Val Phe Val Pro Cys
145                150                155                160
Val Phe Leu Val Asn Arg Leu Pro Phe Cys Arg Thr His Ile Ile Ser
                165                170                175
His Thr Tyr Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp
                180                185                190

```



```

Ile Ser Ile Asn Ile Trp Cys Gly Phe Cys Val Pro Ile Met Thr Val
    195                200                205
Met Thr Asp Val Ile Leu Ile Ala Val Ser Tyr Thr Leu Met Leu Cys
    210                215                220
Gly Val Phe Cys Leu Pro Ser Gln Asp Ala Arg Gln Lys Ala Leu Cys
    225                230                235                240
Ser Cys Gly Ser His Val Cys Val Ile Leu Ile Phe Tyr Thr Pro Ala
    245                250                255
Phe Phe Ser Ile Leu Ala His Arg Phe Gly His Asn Val Pro His Thr
    260                265                270
Phe His Ile Met Phe Ala Asn Leu Tyr Val Ile Ile Pro Pro Ala Leu
    275                280                285
Asn Pro Ile Val Tyr Arg Ile Lys Thr Lys Gln Ile Gln Asn Arg Ile
    290                295                300
Leu Leu Leu Phe Pro Lys Gly Ser Gln Xaa Xaa Val Pro Glu Leu
    305                310                315

```

&lt;210&gt; 1813

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g731 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1813

```

Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
.1      5      10      15
Leu Val Gly Phe Ser Asn Trp Pro His Leu Glu Val Val Ile Phe Val
    20      25      30
Val Val Leu Ile Phe Tyr Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
    35      40      45
Ile Ile Leu Ser Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe
    50      55      60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser
    65      70      75      80
Ile Pro Gln Leu Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser
    85      90      95
Tyr Ala Gly Cys Met Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr
    100     105     110
Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala
    115     120     125
Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys
    130     135     140
His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Ser Ala
    145     150     155     160
Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln
    165     170     175
Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys
    180     185     190
Val Asp Thr His Val Asn Glu Leu Thr Leu Met Ile Thr Ser Ser Ile
    195     200     205
Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile
    210     215     220
Val Arg Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val
    225     230     235     240
Phe Gly Thr Cys Gly Ala His Leu Met Ala Val Ser Leu Phe Phe Ile
    245     250     255
Pro Ala Met Cys Ile Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp
    260     265     270
Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu

```

275                      280                      285  
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Val Val Arg Gly Ala Val  
     290                      295                      300  
 Lys Arg Leu Met Gly Trp Glu  
 305                      310

<210> 1814  
 <211> 88  
 <212> PRT  
 <213> Unknown (H38g732 protein)

<220>  
 <223> Synthetic construct

<400> 1814  
 Phe Ile His Ala Leu Ser Val Ile Glu Ser Ile Ile Val Leu Ala Met  
     1                      5                      10                      15  
 Ala Phe Glu Arg Tyr Val Ala Ile Cys His Pro Leu Cys His Ala Glu  
                     20                      25                      30  
 Val Leu Asn Ser Thr Val Thr Ala His Ile Gly Ile Val Ala Gly Val  
     35                      40                      45  
 Arg Gly Ser Leu Phe Phe Ser Pro Leu Ala Leu Leu Ile Lys Thr Leu  
     50                      55                      60  
 Gly Leu Cys His Ser Tyr Val Leu Ser His Ser Tyr Ser Leu His Gln  
 65                      70                      75                      80  
 Asp Val Ala Asn Leu Ser Tyr Ala  
                     85

<210> 1815  
 <211> 159  
 <212> PRT  
 <213> Unknown (H38g733 protein)

<220>  
 <223> Synthetic construct

<400> 1815  
 Val Ala Ile Cys Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln  
     1                      5                      10                      15  
 Leu Cys Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His  
                     20                      25                      30  
 Ser Ile Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro  
     35                      40                      45  
 Asn Glu Leu Asp Asn Phe Tyr Cys Asp Val Leu Gln Ile Ile Lys Leu  
     50                      55                      60  
 Ala Cys Met Asp Thr Tyr Val Val Glu Val Leu Val Ile Ala Asn Ser  
 65                      70                      75                      80  
 Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala  
                     85                      90                      95  
 Ile Ile Leu Ile Thr Leu Arg Thr Arg Phe Cys Gln Gly Gln Asn Lys  
                     100                      105                      110  
 Val Leu Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe  
                     115                      120                      125  
 Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val  
     130                      135                      140  
 Asp Lys Ile Phe Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu  
 145                      150                      155

<210> 1816  
 <211> 316  
 <212> PRT

<213> Unknown (H38g734 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1816

```

Met Ser Ala Pro Asn His Ser Thr Ala Asn His Asp Met Phe Val Leu
 1           5           10           15
Ile Gly Val Pro Gly Leu Lys Glu Leu His Val Trp Ile Ser Ile Pro
          20           25           30
Phe Cys Leu Met Tyr Leu Val Ala Val Ser Gly Asn Gly Leu Leu Val
          35           40           45
Cys Val Val Ala Val Glu His Ser Leu His Glu Pro Met Tyr Leu Phe
          50           55           60
Leu Ser Met Leu Ala Phe Trp Asp Leu Ile Leu Ser Thr Ser Ala Val
          65           70           75           80
Pro Lys Ala Leu Ser Ile Phe Trp Phe Asp Asp Val Asp Ile Ser Phe
          85           90           95
Gly Gly Cys Val Thr Gln Leu Phe Phe Met His Phe Ala Phe Val Ala
          100          105          110
Glu Ser Gly Ile Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Ser His Ser Val Ile Gly
          130          135          140
Lys Ile Gly Gly Val Val Phe Arg Ser Phe Ala Thr Val Phe Ser
          145          150          155          160
Ile Val Phe Leu Val Lys Arg Leu Pro Phe Cys Arg Thr Asn Ile Ile
          165          170          175
Ala His Thr Phe Cys Glu His Met Gly Leu Ala Lys Leu Gly Cys Ser
          180          185          190
Glu Ile Thr Ile Asn Ile Trp Tyr Gly Ile Ser Val Pro Leu Leu Ser
          195          200          205
Val Thr Leu Asp Met Val Thr Ile Val Ile Ser Xaa Gly Leu Ile Val
          210          215          220
Gln Ala Val Phe Arg Leu Pro Ser Leu Gly Ala Trp Met Lys Ala Leu
          225          230          235          240
Ser Thr Cys Gly Ser His Gly Ser Val Ile Leu Met Phe Cys Leu Pro
          245          250          255
Gly Ile Phe Thr Val Ile Val Gln Arg Phe Ala Xaa Lys Phe Pro Lys
          260          265          270
Tyr Val His Ile Leu Leu Ala Asn Leu Tyr Val Leu Val Pro Pro Met
          275          280          285
Met Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gln Lys Gly
          290          295          300
Val Ala Leu Val Phe Ser Pro Lys Gly Lys Cys Cys
          305          310          315

```

<210> 1817

<211> 364

<212> PRT

<213> Unknown (H38g735 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(364)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1817

```

Met Pro Leu Thr Asn Glu Ser His Pro Glu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ala Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Thr Ser Leu Leu
      20           25           30
Ile Met Tyr Pro Ile Ala Val Met Gly Asn Ile Thr Ile Ile Leu Met
      35           40           45
Ser Arg Leu Asp Ser Arg Leu His Ser Pro Met Tyr Phe Phe Leu Thr
      50           55           60
Asn Leu Ser Phe Leu Asp Met Cys Tyr Thr Thr Ser Ile Val Pro Gln
      65           70           75           80
Met Leu Phe Asn Leu Gly Ser Ser Lys Lys Thr Ile Ser Tyr Met Gly
      85           90           95
Cys Ala Val Gln Leu Tyr Phe Phe His Ile Met Gly Gly Thr Glu Cys
      100          105          110
Leu Leu Leu Ala Ile Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Arg
      115          120          125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Arg Val Cys Ile His Xaa
      130          135          140
Phe Pro Pro Cys Trp Leu Ile Gly Ile Ile Tyr Ala Val Ser Glu Ala
      145          150          155          160
Thr Ala Thr Leu Gln Leu Pro Leu Cys Gly Ser Asn Lys Leu Asp His
      165          170          175
Leu Val Cys Glu Ile Pro Val Leu Ile Lys Ile Ala Cys Gly Glu Lys
      180          185          190
Gly Ser Asn Glu Leu Thr Leu Ser Val Val Cys Ile Phe Met Leu Ala
      195          200          205
Val Pro Leu Cys Leu Ile Leu Ala Ser Tyr Ala Ser Ile Gly Ser Ala
      210          215          220
Val Phe Lys Ile Lys Ser Ser Lys Gly Arg Lys Lys Ala Phe Gly Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Pro Ala Ile
      245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Ile Ser Arg Asp Gln Pro Lys
      260          265          270
Phe Met Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Phe
      275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asn Val Lys Gly Ala Leu Arg Asn Leu
      290          295          300
Val Arg Ser Ile Phe Ser Phe Lys Xaa Xaa Trp Val Asp Ile Thr Met
      305          310          315          320
Lys Leu Leu Asn Ser Xaa Ser Arg Leu Leu Trp Phe Tyr Leu Thr Asn
      325          330          335
Ser Cys Leu Ile Ile Lys Tyr Arg Phe Thr Cys Ser Cys Lys Ile Cys
      340          345          350
Tyr Val Ser Glu Thr Leu Cys Lys His Val Gln Gln
      355          360

```

&lt;210&gt; 1818

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g736 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(166)

&lt;223&gt; Xaa = Any Amino Acid

<400> 1818  
 Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr Ile Leu Leu Ala Met  
 1 5 10 15  
 Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Ala  
 20 25 30  
 Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly Ile Val Ala Val Val  
 35 40 45  
 Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu Leu Ile Lys Arg Leu  
 50 55 60  
 Ala Phe Cys His Ser Asn Val Leu Ser His Ser Tyr Cys Val His Gln  
 65 70 75 80  
 Asp Val Leu Lys Leu Ala Tyr Ala Asp Thr Leu Pro Asn Val Val Tyr  
 85 90 95  
 Gly Leu Thr Ala Ile Leu Leu Ala Met Gly Val Asp Ala Met Phe Ile  
 100 105 110  
 Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val Leu Gln Leu Pro Ser  
 115 120 125  
 Lys Ser Xaa Arg Ala Lys Ala Phe Gly Thr Cys Val Val His Ile Gly  
 130 135 140  
 Val Val Leu Gly Leu Tyr Val Pro Leu Ile Gly Thr Ser Ser Gly His  
 145 150 155 160  
 Arg Phe Gly Asn Lys Leu  
 165

<210> 1819  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g737 protein)

<220>  
 <223> Synthetic construct

<400> 1819  
 Met Met Ile Lys Lys Asn Ala Ser Ser Glu Asp Phe Phe Ile Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asn Trp Pro Gln Leu Glu Val Val Leu Phe Val Val Ile  
 20 25 30  
 Leu Ile Phe Tyr Leu Met Thr Leu Thr Gly Asn Leu Phe Ile Ile Ile  
 35 40 45  
 Leu Ser Tyr Val Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Leu Asp Leu Cys His Thr Thr Ser Ser Ile Pro  
 65 70 75 80  
 Gln Leu Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Met Val Gln Leu Tyr Phe Val Leu Ala Leu Gly Ile Ala Glu  
 100 105 110  
 Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys  
 115 120 125  
 Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys His Leu  
 130 135 140  
 Leu Ala Ala Ala Ser Trp Val Ile Gly Phe Thr Ile Ser Ala Leu His  
 145 150 155 160  
 Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Leu Val Asp  
 165 170 175  
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys Val Asp  
 180 185 190  
 Thr His Ala Asn Glu Leu Thr Leu Met Val Met Ser Ser Ile Phe Val  
 195 200 205  
 Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala Tyr Gly Ala Ile Ala Arg

```

      210              215              220
Ala Val Leu Ser Met Gln Ser Thr Thr Gly Leu Gln Lys Val Phe Arg
225              230              235              240
Thr Cys Gly Ala His Leu Met Val Val Ser Leu Phe Phe Ile Pro Val
      245              250              255
Met Cys Met Tyr Leu Gln Pro Pro Ser Glu Asn Ser Pro Asp Gln Gly
      260              265              270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro
      275              280              285
Leu Ile Tyr Thr Leu Arg Asn Lys His Val Lys Gly Ala Ala Lys Arg
      290              295              300
Leu Leu Gly Trp Glu Trp Gly Lys
305              310

```

<210> 1820  
 <211> 151  
 <212> PRT  
 <213> Unknown (H38g738 protein)

<220>  
 <223> Synthetic construct

```

<400> 1820
Arg Pro Leu Cys Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu
 1              5              10              15
Pro Ala Leu Leu Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu
      20              25              30
Asn Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu Arg Gly Val Ala
      35              40              45
Val Ile Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met
      50              55              60
Arg Phe Asn Gly Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His
      65              70              75              80
Leu Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu
      85              90              95
Gln Pro Ala Gln Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu
      100              105              110
Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu
      115              120              125
Arg Asn Lys Lys Met Lys Gly Ala Pro Arg Arg Leu Leu Arg Ser Leu
      130              135              140
Gly Arg Gly Gln Ala Gly Gln
145              150

```

<210> 1821  
 <211> 341  
 <212> PRT  
 <213> Unknown (H38g739 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(341)  
 <223> Xaa = Any Amino Acid

```

<400> 1821
Met Met Glu Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile Leu Val
 1              5              10              15
Gly Phe Ser Asn Trp Pro Tyr Leu Glu Val Val Leu Phe Val Val Ile
      20              25              30

```

Leu Ile Phe Cys Leu Met Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile  
 35 40 45  
 Leu Thr Tyr Leu Asp Ser His Leu His Thr Pro Leu Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro  
 65 70 75 80  
 Gln Leu Leu Val Ser Leu Trp Gly Val Glu Lys Thr Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Met Val Gln Leu Tyr Phe Phe Leu Thr Leu Gly Thr Thr Glu  
 100 105 110  
 Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys  
 115 120 125  
 Arg Pro Leu His Tyr Thr Val Leu Met His Ser Arg Phe Cys His Leu  
 130 135 140  
 Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Pro Ala Leu His  
 145 150 155 160  
 Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln Ile Asp  
 165 170 175  
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Xaa Leu Ser Phe Val Asn  
 180 185 190  
 Thr Arg Glu Asn Lys Leu Thr Leu Met Ile Thr Ser Ser Ile Phe Val  
 195 200 205  
 Leu Leu Leu Leu Thr Leu Ile Phe Thr Ser Tyr Gly Ala Ile Ala Gln  
 210 215 220  
 Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val Phe Gly  
 225 230 235 240  
 Thr Cys Gly Ala His His Met Val Val Ser Leu Phe Phe Ile Pro Ala  
 245 250 255  
 Met Cys Met Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp Gln Gly  
 260 265 270  
 Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Gly Val Val Lys Arg  
 290 295 300  
 Leu Arg Gly Trp Glu Xaa Ala Cys Val Cys Val Ile Leu Thr Ile Xaa  
 305 310 315 320  
 Trp Ser Leu Ser Ser Gln Xaa Phe Ile His Leu Phe Ile Tyr Gln Pro  
 325 330 335  
 Phe Phe Tyr Ser Leu  
 340

&lt;210&gt; 1822

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g740 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(219)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1822

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Asp Ser Ile Leu  
 35 40 45  
 Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys Cys His Pro Leu

```

      50              55              60
Tyr His Ser Ala Ile Met Asn Pro Cys Leu Cys Gly Phe Leu Leu Leu
65              70              75              80
Leu Ser Ile Phe Phe Ser Leu Ser Leu Leu Asp Ala Gln Leu Tyr Asn
      85              90
Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn
      100              105              110
Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr
      115              120              125
Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala Ile Phe Gly Phe
      130              135              140
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Ser Ser
145              150              155              160
Ile Leu Arg Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Leu Ser Thr
      165              170              175
Cys Gly Ser His Val Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val
      180              185              190
Gly Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro Arg Lys Gly Ala
      195              200              205
Val Ala Ser Val Met Tyr Ala Val Val Thr Pro
      210              215

```

&lt;210&gt; 1823

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g741 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1823

```

Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu Leu Gly
1              5              10              15
Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Val Ile Ile Phe
      20              25              30
Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val Leu Val
      35              40              45
Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser
50              55              60
Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val Pro Gln
65              70              75              80
Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ile Gly
      85              90              95
Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Tyr
      100              105              110
Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val Cys His
      115              120              125
Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu Gln Leu
130              135              140
Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile Gln Ser
145              150              155              160
Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val Asp Asp
      165              170              175
Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr Asp Thr
      180              185              190
Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu Leu Val
195              200              205

```



```

Met Pro Leu Ile Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala Lys Ala
  210                215                220
Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe Gly Thr
  225                230                235                240
Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr Val Thr
                245                250                255
Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp Gly Lys
  260                265                270
Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu
  275                280                285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile Arg Leu
  290                295                300
Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn Xaa Gln Gly Xaa His Met
  305                310                315                320
Phe Thr Phe Ala

```

&lt;210&gt; 1824

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g742 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(218)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1824

```

Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Met Val
  1                5                10                15
Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr
  20                25                30
Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp Asp Met Leu Leu
  35                40                45
Thr Val Met Ala Tyr Asn Xaa Phe Val Ala Ile Cys His Pro Leu His
  50                55                60
Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu Val Leu Val
  65                70                75                80
Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val
  85                90                95
Leu Gln Gln Leu Thr Phe Phe Lys Asn Val Glu Ile Ser Xaa Phe Phe
  100               105               110
Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Ile
  115               120               125
Ile Asn Asn Ile Leu Cys Ile Leu Asp Ile Pro Ile Phe Gly Phe Leu
  130               135               140
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile
  145               150               155               160
Pro Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
  165               170               175
Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu Val
  180               185               190
Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser Met Val
  195               200               205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
  210               215

```

&lt;210&gt; 1825

&lt;211&gt; 124

<212> PRT  
 <213> Unknown (H38g743 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(124)  
 <223> Xaa = Any Amino Acid

<400> 1825  
 Phe Leu Leu Xaa Ala Asn Tyr Ser Ala Glu Glu Arg Phe Leu Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val  
 20 25 30  
 Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ser Ala Leu Val Leu  
 35 40 45  
 Leu Ala Glu Lys Asp Pro Arg Leu Gln Thr Pro Arg Cys Met Asn Tyr  
 50 55 60  
 Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe Thr Thr Ser Val  
 65 70 75 80  
 Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu Leu Xaa Pro  
 85 90 95  
 Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala Leu Gly Ser  
 100 105 110  
 Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Glu  
 115 120

<210> 1826  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g744 protein)

<220>  
 <223> Synthetic construct

<400> 1826  
 Ile Leu Glu Ile Ser Phe Thr Thr Val Ser Ile Pro Lys Phe Leu Gly  
 1 5 10 15  
 Asn Ile Ile Ser Gly Asp Lys Thr Ile Ser Phe Asn Asn Cys Ile Val  
 20 25 30  
 Gln Leu Phe Phe Phe Ile Leu Leu Gly Val Thr Glu Phe Tyr Leu Leu  
 35 40 45  
 Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His  
 50 55 60  
 Tyr Leu Ser Ile Met Asn Arg Arg Val Cys Thr Leu Leu Val Phe Thr  
 65 70 75 80  
 Ser Trp Leu Val Ser Phe Leu Ile Ile Phe Pro Ala Leu Met Leu Leu  
 85 90 95  
 Leu Lys Leu Asp Tyr Cys Arg Ser Asn Ile Ile Asp His Phe Thr Cys  
 100 105 110  
 Asp Tyr Phe Pro Leu Leu Gln Leu Ala Cys Ser Asp Thr Lys Phe Leu  
 115 120 125  
 Glu Val Met Gly Phe Ser Cys Ala Ala Phe Thr Leu Met Phe Thr Leu  
 130 135 140  
 Ala Leu Ile Phe Leu Ser Tyr Ile Tyr Ile Ile Arg Thr Ile Leu Arg  
 145 150 155 160  
 Ile Pro Ser Thr Ser Gln Arg Thr Lys Ala Phe Ser Thr Cys Ser Ser  
 165 170 175  
 His Met Val Val Ile Ser Ile Ser Tyr Gly Ser Cys Ile Phe Met Tyr  
 180 185 190

Ile Lys Pro Ser Ala Lys Asp Arg Val Ser Leu Ser Lys Gly Val Ala  
 195 200 205  
 Ile Leu Asn Thr Ser Val Ala Pro  
 210 215

<210> 1827  
 <211> 219  
 <212> PRT  
 <213> Unknown (H38g745 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(219)  
 <223> Xaa = Any Amino Acid

<400> 1827  
 Phe Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu  
 35 40 45  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu  
 50 55 60  
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu  
 65 70 75 80  
 Leu Ser Phe Phe Phe Ser Leu Ser Leu Leu Asp Ser Gln Leu His Asn  
 85 90 95  
 Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn  
 100 105 110  
 Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr  
 115 120 125  
 Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe  
 130 135 140  
 Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser  
 145 150 155 160  
 Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala Phe Ser Thr  
 165 170 175  
 Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val  
 180 185 190  
 Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala  
 195 200 205  
 Val Ala Ser Val Met Tyr Met Val Val Thr Pro  
 210 215

<210> 1828  
 <211> 268  
 <212> PRT  
 <213> Unknown (H38g746 protein)

<220>  
 <223> Synthetic construct

<400> 1828  
 Met Met Ala Leu Ile Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr  
 1 5 10 15  
 Phe Phe Leu Asn Val Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val  
 20 25 30  
 Val Thr Pro Lys Leu Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile

35 40 45  
 Ser Phe Glu Gly Cys Val Val Gln Leu Ala Phe Phe Val Val His Val  
 50 55 60  
 Thr Ala Glu Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu  
 65 70 75 80  
 Ala Ile Cys Gln Pro Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr  
 85 90 95  
 Cys Leu Gln Leu Val Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser  
 100 105 110  
 Ala Ile Gln Thr Gly Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn  
 115 120 125  
 Gln Leu Thr His Tyr Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala  
 130 135 140  
 Cys Ala Asn Thr Ala Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala  
 145 150 155 160  
 Leu Val Thr Leu Leu Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu  
 165 170 175  
 Val Leu Val Ala Ile Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys  
 180 185 190  
 Asp Leu Ser Thr Cys Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr  
 195 200 205  
 Gly Thr Val Val Phe Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn  
 210 215 220  
 Thr Asn Gly Gln Val Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met  
 225 230 235 240  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala  
 245 250 255  
 Leu Gln Arg Lys Leu Gln Val Asn Ile Phe Pro Gly  
 260 265

&lt;210&gt; 1829

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g747 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1829

Met Asp Leu Gly Asn Gln Thr Arg Val Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Phe Ser Gln Asp Leu Glu Asp Gln Gln Leu Leu Phe Ala Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ser Asp Ser His Leu His Thr Pro Arg Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Ala Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Val Gln Ser Asn Ala Ile Ser Tyr Ala Asp  
 85 90 95  
 Cys Ile Ala Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr  
 100 105 110  
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Tyr Tyr Cys Val Thr Arg Asn Pro Cys Leu Cys Gly Leu Leu  
 130 135 140

Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser  
 145 150 155 160  
 Leu Leu Val Leu Arg Val Ser Phe Cys Thr Ser Xaa Val Ile Gln His  
 165 170 175  
 Phe Tyr Cys Glu Leu Ala Gln Val Leu Arg Leu Thr Cys Ser Asp Thr  
 180 185 190  
 His Val Asn Tyr Ile Leu Leu Tyr Val Val Ala Gly Leu Leu Asp Phe  
 195 200 205  
 Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Tyr  
 210 215 220  
 Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Phe Val Val Ser Leu Phe Tyr Gly Thr Gly Leu  
 245 250 255  
 Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser Trp Trp Gly Met  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Cys Leu Arg Asn Arg Asp Ile Lys Arg Thr Leu Glu Thr Leu  
 290 295 300  
 Leu Gly Arg Met Leu Tyr Ala Gln Xaa Arg Gly His  
 305 310 315

<210> 1830

<211> 309

<212> PRT

<213> Unknown (H38g748 protein)

<220>

<223> Synthetic construct

<400> 1830

Met Glu Asn Cys Thr Glu Val Thr Lys Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Ser Val Pro Glu Leu Gln Ile Pro Leu Phe Ile Leu Phe Thr Phe Ile  
 20 25 30  
 Tyr Leu Leu Thr Leu Cys Gly Asn Leu Gly Met Met Leu Leu Ile Leu  
 35 40 45  
 Met Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met  
 65 70 75 80  
 Ala Gly Phe Leu Arg Gly Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala  
 85 90 95  
 Val Gln Met Phe Phe Phe Val Ala Leu Ala Thr Val Glu Asn Tyr Leu  
 100 105 110  
 Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Thr Thr Met Thr Ala Ser Val Gly Ala Cys Leu Ala Leu  
 130 135 140  
 Gly Ser Tyr Val Cys Gly Phe Leu Asn Ala Ser Phe His Ile Gly Gly  
 145 150 155 160  
 Ile Phe Ser Leu Ser Phe Cys Lys Ser Asn Leu Val His His Phe Phe  
 165 170 175  
 Cys Asp Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Lys His Thr  
 180 185 190  
 Ser Glu Val Ile Leu Val Phe Thr Ser Ser Phe Asn Ile Phe Phe Val  
 195 200 205  
 Leu Leu Val Ile Phe Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu  
 210 215 220  
 Lys Met His Ser Ala Lys Gly His Gln Lys Ala Leu Ser Thr Cys Ala

225                      230                      235                      240  
 Ser His Phe Thr Ala Val Ser Val Phe Tyr Gly Thr Val Ile Phe Ile  
                                  245                      250                      255  
 Tyr Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala  
                                  260                      265                      270  
 Ser Val Phe Tyr Ala Met Ile Ile Pro Met Leu Asn Pro Val Val Tyr  
                                  275                      280                      285  
 Ser Leu Arg Asn Arg Glu Val Gln Asn Ala Phe Lys Lys Val Leu Arg  
                                  290                      295                      300  
 Arg Gln Lys Phe Leu  
 305

<210> 1831

<211> 313

<212> PRT

<213> Unknown (H38g749 protein)

<220>

<223> Synthetic construct

<400> 1831

Met His Thr Met Val Glu Asn His Thr Gln Val Thr Trp Phe Arg Leu  
 1                      5                      10                      15  
 Leu Gly Leu Thr Glu Gln Glu Glu Leu Arg Gly Ile Leu Phe Val Leu  
                                  20                      25                      30  
 Phe Leu Leu Met His Ser Val Thr Val Met Gly Asn Leu Gly Met Ile  
                                  35                      40                      45  
 Thr Leu Ile His Ala Asp Pro Gln Leu His Thr Pro Met Tyr Phe Phe  
                                  50                      55                      60  
 Leu Ser Val Leu Ser Phe Ile Asp Ser Ser Phe Ser Thr Val Asp Thr  
 65                      70                      75                      80  
 Pro Arg Leu Leu Glu Ser Phe Leu Ile Ser Ser Gln Ser Ile Ser Phe  
                                  85                      90                      95  
 Ala Gly Cys Met Val Gln Met Ala Leu Met Ile Leu His Gly Thr Ala  
                                  100                      105                      110  
 Glu Cys Leu Leu Leu Ala Ile Met Ala Tyr Asp Arg Phe Thr Ala Ile  
                                  115                      120                      125  
 Cys His Pro Leu Leu Tyr His Thr Ile Ile Ser Gln Cys Leu Cys Ala  
                                  130                      135                      140  
 Leu Leu Val Val Thr Cys Tyr Thr Val Ser Val Ala Asn Ser Ala Leu  
 145                      150                      155                      160  
 Leu Thr Gly Cys Ile Phe Lys Leu Pro Tyr Cys Gly Pro Asn Val Ile  
                                  165                      170                      175  
 Asn His Tyr Phe Cys Asp Ile Pro Pro Val Leu Gln Leu Ala Gly Ala  
                                  180                      185                      190  
 Asp Thr Tyr Glu Val Glu Thr Ile Ile Phe Ser Leu Cys Ala Leu Leu  
                                  195                      200                      205  
 Ile Leu Phe Thr Ile Thr Ile Ile Pro Val Ser Tyr Ala Tyr Ile Leu  
                                  210                      215                      220  
 Val Thr Ile Cys Arg Met Arg Ser Leu Gln Ala Gln Ser Lys Ala Leu  
 225                      230                      235                      240  
 Ser Thr Cys Ala Ser His Leu Thr Ile Ile Cys Leu Phe Tyr Ser Thr  
                                  245                      250                      255  
 Ile Thr Phe Met Tyr Ala Gln Pro Ser Ser His Asn Ser Met Glu His  
                                  260                      265                      270  
 Asn Lys Val Met Ser Val Phe Tyr Thr Val Val Ile Arg Arg Leu Asn  
                                  275                      280                      285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Lys  
                                  290                      295                      300  
 Arg Arg Cys Leu Cys Lys Leu Ser Ser  
 305                      310

<210> 1832  
 <211> 314  
 <212> PRT  
 <213> Unknown (H38g750 protein)

<220>  
 <223> Synthetic construct

<400> 1832  
 Met Glu Asn Lys Thr Glu Val Thr Gln Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Asn Asp Ser Glu Leu Gln Val Pro Leu Phe Ile Thr Phe Pro Phe Ile  
 20 25 30  
 Tyr Ile Ile Thr Leu Val Gly Asn Leu Gly Ile Ile Val Leu Ile Phe  
 35 40 45  
 Trp Asp Ser Cys Leu His Asn Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Ile Val Met  
 65 70 75 80  
 Ala Gly Phe Leu Ile Glu Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala  
 85 90 95  
 Ala Gln Met Tyr Ile Phe Val Ala Phe Ala Thr Val Glu Asn Tyr Leu  
 100 105 110  
 Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Thr Thr Met Thr Thr Thr Val Cys Ala Arg Leu Ala Ile  
 130 135 140  
 Gly Ser Tyr Leu Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asp  
 145 150 155 160  
 Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Glu Val His His Phe Phe  
 165 170 175  
 Cys Asp Ile Pro Ala Val Met Val Leu Ser Cys Ser Asp Arg His Ile  
 180 185 190  
 Ser Glu Leu Val Leu Ile Tyr Val Val Ser Phe Asn Ile Phe Ile Ala  
 195 200 205  
 Leu Leu Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Ile Thr Ile Leu  
 210 215 220  
 Lys Met His Ser Ala Ser Val Tyr Gln Lys Pro Leu Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Phe Ile Ala Val Gly Ile Phe Tyr Gly Thr Ile Ile Phe Met  
 245 250 255  
 Tyr Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala  
 260 265 270  
 Pro Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Glu Val Lys Ser Ala Phe Lys Lys Val Val Glu  
 290 295 300  
 Lys Ala Lys Leu Ser Val Gly Trp Ser Val  
 305 310

<210> 1833  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g751 protein)

<220>  
 <223> Synthetic construct

<400> 1833  
 Met Asn Asn Ser Asp Thr Arg Ile Ala Gly Cys Phe Leu Thr Gly Ile

```

1           5           10           15
Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile
20           25           30
Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile
35           40           45
Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met
50           55           60
Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala
65           70           75           80
Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys
85           90           95
Leu Thr Gln Lys Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val
100          105          110
Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
115          120          125
Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr
130          135          140
Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu
145          150          155          160
Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe
165          170          175
Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile
180          185          190
Asn Val Trp Tyr Gly Leu Ala Ala Ala Leu Leu Ser Thr Gly Leu Asp
195          200          205
Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe
210          215          220
Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly
225          230          235          240
Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser
245          250          255
Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His
260          265          270
Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro
275          280          285
Val Ile Tyr Gly Val Arg Thr Lys Pro Ile Leu Glu Gly Ala Lys Gln
290          295          300
Met Phe Ser Asn Leu Ala Lys Gly
305          310

```

&lt;210&gt; 1834

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g752 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1834

```

Ser Ile Leu Phe Leu Tyr Phe Ser Leu Leu Gln Ala Ser Ser Asp Phe
1           5           10           15
Leu Ile Thr Leu Met Lys Asn Cys Thr Glu Val Thr Glu Phe Ile Leu
20           25           30
Leu Gly Leu Thr Asn Ala Pro Glu Leu Gln Val Pro Leu Leu Ile Met
35           40           45
Phe Thr Leu Ile Tyr Leu Val Asn Val Val Gly Asn Leu Gly Met Ile
50           55           60
Val Leu Ile Val Trp Asp Ile His Leu His Thr Pro Met Tyr Phe Phe
65           70           75           80
Leu Ser His Leu Ser Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr
85           90           95

```



```

Pro Thr Val Ile Ala Gly Leu Val Ile Gly Asp Lys Val Ile Ser Tyr
      100      105      110
Asn Ala Cys Ala Ala Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val
      115      120      125
Glu Asn Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val
      130      135      140
Cys Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala
      145      150      155      160
Cys Leu Ala Ile Ile Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile
      165      170      175
His Ile Gly Glu Thr Phe Ser Leu Ser Phe Cys Met Ser Asn Glu Val
      180      185      190
His Cys Phe Phe Cys Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys
      195      200      205
Asp Arg His Val Asn Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn
      210      215      220
Ile Phe Ser Ala Ile Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe
      225      230      235      240
Ile Thr Ile Leu Lys Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu
      245      250      255
Ser Thr Cys Ala Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr
      260      265      270
Ile Ile Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr
      275      280      285
Asp Lys Leu Ala Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Asn
      290      295      300
Pro Leu Val Tyr Ser Leu Arg Asn Asn Glu Val Lys Ser Ala Phe Lys
      305      310      315      320
Lys Val Ile Glu Lys Ala Lys Leu Ser Leu Leu Leu
      325      330

```

&lt;210&gt; 1835

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g753 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1835

```

Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
  1      5      10      15
Leu Thr Gly Ile Pro Gly Leu Glu Ala His Phe Trp Ile Ala Ile
      20      25      30
Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu
      35      40      45
Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
      50      55      60
Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
      65      70      75      80
Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
      85      90      95
Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
      100      105      110
Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
      115      120      125
Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
      130      135      140
Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
      145      150      155      160
Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val

```

```

      165      170      175
Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
      180      185      190
Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu
      195      200      205
Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile
      210      215      220
Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala
      225      230      235      240
Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile
      245      250      255
Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val
      260      265      270
Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro
      275      280      285
Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
      290      295      300
Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile
      305      310      315

```

&lt;210&gt; 1836

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g754 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1836

```

His Ile Glu Pro Gly Asn Asp Thr Gln Ile Ser Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Asp Lys Pro Glu Leu Gln Pro Phe Leu Phe Gly Leu Phe
      20      25      30
Phe Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Thr Ile Ser Asp Ser His Leu His Thr Pro Val Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Phe Ala Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro
      65      70      75      80
Lys Met Leu Val Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala
      85      90      95
Gly Cys Ile Thr Gln Met Cys Phe Phe Val Leu Leu Glu Ala Leu Asp
      100      105      110
Ser Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Met Val Ile Met Ser Pro Trp Phe Cys Gly Leu
      130      135      140
Leu Val Leu Ala Ser Trp Ile Ile Met Ser Pro Trp Leu Cys Gly Leu
      145      150      155      160
Leu Val Leu Ala Ser Trp Ile Ile Ser Asp Leu Asp Ser Ser Leu His
      165      170      175
Ser Leu Met Val Leu Ser Leu Pro Phe Cys Thr Asp Phe Gln Ile Pro
      180      185      190
His Phe Val Tyr Glu Leu Asn Gln Val Ile Arg Leu Ala Gly Ser Asp
      195      200      205
Thr Phe Leu Asn Asp Met Ala Met Tyr Phe Ala Val Gly Pro Leu Gly
      210      215      220
Gly Val Pro Leu Ala Gly Ile Leu Tyr Leu Tyr Cys Lys Ile Val Phe
      225      230      235      240
Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser
      245      250      255

```

Thr Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Arg Ser  
                   260                  265                  270  
 Leu Gly Val Tyr Phe Ser Ser Ala Pro Thr Gln Asn Ser His Ser Gly  
                   275                  280                  285  
 Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
                   290                  295                  300  
 Phe Ile Cys Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Asn Gln  
 305                  310                  315                  320  
 Phe Ile Arg Val Val Pro Phe Phe Arg Lys  
                   325                  330

&lt;210&gt; 1837

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g755 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1837

Thr Thr Ser Ile Asp Asp Asn Thr Glu Val Asn Glu Phe Ile Xaa Leu  
 1                  5                  10                  15  
 Gly Leu Thr Lys Ala Pro Glu Leu Gln Val His Leu Phe Val Leu Phe  
                   20                  25                  30  
 Asn Phe Ile Tyr Leu Phe Thr Leu Ser Gly Asn Leu Gly Met Met Leu  
                   35                  40                  45  
 Leu Ile Leu Leu Asp Ser Arg Leu His Thr Ser Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Glu Thr Val Thr Pro  
 65                  70                  75                  80  
 Lys Met Met Ala Gly Leu Leu Ile Ala His Lys Val Ile Ser Tyr Asn  
                   85                  90                  95  
 Val Cys Ala Ala Gln Met Phe Phe Phe Ala Val Phe Ala Thr Val Glu  
                   100                  105                  110  
 Ser Tyr Phe Leu Thr Ser Val Ala Tyr Asp Cys Tyr Arg Val Met Cys  
                   115                  120                  125  
 Lys Pro Leu His Tyr Thr Thr Met Thr Thr Asn Val Cys Ala Ser  
                   130                  135                  140  
 Leu Ala Ile Ala Cys Tyr Val Leu Gly Leu Leu Thr Ala Ala Val Asp  
 145                  150                  155                  160  
 Ile Gly Asp Ile Cys Met Ser Asn Glu Ile His His Phe Phe Cys Asp  
                   165                  170                  175  
 Ile Leu Ala Val Met Thr Leu Thr Cys Ser Asn Lys His Ile Asn Glu  
                   180                  185                  190  
 Leu Ile Leu Val Leu Leu Gln Ala Ile Phe Phe Thr Leu Leu Val Ile  
                   195                  200                  205  
 Leu Ile Ser Cys Leu Phe Val Phe Val Phe Val Thr Ile Leu Lys Met  
                   210                  215                  220  
 His Leu Phe Lys Ser Tyr Lys Lys Val Leu Ser Thr Tyr Gly Ser His  
 225                  230                  235                  240  
 Leu Thr Ala Val Pro Leu Phe Tyr Glu Thr Val Leu Ile Thr Tyr Val  
                   245                  250                  255  
 Gln Pro Ser Ser Ser His Phe Met Asn Thr Glu Lys Ile Val Ser Val  
                   260                  265                  270  
 Phe His Ile Met Val Ile Pro Met Leu Ile Pro Val Val Tyr Ser Leu  
                   275                  280                  285  
 Arg Asn Asn Glu Val Lys Ser Ala Phe Lys Thr Val Val Glu Glu Thr

290 295 300  
 Lys Tyr Phe Leu Gly Leu Val Phe  
 305 310

<210> 1838  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g756 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(315)  
 <223> Xaa = Any Amino Acid

<400> 1838  
 Met Gly Gly Phe Gly Thr Asn Ile Ser Ser Thr Thr Ser Phe Thr Leu  
 1 5 10 15  
 Thr Gly Phe Pro Glu Met Lys Gly Leu Glu His Trp Leu Ala Ala Leu  
 20 25 30  
 Leu Leu Leu Cys Ala Ile Ser Phe Leu Gly Asn Ile Leu Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Glu Glu Gln Ser Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Leu Phe Ser Val Asn Asp Leu Gly Val Ser Phe Ser Thr Leu  
 65 70 75 80  
 Pro Thr Val Leu Ala Ala Val Cys Phe His Ala Pro Glu Thr Thr Phe  
 85 90 95  
 Asp Ala Cys Leu Ala Gln Thr Phe Phe Ile His Phe Ser Ser Trp Thr  
 100 105 110  
 Glu Phe Gly Ile Leu Leu Ala Met Ser Phe Asp His Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg Tyr Ala Thr Val Leu Thr Asp Val Arg Val Ala  
 130 135 140  
 His Asn Gly Ile Ser Ile Val Ile Arg Ser Phe Cys Met Val Phe Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Lys Arg Leu Pro Phe Cys Lys Ala Ser Val Val  
 165 170 175  
 Leu Ala His Ser Tyr Cys Leu His Ala Asp Leu Ile Arg Leu Pro Cys  
 180 185 190  
 Gly Asp Thr Thr Ile Asn Ser Met Tyr Gly Leu Phe Ile Val Ile Ser  
 195 200 205  
 Ala Phe Gly Val Asp Ser Leu Leu Ile Leu Leu Ser Tyr Val Leu Ile  
 210 215 220  
 Leu His Ser Val Leu Ala Ile Ala Ser Arg Gly Glu Arg Leu Lys Thr  
 225 230 235 240  
 Leu Asn Thr Cys Val Ser His Ile Tyr Ala Val Leu Ile Phe Tyr Val  
 245 250 255  
 Pro Met Val Ser Val Ser Met Val His Arg Phe Gly Arg His Ala Pro  
 260 265 270  
 Glu Tyr Val His Lys Phe Met Ser Ser Leu Tyr Leu Pro Met Leu Tyr  
 275 280 285  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile Arg Arg Arg Leu His  
 290 295 300  
 Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Lys  
 305 310 315

<210> 1839  
 <211> 329  
 <212> PRT

<213> Unknown (H38g757 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1839

```

Met Glu Pro Glu Asn Asp Thr Arg Ile Ser Glu Phe Arg Leu Leu Gly
 1           5           10           15
Phe Ser Glu Glu Pro Arg Leu Gln Arg Phe Arg Phe Leu Phe Gly Val
           20           25           30
Phe Leu Ser Met Tyr Leu Ile Ile Val Phe Gly Asn Leu Leu Ile Ile
 35           40           45
Leu Val Ile Ile Leu Cys Ser His Leu His Thr Ser Met Tyr Phe Phe
 50           55           60
Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Arg Val
 65           70           75           80
Pro Lys Met Leu Val Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Ser
           85           90           95
Ala Gly Cys Ile Thr Gln Met Tyr Phe Phe Ile His Phe Val Gly Leu
           100           105           110
Asp Ser Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile
           115           120           125
Cys His Pro Leu Tyr Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly
           130           135           140
Leu Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu His Ser Leu Leu
 145           150           155           160
His Ser Leu Met Val Leu Gln Leu Ser Leu Cys Arg Glu Leu Glu Ile
           165           170           175
Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser
           180           185           190
Asp Thr Phe Leu Asn Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu
           195           200           205
Gly Gly Gly Ser Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Thr Val
           210           215           220
Ser Ser Ile Cys Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe
 225           230           235           240
Ser Thr Cys Pro Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr
           245           250           255
Ser Leu Gly Val Tyr Leu Ser Ser Ala Ala Ser His Asn Ser His Ser
           260           265           270
Gly Ala Ile Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
           275           280           285
Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys
           290           295           300
Asn Ser Leu Gly Gly Lys Leu Glu Lys Gly Gln Leu Ser Leu Gly Leu
 305           310           315           320
Lys Leu Tyr Pro Xaa Leu Gln Gly Ser
           325

```

<210> 1840

<211> 320

<212> PRT

<213> Unknown (H38g758 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1840

```

Met Glu Arg Gly Asn Gln Thr Glu Val Gly Asn Phe Leu Leu Leu Gly
 1           5           10           15
Phe Ala Glu Asp Ser Asp Met Gln Leu Leu Leu His Gly Leu Phe Leu
 20           25           30
Ser Met Tyr Leu Val Thr Ile Ile Gly Asn Leu Leu Ile Ile Leu Thr
 35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
 65           70           75           80
Met Leu Val Asn Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly
 85           90           95
Cys Leu Thr Gln Ile Phe Phe Phe Ile Ala Phe Gly Cys Leu Asp Asn
100           105           110
Leu Leu Leu Thr Met Thr Ala Tyr Asp Arg Phe Val Ala Ile Cys Tyr
115           120           125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
130           135           140
Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr
145           150           155           160
Leu Thr Ile Leu Arg Leu Ser Ser Cys Thr Asn Met Glu Ile Pro His
165           170           175
Phe Phe Cys Asp Pro Ser Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
180           185           190
Phe Ile Asn Asn Ile Val Met Cys Phe Val Thr Ile Val Leu Gly Val
195           200           205
Phe Pro Leu Cys Gly Ile Leu Phe Ser Tyr Ser Gln Ile Phe Ser Ser
210           215           220
Val Leu Arg Val Ser Ser Ala Arg Gly Gln His Lys Ala Phe Thr Thr
225           230           235           240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
245           250           255
Gly Val Tyr Leu Ser Ser Ala Val Thr Pro Pro Ser Arg Thr Ser Leu
260           265           270
Ala Ala Ser Val Met His Thr Met Val Thr Pro Met Leu Asn Pro Phe
275           280           285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ser Leu Gly Arg Leu
290           295           300
Leu Leu Arg Ala Thr Ser Leu Lys Glu Gly Thr Ile Ala Lys Leu Ser
305           310           315           320

```

&lt;210&gt; 1841

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g759 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1841

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
 1           5           10           15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
 20           25           30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
 35           40           45

```

Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys  
 50 55 60  
 Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu  
 100 105 110  
 Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe  
 130 135 140  
 Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu  
 145 150 155 160  
 Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile  
 165 170 175  
 Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys  
 180 185 190  
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe  
 195 200 205  
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val  
 210 215 220  
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe  
 225 230 235 240  
 Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr  
 245 250 255  
 Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys  
 260 265 270  
 Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn  
 275 280 285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp  
 290 295 300  
 Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His  
 305 310 315 320  
 Leu Phe His Ser Phe Cys Arg Met  
 325

&lt;210&gt; 1842

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g760 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1842

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met  
 1 5 10 15  
 Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu  
 20 25 30  
 Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu  
 35 40 45  
 Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu  
 50 55 60  
 Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro  
 65 70 75 80  
 Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile

85 90 95  
 Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Ile Glu  
 100 105 110  
 Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys  
 115 120 125  
 Lys Pro Pro Arg Tyr Thr Ile Ile Asp His Lys Val Cys Leu His  
 130 135 140  
 Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln  
 145 150 155 160  
 Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile  
 165 170 175  
 Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr  
 180 185 190  
 Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly  
 195 200 205  
 Glu Leu  
 210

&lt;210&gt; 1843

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g761 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1843

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly  
 1 5 10 15  
 Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu  
 20 25 30  
 Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
 50 55 60  
 Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His  
 115 120 125  
 Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu  
 130 135 140  
 Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr  
 145 150 155 160  
 Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His  
 165 170 175  
 Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr  
 180 185 190  
 His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr  
 195 200 205  
 Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr  
 210 215 220  
 Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe  
 245 250 255  
 Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys  
 260 265 270



Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu  
 290 295 300  
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro  
 305 310 315

<210> 1844  
 <211> 316  
 <212> PRT  
 <213> Unknown (H38g762 protein)

<220>  
 <223> Synthetic construct

<400> 1844  
 Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Val Asp Gly Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys Leu  
 20 25 30  
 Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala Leu  
 35 40 45  
 Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu Gly  
 50 55 60  
 His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro Arg  
 65 70 75 80  
 Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln Ala  
 85 90 95  
 Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu Ser  
 100 105 110  
 Tyr Leu Leu Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys Arg  
 115 120 125  
 Pro Leu Arg Tyr Gly Ala Leu Val Thr Pro Trp Ala Cys Ala Ser Leu  
 130 135 140  
 Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His Thr  
 145 150 155 160  
 Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg Pro  
 165 170 175  
 Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp Thr  
 180 185 190  
 Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val Leu  
 195 200 205  
 Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val Ala  
 210 215 220  
 Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Tyr Cys Gly Ala  
 225 230 235 240  
 His Leu Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser Val Leu Ser  
 245 250 255  
 Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr Asp Arg Leu  
 260 265 270  
 Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn Pro Phe Ile  
 275 280 285  
 Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Arg Gly Leu  
 290 295 300  
 Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala  
 305 310 315

<210> 1845  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g763 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1845

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1              5              10              15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
      20              25              30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
      35              40              45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
      50              55              60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
65              70              75              80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
      85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100             105             110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
      115             120             125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
      130             135             140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
145             150             155             160
Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser
      165             170             175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
      180             185             190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
      195             200             205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
      210             215             220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225             230             235             240
Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe
      245             250             255
Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
      260             265             270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
      275             280             285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
      290             295             300
Leu Val Ile Tyr Lys Arg Ile Ser
305             310

```

&lt;210&gt; 1846

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g764 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1846

```

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1              5              10              15
Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
      20              25              30
Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
      35              40              45

```

```

Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50          55          60
Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Thr Ile Leu Lys
65          70          75          80
Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
          85          90          95
Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
          130          135          140
Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
145          150          155          160
Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His
          165          170          175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
          180          185          190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu Leu
          195          200          205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
210          215          220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
          245          250          255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
          260          265          270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
          275          280          285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
          290          295          300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
305          310          315

```

&lt;210&gt; 1847

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g765 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(105)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1847

```

Thr Leu Cys Ala Thr Ala Xaa Leu Asp His Phe Ile Cys Glu Leu Pro
 1          5          10          15
Ala Leu Leu Lys Leu Ala Arg Gly Gly Ile Gly Asp Thr Thr Glu Asn
          20          25          30
Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val
          35          40          45
Ile Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg
          50          55          60
Phe Ser Gly Gly Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu
65          70          75          80
Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln
          85          90          95
Pro Ala Gln Arg Asn Asn Gln Ala Arg

```

100

105

<210> 1848  
 <211> 104  
 <212> PRT  
 <213> Unknown (H38g766 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(104)  
 <223> Xaa = Any Amino Acid

<400> 1848  
 Ile His Ala Leu Ser Ala Ile Glu Ser Thr Ile Leu Leu Ala Met Ala  
 1 5 10 15  
 Phe Asn Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Ala Val  
 20 25 30  
 Leu Asn Asn Thr Val Thr Ala Gln Ile Gly Ile Val Ala Val Val Arg  
 35 40 45  
 Gly Ser Leu Phe Phe Phe Pro Leu Leu Ile Lys Arg Leu Ala  
 50 55 60  
 Phe Cys His Ser Asn Val Leu Ser His Ser Tyr Cys Val His Gln Asp  
 65 70 75 80  
 Val Met Lys Leu Ala Tyr Ala Asp Asn Leu Pro Asn Val Val Tyr Gly  
 85 90 95  
 Leu Asn Xaa Pro Phe Trp Leu Val  
 100

<210> 1849  
 <211> 320  
 <212> PRT  
 <213> Unknown (H38g767 protein)

<220>  
 <223> Synthetic construct

<400> 1849  
 Met Glu Thr Gly Asn Gln Thr His Ala Gln Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Phe Ser Ala Thr Ser Glu Ile Gln Phe Ile Leu Phe Gly Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Phe Thr Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Cys Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Leu Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly  
 85 90 95  
 Cys Leu Ser Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn  
 100 105 110  
 Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu  
 130 135 140  
 Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr  
 145 150 155 160  
 Leu Thr Val Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His  
 165 170 175

```

Phe Phe Cys Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
      180      185      190
Phe Ile Asn Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val
      195      200      205
Ile Ser Phe Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser
      210      215      220
Ile Leu Arg Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu
      260      265      270
Val Ala Ser Val Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Thr Asp Met Lys Arg Ala Leu Gly Arg Leu
      290      295      300
Leu Ser Arg Ala Thr Phe Phe Asn Gly Asp Ile Thr Ala Gly Leu Ser
      305      310      315      320

```

&lt;210&gt; 1850

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g768 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1850

```

Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
  1      5      10      15
Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
      20      25      30
Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
      35      40      45
Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met
      65      70      75      80
Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys
      85      90      95
Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met
      100      105      110
Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
      115      120      125
Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala
      130      135      140
Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile
      145      150      155      160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
      165      170      175
Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
      180      185      190
Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly
      195      200      205
Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile
      210      215      220
Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys

```

```

225          230          235          240
Ser Ser His Leu Cys Val Val Gly Leu Tyr Phe Gly Met Ala Met Val
          245          250          255
Val Tyr Leu Val Pro Asp Asn Ser Gln Arg Gln Lys Gln Gln Lys Ile
          260          265          270
Leu Thr Leu Phe Tyr Ser Leu Phe Asn Pro Leu Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu Tyr Arg Ala Leu
          290          295          300
Gln Lys Lys Arg Thr Met Xaa Met
305          310

```

&lt;210&gt; 1851

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g769 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1851

```

Met Glu Pro Gly Asn Asp Thr Gln Ile Ser Glu Phe Leu Leu Leu Gly
 1          5          10          15
Phe Ser Gln Glu Pro Gly Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu
          20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
          35          40          45
Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ala Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys
          65          70          75          80
Met Leu Met Asn Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ile Ala
          85          90          95
Cys Leu Met Gln Met Tyr Phe Phe Ile Leu Phe Ala Gly Phe Glu Asn
          100          105          110
Phe Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Met Val Ile Met Asn Pro His Leu Cys Gly Leu Leu
          130          135          140
Val Leu Ala Ser Trp Thr Met Ser Ala Leu Tyr Ser Leu Leu Gln Ile
          145          150          155          160
Leu Met Val Val Arg Leu Ser Phe Cys Thr Ala Leu Glu Ile Pro His
          165          170          175
Phe Phe Cys Glu Leu Asn Gln Val Ile Gln Leu Ala Cys Ser Asp Ser
          180          185          190
Phe Leu Asn His Met Val Ile Tyr Phe Thr Val Ala Leu Leu Gly Gly
          195          200          205
Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ile Ser Ser
          210          215          220
Ile His Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Leu
          245          250          255
Gly Val Tyr Leu Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala
          260          265          270
Thr Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Gly Ile His
          290          295          300
Leu Leu Trp Gly Thr Met Lys Gly Gln Phe Phe Lys Lys Cys Pro
          305          310          315

```

<210> 1852  
 <211> 74  
 <212> PRT  
 <213> Unknown (H38g770 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(74)  
 <223> Xaa = Any Amino Acid

<400> 1852  
 Gly Asp Thr Thr Glu Asn Gln Met Phe Ala Ala Arg Val Val Ile Leu  
 1 5 10 15  
 Leu Leu Pro Tyr Asp Val Ile Leu Ala Ser Xaa Gly Ala Val Ala Arg  
 20 25 30  
 Ala Val Cys Cys Met Arg Phe Ser Gly Gly Pro Arg Arg Ala Leu Gly  
 35 40 45  
 Thr Cys Gly Ser His Pro Thr Ala Val Trp Leu Phe Xaa Gly Ser Gly  
 50 55 60  
 Lys Xaa Thr Tyr Leu Gln Ala Ala Gln Leu  
 65 70

<210> 1853  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g771 protein)

<220>  
 <223> Synthetic construct

<400> 1853  
 Met Lys Ser Trp Asn Asn Thr Ile Ile Leu Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Val Gly Ile Cys Phe Val Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly  
 85 90 95  
 Cys Ile Thr Gln Met Cys Phe Phe Leu Phe Val Gly Leu Asp Asn  
 100 105 110  
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu  
 130 135 140  
 Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser  
 145 150 155 160  
 Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly  
 195 200 205  
 Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser

```

      210              215              220
Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu
      245              250              255
Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala
      260              265              270
Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe
      290              295              300
Phe Arg Gly Lys Gln
305

```

<210> 1854  
 <211> 82  
 <212> PRT  
 <213> Unknown (H38g772 protein)

<220>  
 <223> Synthetic construct

```

<400> 1854
Met Val Thr Glu Phe Leu Pro Leu Gly Phe Leu Leu Gly Pro Arg Ile
1              5              10              15
Gln Met Leu Leu Leu Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Pro
      20              25              30
Leu Gly Asn Gly Thr Ile Pro Gly Leu Ile Ser Leu Asp Ser Arg Leu
      35              40              45
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile
      50              55              60
Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
65              70              75              80
Pro Ala

```

<210> 1855  
 <211> 216  
 <212> PRT  
 <213> Unknown (H38g773 protein)

<220>  
 <223> Synthetic construct

```

<400> 1855
Leu Met Asp Leu Lys Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe
1              5              10              15
Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Val Thr
      20              25              30
Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys Phe Leu Leu
      35              40              45
Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
      50              55              60
Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met Ala Thr Phe
65              70              75              80
Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala Val Ala Thr
      85              90              95
Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
      100              105              110
Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
      115              120              125

```



Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val Phe Pro Val  
 130 135 140  
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His  
 145 150 155 160  
 Met Gly Ser Gly Gly Arg Cys Lys Ala Phe Thr Thr Cys Ser Ser  
 165 170 175  
 His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr  
 180 185 190  
 Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys Met Val Ser  
 195 200 205  
 Val Phe Tyr Thr Ile Leu Thr Pro  
 210 215

<210> 1856  
 <211> 305  
 <212> PRT  
 <213> Unknown (H38g774 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(305)  
 <223> Xaa = Any Amino Acid

<400> 1856  
 Met Lys Pro Gly Asn Asp Thr Arg Ile Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ala Glu Pro Glu Leu Gln Pro Phe Phe Phe Gly Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ala Asp Ile Ser Phe Val Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly  
 85 90 95  
 Cys Ile Thr Gln Met Cys Phe Phe Leu Leu Phe Ala Val Leu Asp Ser  
 100 105 110  
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Tyr Tyr Thr Ile Ile Met Asn Pro Gln Phe Tyr Ser Trp Ile  
 130 135 140  
 Leu Ser Val Leu Asn Ser Leu Leu Gln Ser Leu Met Val Leu Pro Leu  
 145 150 155 160  
 Pro Phe Tyr Thr Asp Ile Ala Ile Pro His Phe Phe Cys Glu Leu Asn  
 165 170 175  
 Gln Ile Ile Cys Ile Ala Cys Ser Asp Thr Phe Leu Asn Asp Ile Met  
 180 185 190  
 Ile Tyr Cys Ala Thr Val Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile  
 195 200 205  
 Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser  
 210 215 220  
 Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser  
 225 230 235 240  
 Val Val Ser Leu Phe Tyr Gly Thr Ser Leu Gly Met Tyr Leu Ser Ser  
 245 250 255  
 Ala Ala Thr His Asn Ser Pro Ser Ser Ala Thr Ala Ser Val Met Tyr  
 260 265 270  
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn

275                      280                      285  
 Lys Asp Leu Lys Asp Ala Leu Lys Arg Phe Phe Arg Arg Lys Gln Xaa  
 290                      295                      300  
 Lys  
 305

<210> 1857  
 <211> 120  
 <212> PRT  
 <213> Unknown (H38g775 protein)

<220>  
 <223> Synthetic construct

<400> 1857  
 Phe Ser Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn  
 1                      5                      10                      15  
 Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile  
 20                      25                      30  
 Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala  
 35                      40                      45  
 Val Thr Glu Cys Phe Leu Leu Val Val Lys Ser Asn Asp Leu Tyr Val  
 50                      55                      60  
 Ala Ile Cys His Pro Ser Arg Tyr Leu Ala Ile Met Thr Trp Arg Val  
 65                      70                      75                      80  
 Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser  
 85                      90                      95  
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln  
 100                      105                      110  
 Lys Ile Tyr His Phe Phe Cys Glu  
 115                      120

<210> 1858  
 <211> 214  
 <212> PRT  
 <213> Unknown (H38g776 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(214)  
 <223> Xaa = Any Amino Acid

<400> 1858  
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val  
 1                      5                      10                      15  
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr  
 20                      25                      30  
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu  
 35                      40                      45  
 Pro Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu  
 50                      55                      60  
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
 65                      70                      75                      80  
 Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn Leu Ile Ala Leu  
 85                      90                      95  
 Gln Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn Phe Leu Cys Asp  
 100                      105                      110  
 Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr Phe Thr Asn His  
 115                      120                      125

```

Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser
  130                135                140
Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser Ile Leu Arg Val
 145                150                155                160
Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Tyr Gly Ser His
                165                170                175
Leu Ser Asp Val Ser Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu
                180                185                190
Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val Ala Ser Val
                195                200                205
Met Tyr Ala Val Val Thr
                210

```

<210> 1859  
 <211> 166  
 <212> PRT  
 <213> Unknown (H38g777 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(166)  
 <223> Xaa = Any Amino Acid

```

<400> 1859
Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe Phe
  1                5                10                15
Leu Ser Pro Arg Ile His Met Leu Leu Phe Gly Leu Phe Tyr Leu Phe
                20                25                30
Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser
                35                40                45
Leu Asp Ser Ile Leu His Thr Pro Met Tyr Phe Phe Leu Xaa His Leu
                50                55                60
Ser Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu
                65                70                75                80
Val Asn Leu Leu His Ser Ala Lys Pro Ile Tyr Phe Ala Gly Cys Met
                85                90                95
Thr Tyr Thr Phe Leu Phe Leu Arg Phe Ala His Thr Glu Cys Leu Leu
                100                105                110
Leu Val Leu Met Ser Tyr Asp Trp Tyr Val Ala Ile Leu Thr Pro Leu
                115                120                125
Arg Tyr Ile Ile Ile Met Thr Trp Lys Val Phe Ile Ile Ser Ala Ile
                130                135                140
Thr Ser Trp Thr Cys Gly Ser Phe Leu Ser Met Val His Val Ser Leu
                145                150                155                160
Ile Leu Arg Leu Pro Phe
                165

```

<210> 1860  
 <211> 93  
 <212> PRT  
 <213> Unknown (H38g778 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(93)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 1860

Gln Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Leu Phe  
 1 5 10 15  
 Lys Leu Ala Leu Ala Tyr Arg Pro Xaa Cys Tyr Cys His Leu Cys Thr  
 20 25 30  
 His Pro Phe Tyr His Ile Asp His Val Xaa Glu Ala Ile Ile Phe Phe  
 35 40 45  
 Leu Val Ala Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val  
 50 55 60  
 Thr Thr Ser Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val His Leu  
 65 70 75 80  
 His Phe Phe Cys Asp Ile Pro Ser Phe Cys Ser Tyr Ser  
 85 90

&lt;210&gt; 1861

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g779 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1861

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln  
 1 5 10 15  
 Asn Met Gln Ser Gln Val Pro Thr Ile Ser Tyr Ala Asp Cys Leu Thr  
 20 25 30  
 Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu  
 35 40 45  
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
 50 55 60  
 Tyr Thr Ser Ile Met Ser Thr Lys Phe Cys Ala Leu Leu Val Leu Leu  
 65 70 75 80  
 Leu Trp Met Leu Thr Ile Ser His Ala Leu Leu His Thr Leu Leu Met  
 85 90 95  
 Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His Phe Phe Cys  
 100 105 110  
 Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Tyr Val Asn  
 115 120 125  
 Glu Leu Met Ile Phe Ile Met Gly Gly Ile Ile Ser Ile Ile Pro Phe  
 130 135 140  
 Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys  
 145 150 155 160  
 Val Pro Ser Ser Gln Asp Ile His Lys Val Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr  
 180 185 190  
 Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Asn Glu Ile Ser Met Ala  
 195 200 205  
 Met Met Tyr Thr Val Val Ala  
 210 215

&lt;210&gt; 1862

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g780 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(219)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1862

```

Ser Asn Leu Ser Phe Thr Asp Leu Xaa Phe Ser Ser Val Thr Met Pro
 1              5              10              15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
      20              25              30
Gly Cys Leu Thr Gln Met Tyr Phe Leu Leu Phe Phe Gly Asp Leu Glu
      35              40              45
Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      50              55              60
Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser
      65              70              75              80
Leu Val Leu Leu Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His
      85              90              95
Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro
      100             105             110
His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
      115             120             125
Ile His Ile Asn Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val
      130             135             140
Ile Leu Pro Phe Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser
      145             150             155             160
Ser Ile Leu Lys Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser
      165             170             175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
      180             185             190
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp
      195             200             205
Thr Val Met Ser Met Met Tyr Thr Val Val Thr
      210             215

```

&lt;210&gt; 1863

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g781 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1863

```

Met Glu Asn Asn Thr Glu Val Thr Glu Phe Ile Leu Val Gly Leu Thr
 1              5              10              15
Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Ile Val Phe Leu Phe Ile
      20              25              30
Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Glu Leu Ile Leu
      35              40              45
Leu Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
      50              55              60
Ser Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met
      65              70              75              80
Val Gly Phe Leu Thr Gly Asp Lys Phe Ile Leu Tyr Asn Ala Cys Ala
      85              90              95
Thr Gln Phe Phe Phe Val Ala Phe Ile Thr Ala Glu Ser Phe Leu
      100             105             110
Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Leu Cys Lys Pro Leu
      115             120             125
His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Cys Leu Ala Ile
      130             135             140
Gly Ser Tyr Ile Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asn

```

```

145          150          155          160
Thr Phe Arg Leu Ser Phe Cys Arg Ser Asn Val Val Glu His Phe Phe
          165          170          175
Cys Asp Ala Pro Pro Leu Leu Thr Leu Ser Cys Ser Asp Asn Tyr Ile
          180          185          190
Ser Glu Met Val Ile Phe Phe Val Val Gly Phe Asn Asp Leu Phe Ser
          195          200          205
Ile Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Met
          210          215          220
Lys Met Arg Ser Pro Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala
225          230          235          240
Ser His Leu Thr Ala Val Ser Ile Phe Tyr Gly Thr Gly Ile Phe Met
          245          250          255
Tyr Leu Arg Pro Asn Ser Ser His Phe Met Gly Thr Asp Lys Met Ala
          260          265          270
Ser Val Phe Tyr Ala Ile Val Ile Pro Met Leu Asn Pro Leu Val Tyr
          275          280          285
Ser Leu Arg Asn Lys Glu Val Lys Ser Ala Phe Lys Lys Thr Val Gly
          290          295          300
Lys Ala Lys Ala Ser Ile Gly Phe Ile Phe
305          310

```

&lt;210&gt; 1864

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g782 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(189)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1864

```

Ala Thr Lys Glu Leu Cys Phe Leu Gly Val Tyr Ile Pro Lys Gly Asp
 1          5          10          15
Ala Cys Trp Lys Xaa Leu Xaa Leu Gly Leu His Leu Leu Leu Gly
          20          25          30
Xaa Gln Val Val Ser Met Val Gly Asn Leu Ala Leu Ile Ala Leu Ile
          35          40          45
Gly Xaa Asn Ser Tyr Leu His His Pro Gln Ala Leu Phe Ser Phe Thr
          50          55          60
Gln Ser Phe Pro Asp Leu Tyr Cys Pro Val Cys Thr Pro Arg Met Leu
65          70          75          80
Met Thr Phe Val Ser Lys Lys Asn Ile Phe Tyr Val Arg Cys Met Thr
          85          90          95
Gln Leu Ser Gln Leu Phe Phe Leu Phe Ile Val Leu Ser Ile Lys Tyr
          100          105          110
His Val Leu Met Phe Ile Ala Cys Gly Cys Leu Val Ala Ile Tyr Asn
          115          120          125
Pro Ser Leu His Glu Val Thr Met Ser Pro Gln Val Arg Glu Met Arg
          130          135          140
Glu Ser Gly Phe Ala Gly Thr Thr Ala His Thr Gly His Ile Leu Arg
145          150          155          160
Pro Asn Leu Cys Asn Ile Asp Val Ile Asn His His Leu Thr Asp Ser
          165          170          175
Leu Leu Val Leu Xaa Val Ser Cys Thr Ser Thr Cys Ala
          180          185

```

&lt;210&gt; 1865

<211> 311  
 <212> PRT  
 <213> Unknown (H38g783 protein)

<220>  
 <223> Synthetic construct

<400> 1865  
 Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe  
 20 25 30  
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val  
 35 40 45  
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro  
 65 70 75 80  
 Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val  
 85 90 95  
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu  
 100 105 110  
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
 115 120 125  
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp  
 130 135 140  
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln  
 145 150 155 160  
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg  
 165 170 175  
 His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp  
 180 185 190  
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly  
 195 200 205  
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile  
 210 215 220  
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Pro Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly  
 245 250 255  
 Ile Phe Val Tyr Leu Arg Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp  
 260 265 270  
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg  
 290 295 300  
 Leu Gln Lys Arg Lys Cys Cys  
 305 310

<210> 1866  
 <211> 312  
 <212> PRT  
 <213> Unknown (H38g784 protein)

<220>  
 <223> Synthetic construct

<400> 1866  
 Met Thr Gly Glu Arg Asn Ser Thr Arg Ile Thr Lys Phe Ile Leu Leu  
 1 5 10 15  
 Gly Phe Ser Glu Phe Pro Lys Asn Pro Ile Phe Leu Phe Ser Ile Phe

```

      20      25      30
Leu Gly Ile Tyr Leu Leu Thr Val Ser Trp Asn Ile Asn Leu Ile Thr
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Thr Ile Ala Pro
65      70      75      80
Lys Met Leu Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
      85      90      95
Gly Cys Ser Met Gln Tyr Phe Phe Phe Ser Ser Leu Gly Leu Thr Glu
      100      105      110
Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
      115      120      125
Asn Pro Leu Leu Tyr Arg Ala Ile Met Phe Pro Thr Leu Cys Val Gln
      130      135      140
Met Val Ala Gly Ser Cys Ile Thr Gly Phe Leu Gly Ser Phe Ile Gln
145      150      155      160
Leu Cys Ala Leu Leu Gln Leu His Phe Cys Gly Pro Asn Val Ile Asn
      165      170      175
His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser Asp
      180      185      190
Thr Phe Phe Gln Val Met Thr Ser Val Leu Thr Val Ile Phe Gly
      195      200      205
Leu Thr Ser Val Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Ile Ala
      210      215      220
Thr Ile Leu Lys Ile Thr Ser Ala Glu Gly Arg Ala Lys Ser Phe Asn
225      230      235      240
Thr Cys Ala Ser His Leu Thr Ala Val Ile Leu Phe Phe Gly Ser Gly
      245      250      255
Ile Phe Val Tyr Met Tyr Pro Asn Ala Gly Asp Ser Leu Ser Gln Asn
      260      265      270
Lys Leu Ala Ser Val Leu Tyr Thr Val Thr Ile Pro Met Leu Asn Pro
      275      280      285
Val Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Asn Arg
      290      295      300
Trp Lys Lys Arg Ile Phe Ser Trp
305      310

```

&lt;210&gt; 1867

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g785 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(444)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1867

```

Met Thr Val Glu Arg Ser Ser Met Thr Ile Thr Lys Phe Ile Leu Leu
1      5      10      15
Gly Phe Ser Glu Tyr Ser Lys Thr Thr Ile Phe Leu Phe Ser Val Phe
      20      25      30
Leu Gly Ile Tyr Leu Leu Thr Met Ser Xaa Asn Val Ser Leu Ile Ala
      35      40      45
Leu Ile Arg Thr Asp Ser His Leu His Ala Pro Val Tyr Phe Phe Leu
      50      55      60
Ser Asn Pro Ser Phe Leu Asp Ile Cys Cys Val Ser Thr Ile Ala Pro
65      70      75      80

```



Lys Met Pro Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met  
 85 90 95  
 Gly Cys Thr Met Gln Tyr Phe Ser Ser Leu Asn Val Thr Glu Cys Cys  
 100 105 110  
 Leu Leu Thr Ala Met Ala Tyr Asp Xaa Tyr Ala Ala Ile Cys Asp Pro  
 115 120 125  
 Leu Leu Tyr Thr Ala Ile Met Ser Pro Ala Leu Cys Met Pro Met Val  
 130 135 140  
 Ala Gly Ser Cys Thr Thr Gly Tyr Phe Val Ser Phe Ile Gln Leu Cys  
 145 150 155 160  
 Ala Leu Leu Leu Leu His Phe Cys Glu Ser Asn Ser Ser His Phe Phe  
 165 170 175  
 Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser His Thr Val Phe  
 180 185 190  
 Phe Phe Ser Ser His Asp His Tyr Ala His Ser Asn Leu Tyr Thr His  
 195 200 205  
 Leu Tyr Leu Gly Tyr His Asp Asn Leu Trp Leu Tyr His Cys Gln His  
 210 215 220  
 Ser Ser Leu Leu Trp Asp Ala Pro Cys Asn Thr Ser Ser Leu Ala Trp  
 225 230 235 240  
 Val Xaa Leu Ser Ala Val Phe Trp Lys Leu Trp Leu Ile Ile Asp Met  
 245 250 255  
 Leu Pro Phe Val Thr Leu Cys Ser Thr Trp Pro Ser Met Ser Pro Thr  
 260 265 270  
 Ser Val Cys Thr Xaa Trp Leu Glu Pro Val Xaa Leu Leu Ser Leu Ala  
 275 280 285  
 His Leu Ser Asn Tyr Val Leu Cys Phe Ser Ser Ile Ser Val Gly Gln  
 290 295 300  
 Ile Val Asn His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser  
 305 310 315 320  
 Cys Tyr Asp Thr Phe Phe Cys Gln Val Met Thr Ser Met Leu Thr Val  
 325 330 335  
 Val Phe Gly Leu Thr Ser Val Leu Val Ile Met Ile Phe Tyr Gly Tyr  
 340 345 350  
 Val Ile Ala Thr Ile Leu Lys Ile Ile Ser Val Glu Gly Arg Ser Lys  
 355 360 365  
 Val Phe Asn Thr Gly Gly Ser His Leu Ile Ala Val Thr Leu Phe Tyr  
 370 375 380  
 Cys Ser Arg Ile Phe Val Tyr Met Cys Ser His Ser Asp Ala Ser Leu  
 385 390 395 400  
 Ser Arg Asn Lys Val Asp Ser Ile Val Tyr Thr Val Val Ile Pro Arg  
 405 410 415  
 Leu Asn Pro Leu Ile Tyr Ser Leu Ser Asp Lys Xaa Ile Lys Asp Ala  
 420 425 430  
 Leu Lys Arg Trp Thr Lys Arg Ile Phe Ser Trp Pro  
 435 440

&lt;210&gt; 1868

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g786 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1868

Met Gly Glu Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe  
 1 5 10 15  
 Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu  
 20 25 30  
 Phe Tyr Ile Phe Thr Leu Leu Gly Asn Gly Ala Ile Leu Gly Leu Ile

```

      35              40              45
Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
  50              55              60
Leu Ala Val Val Asp Ile Ala Tyr Thr Arg Asn Thr Val Pro Gln Met
  65              70              75              80
Leu Ala Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys
      85              90              95
Met Thr Gln Thr Phe Leu Cys Leu Ser Phe Gly His Ser Glu Cys Leu
      100              105              110
Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115              120              125
Leu Arg Tyr Ser Val Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130              135              140
Val Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Leu Ala His Val Val
      145              150              155              160
Leu Ile Leu Arg Leu Pro Phe Ser Gly Pro His Glu Ile Asn His Phe
      165              170              175
Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp
      180              185              190
Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Phe Leu Val Gly
      195              200              205
Pro Pro Ser Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile
      210              215              220
Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys
      225              230              235              240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Ile
      245              250              255
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val
      260              265              270
Phe Phe Leu Phe Tyr Ser Phe Phe Asn Pro Thr Leu Asn Pro Leu Ile
      275              280              285
Tyr Ser Leu Arg Asn Gly Glu Val Lys Gly Ala Leu Arg Arg Ala Leu
      290              295              300
Gly Lys Glu Ser His Ser
      305              310

```

&lt;210&gt; 1869

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g787 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1869

```

Met Glu Arg Gln Asn Gln Ser Cys Val Val Glu Phe Ile Leu Leu Gly
  1              5              10              15
Phe Ser Asn Tyr Pro Glu Leu Gln Gly Gln Leu Phe Val Ala Phe Leu
      20              25              30
Val Ile Tyr Leu Val Thr Leu Ile Gly Asn Ala Ile Ile Ile Val Ile
      35              40              45
Val Ser Leu Asp Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu Leu
      50              55              60
Asn Leu Ser Val Val Asp Leu Ser Phe Ser Ala Val Ile Met Pro Glu
      65              70              75              80
Met Leu Val Val Leu Ser Thr Glu Lys Thr Thr Ile Ser Phe Gly Gly
      85              90              95
Cys Phe Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Ala Glu Cys
      100              105              110
Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
      115              120              125

```

```

Pro Leu Asn Tyr Gln Met Ile Met Asn Lys Gly Val Phe Met Lys Leu
 130                135                140
Ile Ile Phe Ser Trp Ala Leu Gly Phe Met Leu Gly Thr Val Gln Thr
145                150                155                160
Ser Trp Val Ser Ser Phe Pro Phe Cys Gly Leu Asn Glu Ile Asn His
                165                170                175
Ile Ser Cys Glu Thr Pro Ala Val Leu Glu Leu Ala Cys Ala Asp Thr
                180                185                190
Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Phe Leu Ile Ile Leu
                195                200                205
Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val Leu Phe Ala
210                215                220
Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser Thr
225                230                235                240
Cys Ala Ala His Leu Thr Ser Val Thr Leu Phe Tyr Gly Thr Ala Ser
                245                250                255
Met Thr Tyr Leu Gln Pro Lys Ser Gly Tyr Ser Pro Glu Thr Lys Lys
                260                265                270
Val Met Ser Leu Ser Tyr Ser Leu Leu Thr Pro Leu Leu Asn Leu Leu
                275                280                285
Ile Tyr Ser Leu Arg Asn Ser Glu Met Lys Arg Ala Leu Met Lys Leu
290                295                300
Trp Arg Arg Arg Val Val Leu His Thr Ile
305                310

```

&lt;210&gt; 1870

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g788 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1870

```

Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1                5                10                15
Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu
                20                25                30
Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu
                35                40                45
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile
                50                55                60
Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
65                70                75                80
Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met Thr Xaa Thr Phe Leu
                85                90                95
Phe Leu Ser Phe Ala His Thr Glu Cys Leu Leu Leu Val Leu Met Ser
                100                105                110
Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Phe Ile Ile
                115                120                125
Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile Thr Ser Trp Thr Cys
130                135                140
Gly Ser Leu Leu Ala Met Val His Val Ser Leu Ile Leu Arg Leu Pro
145                150                155                160
Phe Cys Gly Pro Arg Glu Ile Asn His Phe Phe Cys Glu Ile Leu Ser
                165                170                175
Val Leu Arg Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile

```

```

      180      185      190
Phe Ala Ala Cys Met Phe Ile Leu Val Gly Pro Leu Cys Leu Val Leu
      195      200      205
Val Ser Tyr Ser His Ile Leu Ala Ala Ile Leu Arg Ile Gln Ser Gly
      210      215      220
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val
      225      230      235      240
Val Gly Leu Phe Phe Gly Ser Ala Ser Val Met Tyr Met Ala Pro Lys
      245      250      255
Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Phe Leu Phe Tyr Ser
      260      265      270
Ser Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Asn Leu Arg Asn Val
      275      280      285
Glu Val Lys Gly Ala Leu Arg Arg Ala Leu Cys Lys Glu Ser His Ser
      290      295      300
Xaa Glu Val Xaa His Leu Asn Cys Gln Pro Gln Leu Ser Arg Gly Leu
      305      310      315      320
Leu Met Pro Asn Tyr Cys Leu Asn Pro Glu Lys
      325      330

```

&lt;210&gt; 1871

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g789 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1871

```

Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe
  1      5      10      15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
      20      25      30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
      35      40      45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
      65      70      75      80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
      85      90      95
Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
      100      105      110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115      120      125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130      135      140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145      150      155      160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165      170      175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180      185      190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195      200      205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210      215      220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Cys Thr Cys
      225      230      235      240
Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr Gly Thr Ala Ile Ile
      245      250      255

```

Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr  
                   260                  265                  270  
 Leu Pro Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile  
                   275                  280                  285  
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu  
                   290                  295                  300  
 Gly Val Glu Arg Ala Leu  
 305                  310

&lt;210&gt; 1872

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g790 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1872

Met Lys Arg Gln Asn Gln Ser Cys Val Val Glu Phe Ile Leu Leu Gly  
 1                  5                  10                  15  
 Phe Ser Asn Phe Pro Glu Leu Gln Val Gln Leu Phe Gly Val Phe Leu  
                   20                  25                  30  
 Val Ile Tyr Val Val Thr Leu Met Gly Asn Ala Ile Ile Thr Val Ile  
                   35                  40                  45  
 Ile Ser Leu Asn Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu Leu  
                   50                  55                  60  
 Asn Leu Ser Val Val Glu Val Ser Phe Ser Ala Val Ile Thr Pro Glu  
 65                  70                  75                  80  
 Met Leu Val Val Leu Ser Thr Glu Lys Thr Met Ile Ser Phe Val Gly  
                   85                  90                  95  
 Cys Phe Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Thr Glu Cys  
                   100                  105                  110  
 Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His  
                   115                  120                  125  
 Pro Leu Asn Tyr Pro Val Ile Met Asn Arg Gly Val Phe Met Lys Leu  
                   130                  135                  140  
 Val Ile Phe Ser Trp Ile Ser Gly Ile Met Val Ala Thr Val Gln Thr  
 145                  150                  155                  160  
 Thr Trp Val Phe Ser Phe Pro Phe Cys Gly Pro Asn Glu Ile Asn His  
                   165                  170                  175  
 Leu Phe Cys Glu Thr Pro Pro Val Leu Glu Leu Val Cys Ala Asp Thr  
                   180                  185                  190  
 Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Ile Leu Ile Val Met  
                   195                  200                  205  
 Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val Leu Phe Ala  
                   210                  215                  220  
 Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser Thr  
 225                  230                  235                  240  
 Cys Ala Ser His Leu Thr Ser Val Thr Leu Phe Tyr Gly Thr Ala Asn  
                   245                  250                  255  
 Met Thr Tyr Leu Gln Pro Lys Ser Gly Tyr Ser Pro Glu Thr Lys Lys  
                   260                  265                  270  
 Leu Ile Ser Leu Ala Tyr Thr Leu Leu Thr Pro Leu Leu Asn Pro Leu  
                   275                  280                  285  
 Ile Tyr Ser Leu Arg Asn Ser Glu Met Lys Arg Thr Leu Ile Lys Leu  
                   290                  295                  300  
 Trp Arg Arg Lys Val Ile Leu His Thr Phe  
 305                  310

&lt;210&gt; 1873

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g791 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1873

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
 1           5           10           15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
      20           25           30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
 35           40           45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
 50           55           60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
 65           70           75           80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
      85           90           95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
      100           105           110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
      115           120           125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
      130           135           140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
 145           150           155           160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
      165           170           175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
      180           185           190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
      195           200           205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
      210           215           220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225           230           235           240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
      245           250           255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
      260           265           270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
      275           280           285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
      290           295           300
Gln Lys Thr Val Pro Met Glu Ile
 305           310

```

&lt;210&gt; 1874

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g792 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1874

```

Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ala
 1           5           10           15
Ile Ser Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      20           25           30

```

Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Met Val Pro Lys Met  
 35 40 45  
 Leu Val Asn Ile Gln Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys  
 50 55 60  
 Ile Thr Gln Met Cys Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu  
 65 70 75 80  
 Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro  
 85 90 95  
 Leu His Tyr Thr Val Ile Met Ser Pro Gln Leu Cys Gly Leu Leu Val  
 100 105 110  
 Leu Val Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser Leu  
 115 120 125  
 Val Thr Leu Gln Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe  
 130 135 140  
 Phe Cys Glu Leu Asn Glu Met Ile His Leu Ala Cys Ser Asp Thr Phe  
 145 150 155 160  
 Val Asn Asn Met Val Met His Phe Ala Ala Val Leu Leu Asp Gly Gly  
 165 170 175  
 Pro Leu Val Gly Ile Leu Tyr Ser Tyr Cys Arg Ile Val Ser Ser Ile  
 180 185 190  
 Arg Ala Ile Ser Ser Thr Gln Gly Lys Tyr Lys Ala Leu Ser Thr Cys  
 195 200 205  
 Ala Ser His Leu Ser Val Val Ser Ile Phe Tyr Gly Thr Gly Leu Gly  
 210 215 220  
 Val Tyr Leu Ser Ser Thr Met Thr Gln Asn Leu His Ser Thr Ala Val  
 225 230 235 240  
 Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile  
 245 250 255  
 Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Thr Gln Phe Phe  
 260 265 270  
 Arg Gly Lys Gln  
 275

&lt;210&gt; 1875

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g793 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1875

Ser Ile Thr Trp Glu Asn His Ser Val Leu Met Glu Phe Val Phe Leu  
 1 5 10 15  
 Ala Tyr Pro Ser Cys Pro Glu Leu His Ile Leu Ser Phe Leu Gly Val  
 20 25 30  
 Ser Leu Val Tyr Gly Leu Ile Ile Thr Gly Asn Ile Leu Ile Val Val  
 35 40 45  
 Ser Ile His Thr Glu Thr Cys Leu Cys Thr Ser Met Tyr Tyr Phe Leu  
 50 55 60  
 Gly Ser Leu Ser Gly Ile Glu Ile Cys Tyr Thr Ala Val Val Val Pro  
 65 70 75 80  
 His Ile Leu Ala Asn Thr Leu Gln Ser Glu Lys Thr Ser Leu Ser Val  
 85 90 95  
 Gly Cys Ala Thr Gln Met Ala Phe Phe Ile Ala Leu Gly Ser Ala Asp  
 100 105 110  
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys

115	120	125
His Pro Leu Gln Tyr Pro Leu Leu Met Thr Leu Thr Leu Cys Val His		
130	135	140
Leu Val Val Ala Ser Val Ile Ser Gly Leu Phe Leu Ser Leu Gln Leu		
145	150	155
Val Ala Phe Ile Phe Ser Leu Pro Phe Cys Gln Ala Gln Gly Ile Glu		160
165	170	175
His Phe Phe Cys Asp Val Pro Pro Val Met His Val Val Cys Ala Gln		
180	185	190
Ser His Ile His Glu Gln Ser Val Leu Val Ala Ala Ile Leu Ala Ile		
195	200	205
Ala Val Pro Phe Phe Leu Ile Thr Thr Ser Tyr Thr Phe Ile Val Ala		
210	215	220
Ala Leu Leu Lys Ile His Ser Ala Ala Gly Arg His Arg Ala Phe Ser		
225	230	235
Thr Cys Ser Ser His Leu Thr Val Val Leu Leu Gln Tyr Gly Cys Cys		240
245	250	255
Ala Phe Met Tyr Leu Cys Pro Ser Ser Tyr Asn Pro Lys Gln Asp		
260	265	270
Arg Phe Ile Ser Leu Val Tyr Thr Leu Gly Thr Pro Leu Leu Asn Pro		
275	280	285
Leu Ile Tyr Ala Leu Arg Asn Ser Glu Met Lys Gly Ala Val Gly Arg		
290	295	300
Val Leu Thr Arg Asn Cys Leu Ser Gln Asn Ser Xaa Glu		
305	310	315

&lt;210&gt; 1876

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g794 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1876

Met Glu Pro Glu Asn Asp Thr Gly Ile Ser Glu Phe Val Leu Leu Gly		
1	5	10
Leu Ser Glu Glu Pro Glu Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu		15
20	25	30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala		
35	40	45
Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser		
50	55	60
Asn Leu Ser Phe Ala Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro Lys		
65	70	75
Met Leu Ile Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly		
85	90	95
Cys Ile Thr Gln Met Cys Phe Phe Val Leu Phe Gly Gly Leu Asp Ser		
100	105	110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His		
115	120	125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu		
130	135	140
Val Leu Ala Ser Trp Met Ile Ala Ala Leu Asn Ser Leu Ser Gln Ser		
145	150	155
Leu Met Val Leu Trp Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His		
165	170	175
Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr		
180	185	190
Phe Leu Asn Asp Met Gly Met Tyr Phe Ala Ala Gly Leu Leu Ala Gly		
195	200	205



Gly Pro Leu Val Gly Ile Leu Cys Ser Tyr Ser Lys Ile Val Ser Ser  
 210 215 220  
 Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Cys Cys Thr Gly Leu  
 245 250 255  
 Gly Val Tyr Leu Thr Ser Ala Ala Thr His Asn Ser His Thr Ser Ala  
 260 265 270  
 Thr Ala Ser Val Met Tyr Thr Val Ala Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys Met Ser  
 290 295 300  
 Phe Arg Gly Lys Gln  
 305

&lt;210&gt; 1877

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g795 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1877

Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile  
 20 25 30  
 Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu  
 35 40 45  
 Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu  
 65 70 75 80  
 Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala  
 85 90 95  
 Ala Gln Met Phe Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu  
 100 105 110  
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu  
 115 120 125  
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile  
 130 135 140  
 Gly Cys Tyr Val Ile Gly Phe Leu Asn Ala Ser Ile Gln Ile Gly Asp  
 145 150 155 160  
 Thr Phe Arg Leu Ser Phe Cys Met Ser Asn Val Ile His His Phe Phe  
 165 170 175  
 Cys Asp Lys Pro Ala Val Ile Thr Leu Thr Cys Ser Glu Lys His Ile  
 180 185 190  
 Ser Glu Leu Ile Leu Val Leu Ile Ser Ser Phe Asn Val Phe Phe Ala  
 195 200 205  
 Leu Leu Val Thr Leu Ile Ser Tyr Leu Phe Ile Leu Ile Thr Ile Leu  
 210 215 220  
 Lys Arg His Thr Gly Lys Gly Tyr Gln Lys Pro Leu Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Ile Ala Ile Phe Leu Phe Tyr Ile Thr Val Ile Ile Met  
 245 250 255  
 Tyr Ile Arg Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Ile Ala  
 260 265 270  
 Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Ser Pro Ile Val Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Asp Val Lys Asn Ala Phe Met Lys Val Val Glu

290 295 300  
 Lys Ala Lys Tyr Ser Leu Asp Ser Val Phe  
 305 310

<210> 1878  
 <211> 315  
 <212> PRT  
 <213> Unknown (H38g796 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(315)  
 <223> Xaa = Any Amino Acid

<400> 1878  
 Met Xaa Asn Asn Ser Lys Phe Thr Asp Phe Ile Leu Val Gly Leu Thr  
 1 5 10 15  
 Asn Ala Thr Glu Leu Gln Ile Pro Leu Phe Ile Leu Phe Ile Leu Ile  
 20 25 30  
 His Leu Leu Ile Leu Thr Arg Asn Leu Glu Ile Ile Leu Leu Ile Leu  
 35 40 45  
 Leu Asp Ser Cys Leu His Ile Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Leu Leu Gly Tyr Leu Thr Val Thr Pro Arg Val Thr Ala Ser Arg  
 65 70 75 80  
 Ala Gly Tyr Leu Glu Gly Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys  
 85 90 95  
 Ala Ala Gln Met Phe Phe Phe Val Ala Leu Ala Thr Val Glu Asn Met  
 100 105 110  
 Leu Leu Thr Ser Met Ala Tyr Asp His Tyr Ile Ala Val Cys Lys Pro  
 115 120 125  
 Leu His Tyr Thr Thr Thr Thr Ile Ala Ser Val Cys Ala His Leu Val  
 130 135 140  
 Ile Gly Ser Tyr Val Cys Gly Phe Leu Asn Ala Ser Leu Arg Ile Gly  
 145 150 155 160  
 Asp Ile Phe Ser Leu Ser Phe Cys Lys Ser Asn Leu Val His His Leu  
 165 170 175  
 Phe Cys Asp Val Pro Pro Val Met Ala Val Ser Cys Ser Gly Lys His  
 180 185 190  
 Ile Ser Lys Lys Ile Leu Val Phe Met Ser Ser Phe Asn Val Phe Leu  
 195 200 205  
 Ala Leu Leu Val Ile Leu Thr Ser Tyr Leu Phe Ile Phe Ile Thr Ile  
 210 215 220  
 Leu Lys Met His Ser Ala Gln Gly His Leu Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Ile Ala Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe  
 245 250 255  
 Met His Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Glu Met  
 260 265 270  
 Ala Ser Leu Phe Tyr Ala Val Phe Ile Ser Met Leu Asn Leu Val Phe  
 275 280 285  
 Tyr Ser Leu Arg Ser Lys Glu Val Lys Asn Ala Phe Lys Lys Ala Val  
 290 295 300  
 Glu Lys Ala Lys Phe Phe Leu Glu Leu Xaa Phe  
 305 310 315

<210> 1879  
 <211> 314  
 <212> PRT

&lt;213&gt; Unknown (H38g797 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1879

```

Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu Leu Gly
 1          5          10          15
Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val Phe Ser
          20          25          30
Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile Thr Leu
          35          40          45
Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe Leu Ser
          50          55          60
Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
65          70          75          80
Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly
          85          90          95
Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met Glu Asn
          100          105          110
Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
          115          120          125
Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met
          130          135          140
Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu His Thr
145          150          155          160
Phe Leu Met Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His
          165          170          175
Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr
          180          185          190
Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser
          195          200          205
Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val
          210          215          220
Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser
          245          250          255
Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg
          260          265          270
Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met Lys Trp
          290          295          300
Met Ser Arg Met Gln Thr Phe Phe Phe Arg
305          310

```

&lt;210&gt; 1880

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g798 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1880

```

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
 1          5          10          15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
          20          25          30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val

```

```

      35              40              45
Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu
  50              55              60
Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
  65              70              75              80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser
      85              90              95
Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
      100              105              110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115              120              125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
      130              135              140
Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser
      145              150              155              160
Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu
      165              170              175
Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr
      180              185              190
Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro
      195              200              205
Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu
      210              215              220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
      225              230              235              240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245              250              255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
      260              265              270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
      275              280              285
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
      290              295              300
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
      305              310              315

```

&lt;210&gt; 1881

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g799 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1881

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20              25              30
Leu Ser Leu Ser Met Tyr Met Val Thr Val Leu Arg Asn Leu Leu Ser
      35              40              45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Cys Phe
      50              55              60
Phe Leu Ser Lys Leu Cys Xaa Ala Asp Ile Gly Phe Thr Leu Ala Met
      65              70              75              80
Val Pro Lys Met Ile Val Asn Met Gln Ser His Ser Arg Val Ile Ser
      85              90              95

```

```

Tyr Glu Gly Cys Leu Thr Arg Met Ser Phe Phe Val Leu Phe Ala Cys
      100      105      110
Met Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Pro Leu Asp Ser Gln
145      150      155      160
Leu His Ser Trp Ile Val Leu Leu Phe Thr Ile Ile Lys Asn Val Glu
      165      170      175
Ile Thr Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys
      180      185      190
Ser Asp Ser Val Ile Asn Asn Ile Phe Ile Tyr Phe Asp Ser Thr Met
      195      200      205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
      210      215      220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Gly
225      230      235      240
Phe Ser Thr Cys Gly Ser Tyr Leu Ala Val Val Cys Xaa Phe Asp Gly
      245      250      255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260      265      270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Gly Lys Arg Asp Ile Gln Ser Val Leu
      290      295      300
Arg Arg Leu Cys Ser Arg Thr Val Glu Ser Pro Xaa Tyr Val Pro Ser
305      310      315      320
Phe Phe Leu Cys

```

&lt;210&gt; 1882

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g800 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1882

```

Met Glu Pro Glu Asn Gly Thr Arg Ile Leu Gly Phe Leu Leu Leu Gly
  1      5      10      15
Leu Ser Glu Glu Pro Glu Leu Gln Pro Val Met Phe Gly Leu Phe Leu
      20      25      30
Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
      35      40      45
Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
65      70      75      80
Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
      85      90      95
Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
      100      105      110
Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
      130      135      140
Val Leu Ala Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile
145      150      155

```

<210> 1883  
 <211> 318  
 <212> PRT  
 <213> Unknown (H38g801 protein)

<220>  
 <223> Synthetic construct

<400> 1883

```

Met Met Ser Phe Ala Pro Asn Ala Ser His Ser Pro Val Phe Leu Leu
 1           5           10           15
Leu Gly Phe Ser Arg Ala Asn Ile Ser Tyr Thr Leu Leu Phe Phe Leu
           20           25           30
Phe Leu Ala Ile Tyr Leu Thr Thr Ile Leu Gly Asn Val Thr Leu Val
           35           40           45
Leu Leu Ile Ser Trp Asp Ser Arg Leu His Ser Pro Met Tyr Tyr Leu
           50           55           60
Leu Arg Gly Leu Ser Val Ile Asp Met Gly Leu Ser Thr Val Thr Leu
           65           70           75           80
Pro Gln Leu Leu Ala His Leu Val Ser His Tyr Pro Thr Ile Pro Ala
           85           90           95
Ala Arg Cys Leu Ala Gln Phe Phe Phe Tyr Ala Phe Gly Val Thr
           100          105          110
Asp Thr Leu Val Ile Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile
           115          120          125
Cys Asp Pro Leu His Tyr Ala Leu Val Met Asn His Gln Arg Cys Ala
           130          135          140
Cys Leu Leu Ala Leu Ser Trp Val Val Ser Ile Leu His Thr Met Leu
           145          150          155          160
Arg Val Gly Leu Val Leu Pro Leu Cys Trp Thr Gly Asp Ala Gly Gly
           165          170          175
Asn Val Asn Leu Pro His Phe Phe Cys Asp His Arg Pro Leu Leu Arg
           180          185          190
Ala Ser Cys Ser Asp Ile His Ser Asn Glu Leu Ala Ile Phe Phe Glu
           195          200          205
Gly Gly Phe Leu Met Leu Gly Pro Cys Ala Leu Ile Val Leu Ser Tyr
           210          215          220
Val Arg Ile Gly Ala Ala Ile Leu Arg Leu Pro Ser Ala Ala Gly Arg
           225          230          235          240
Arg Arg Ala Val Ser Thr Cys Gly Ser His Leu Thr Met Val Gly Phe
           245          250          255
Leu Tyr Gly Thr Ile Ile Cys Val Tyr Phe Gln Pro Pro Phe Gln Asn
           260          265          270
Ser Gln Tyr Gln Asp Met Val Ala Ser Val Met Tyr Thr Ala Ile Thr
           275          280          285
Pro Leu Ala Asn Pro Phe Val Tyr Ser Leu His Asn Lys Asp Val Lys
           290          295          300
Gly Ala Leu Cys Arg Leu Leu Glu Trp Val Lys Val Asp Pro
           305          310          315

```

<210> 1884  
 <211> 307  
 <212> PRT  
 <213> Unknown (H38g802 protein)

<220>  
 <223> Synthetic construct

<400> 1884

```

Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
 1           5           10           15

```

Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile  
                   20                  25                  30  
 Tyr Phe Ile Ser Val Thr Gly Asn Gly Ala Val Leu Met Ile Val Ile  
           35                  40                  45  
 Ser Asp Pro Arg Leu His Ser Leu Met Tyr Phe Phe Leu Gly Asn Leu  
       50                  55                  60  
 Ser Tyr Leu Asp Ile Cys Tyr Ser Thr Val Thr Leu Pro Lys Met Leu  
   65                  70                  75                  80  
 Gln Asn Phe Leu Ser Thr His Lys Ala Ile Ser Phe Leu Gly Cys Ile  
                   85                  90                  95  
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ser Met Leu  
           100                  105                  110  
 Phe Ala Val Met Ala Phe Asp Leu Ser Val Ala Ile Cys Lys Pro Leu  
       115                  120                  125  
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile  
       130                  135                  140  
 Thr Ile Trp Val Ile Gly Phe Phe His Ala Leu Leu His Ser Val Met  
   145                  150                  155                  160  
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe Leu  
           165                  170                  175  
 Cys Asp Ile Lys Pro Leu Leu Lys Leu Ala Cys Gly Asn Thr Glu Leu  
       180                  185                  190  
 Asn Gln Trp Leu Leu Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro  
       195                  200                  205  
 Phe Phe Leu Thr Leu Leu Ser Tyr Phe Tyr Ile Ile Thr Tyr Leu Phe  
       210                  215                  220  
 Phe Lys Thr Arg Ser Cys Ser Met Leu Cys Lys Ala Leu Ser Thr Cys  
   225                  230                  235                  240  
 Ala Ser His Phe Met Val Val Ile Leu Phe Tyr Ala Pro Val Leu Phe  
           245                  250                  255  
 Thr Tyr Ile His Pro Ala Leu Glu Ser Phe Met Asp Gln Asp Arg Ile  
       260                  265                  270  
 Val Ala Ile Met Tyr Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile  
       275                  280                  285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Val Ile  
       290                  295                  300  
 Arg Arg Leu  
 305

&lt;210&gt; 1885

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g803 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1885

Gln Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Met Gly Leu  
   1                  5                  10                  15  
 Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser Leu Ser  
       20                  25                  30  
 Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val  
       35                  40                  45  
 Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn  
       50                  55                  60  
 Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys Ile

```

65          70          75          80
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Val Gly Cys
      85          90          95
Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met
      100        105        110
Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro
      115        120        125
Leu His Tyr Pro Val Ile Val Asn Ala His Leu Arg Val Phe Leu Val
      130        135        140
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Xaa
145          150          155          160
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
      165        170        175
Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Ile
      180        185        190
Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu
      195        200        205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Cys Lys Ile Val Pro Ser Ile
      210        215        220
Leu Arg Ile Ser Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Ala Leu Val Cys Leu Phe Tyr Gly Ala Gly Ile Gly
      245        250        255
Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val
      260        265        270
Val Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile
      275        280        285
Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Thr Leu Arg Arg Leu Leu
      290        295        300
Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
305          310          315          320

```

&lt;210&gt; 1886

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g804 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1886

```

Met Ala Pro Gly Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Ala Gly
 1          5          10          15
Leu Thr His Gln Pro Asp Leu Gln Ser Pro Leu Phe Phe Leu Phe Leu
      20        25        30
Val Ile Tyr Val Val Thr Leu Leu Gly Asn Leu Gly Leu Val Thr Leu
      35        40        45
Ile Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
      50        55        60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Ile Pro Lys
65          70          75          80
Met Leu Met Asn Phe Ile Ser Glu Lys Asn Ile Met Ser Phe Lys Gly
      85        90        95
Cys Met Thr Gln Leu Ser Phe Tyr Xaa Phe Phe Val Val Ile Ser Glu
      100        105        110
Gly Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Val Ala Ile Cys Thr
      115        120        125

```



Pro Leu Leu Tyr His Ile Ala Met Ser Pro Thr Val Cys Ser Ser Leu  
 130 135 140  
 Met Phe Gly Ser Tyr Leu Met Pro Phe Ser Gly Ala Met Ala His Thr  
 145 150 155 160  
 Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp His  
 165 170 175  
 Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr  
 180 185 190  
 Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile Ile  
 195 200 205  
 Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser  
 210 215 220  
 Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala  
 245 250 255  
 Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg Lys  
 260 265 270  
 Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys Ala  
 290 295 300  
 Leu Ser Ser Arg Lys Leu Xaa Xaa Val Ile Val Cys Val Cys Val Tyr  
 305 310 315 320  
 Ser His Lys Thr Gly Ile Phe Cys  
 325

&lt;210&gt; 1887

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g805 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1887

Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu  
 20 25 30  
 Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Ser Glu  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser  
 100 105 110  
 Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu  
 130 135 140  
 Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile  
 145 150 155 160  
 Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His  
 165 170 175  
 Phe Phe Cys Asp Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His  
 180 185 190  
 Phe Val Lys Glu Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met

195	200	205
Thr Pro Phe Ser Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr		
210	215	220
Val Leu Lys Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser		240
245	250	255
Tyr Leu Tyr Phe Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile		
260	265	270
Ala Thr Ile Ile Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Phe Ile		
275	280	285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Gln Gly Leu Ala Lys Leu Met		
290	295	300
His Arg Met Lys Cys Gln		
305	310	

&lt;210&gt; 1888

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g806 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1888

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu		
1	5	10
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val		15
20	25	30
Phe Thr Ala Val Tyr Val Phe Ile Ile Ile Gly Asn Met Leu Ile Ile		35
35	40	45
Val Ala Val Val Ser Ser Gln Arg Leu His Lys Pro Met Tyr Ile Phe		50
50	55	60
Leu Ala Asn Leu Ser Phe Leu Asp Ile Leu Tyr Thr Ser Ala Val Met		65
65	70	75
Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser Val Ala		80
85	90	95
Gly Cys Leu Leu Gln Phe Phe Ile Phe Gly Ser Leu Ala Thr Ala Glu		100
100	105	110
Cys Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys		115
115	120	125
Tyr Pro Leu His Tyr Pro Leu Leu Met Gly Pro Arg Arg Tyr Met Gly		130
130	135	140
Leu Val Val Thr Thr Trp Leu Ser Gly Phe Val Val Asp Gly Leu Val		145
145	150	155
Val Ala Leu Val Ala Gln Leu Arg Phe Cys Gly Pro Asn His Ile Asp		160
165	170	175
Gln Phe Tyr Cys Asp Phe Met Leu Phe Val Gly Leu Ala Cys Ser Asp		180
180	185	190
Pro Arg Val Ala Gln Val Thr Thr Leu Ile Leu Ser Val Phe Cys Leu		195
195	200	205
Thr Ile Pro Phe Gly Leu Ile Leu Thr Ser Tyr Ala Arg Ile Val Val		210
210	215	220
Ala Val Leu Arg Val Pro Ala Gly Ala Ser Arg Arg Arg Ala Phe Ser		225
225	230	235
Thr Cys Ser Ser His Leu Ala Val Val Thr Thr Phe Tyr Gly Thr Leu		240
245	250	255
Met Ile Phe Tyr Val Ala Pro Ser Ala Val His Ser Gln Leu Leu Ser		260
260	265	270
Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Phe Asn Pro		275
275	280	285

Val Ile Tyr Thr Met Arg Asn Lys Glu Val His Gln Ala Leu Arg Lys  
 290 295 300  
 Ile Leu Cys Ile Lys Gln Thr Glu Thr Leu Asp  
 305 310 315

<210> 1889  
 <211> 188  
 <212> PRT  
 <213> Unknown (H38g807 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(188)  
 <223> Xaa = Any Amino Acid

<400> 1889  
 His Trp Lys Ile Leu Arg Arg Asn Ser Lys Met Ile His Glu Ile Ile  
 1 5 10 15  
 Xaa Thr Leu Cys Gln Ile Leu Tyr Ser Glu Asp Lys Thr Cys Tyr Ile  
 20 25 30  
 Gln Ile Gln Ser Leu Phe Cys Thr Asp Leu Glu Ile Pro Asn Phe Phe  
 35 40 45  
 Cys Glu Leu Asn Xaa Val Val His Leu Ala Cys Ser Asp Thr Phe Leu  
 50 55 60  
 Lys Asp Ile Val Arg Tyr Cys Thr Thr Met Leu Leu Ser Gly Gly Pro  
 65 70 75 80  
 Ile Ala Gly Ile Phe Tyr Ser Phe Ser Lys Ile Ile Ser Ser Ile Cys  
 85 90 95  
 Ala Ile Pro Ser Ala Gln Gly Lys His Lys Ala Phe Pro Thr Cys Val  
 100 105 110  
 Ser His Leu Ser Asn Met Ser Leu Phe Tyr Cys Arg Ser Thr Gly Leu  
 115 120 125  
 Tyr Leu Ser Phe Ala Ala Thr His Asn Ser Cys Ser Asn Ala Thr Ala  
 130 135 140  
 Ser Val Arg His Thr Val Val Lys Pro Leu Leu Asn Val Phe Ile Leu  
 145 150 155 160  
 Lys Ser Ser Asn Lys Asp Ile Lys Xaa Ala Leu Lys Val Phe Phe Arg  
 165 170 175  
 Gly Lys Gln Trp Lys His His Phe Ser Lys Ser Ala  
 180 185

<210> 1890  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g808 protein)

<220>  
 <223> Synthetic construct

<400> 1890  
 Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu  
 20 25 30  
 Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ala Thr  
 35 40 45  
 Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln

```

65          70          75          80
Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly
      85          90          95
Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser
      100        105        110
Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115        120        125
Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu
      130        135        140
Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr
      145        150        155        160
Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His
      165        170        175
Phe Leu Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Val
      180        185        190
Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Asp Leu Leu Ala Leu
      195        200        205
Thr Pro Leu Val Cys Ile Leu Val Ser Tyr Gly Leu Ile Phe Ser Thr
      210        215        220
Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala Val Ser Thr
      225        230        235        240
Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly Thr Ala Ile
      245        250        255
Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu Ser Asp Thr
      260        265        270
Leu Ser Thr Ile Met Tyr Ser Met Val Ala Pro Met Leu Asn Pro Phe
      275        280        285
Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Arg Gly Leu Gln Lys Met
      290        295        300
Leu Leu Lys Cys Thr Val Phe Gln Gln
305          310

```

&lt;210&gt; 1891

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g809 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1891

```

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
1          5          10          15
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
      20          25          30
Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
      35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
      50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly
      85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
      100        105        110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
      115        120        125
Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
      130        135        140
Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
      145        150        155        160

```

```

Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
      165                      170                      175
Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
      180                      185                      190
Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
      195                      200                      205
Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
      210                      215                      220
Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
      225                      230                      235                      240
Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
      245                      250                      255
Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
      260                      265                      270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
      275                      280                      285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
      290                      295                      300
Asp Lys His Phe Lys Arg Leu Thr
      305                      310

```

&lt;210&gt; 1892

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g810 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1892

```

Met Gly Met Ser Asn Leu Thr Arg Leu Ser Glu Phe Ile Leu Leu Gly
  1          5          10          15
Leu Ser Ser Arg Ser Glu Asp Gln Arg Pro Leu Phe Ala Leu Phe Leu
      20          25          30
Ile Ile Tyr Leu Val Thr Leu Met Gly Asn Leu Leu Ile Ile Leu Ala
      35          40          45
Ile His Ser Asp Pro Arg Leu Gln Asn Pro Met Tyr Phe Phe Leu Ser
      50          55          60
Ile Leu Ser Phe Ala Asp Ile Cys Tyr Thr Thr Val Ile Val Pro Lys
      65          70          75          80
Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala Glu
      85          90          95
Cys Leu Ala Gln Met Tyr Phe Phe Leu Val Phe Gly Asn Ile Asp Ser
      100         105         110
Tyr Leu Leu Ala Ala Met Ala Ile Asn Arg Cys Val Ala Ile Cys Asn
      115         120         125
Pro Phe His Tyr Val Thr Val Met Asn Arg Arg Cys Cys Val Leu Leu
      130         135         140
Leu Ala Phe Pro Ile Thr Phe Ser Tyr Phe His Ser Leu Leu His Val
      145         150         155         160
Leu Leu Val Asn Arg Leu Thr Phe Cys Thr Ser Asn Val Ile His His
      165         170         175
Phe Phe Cys Asp Val Asn Pro Val Leu Lys Leu Ser Cys Ser Ser Thr
      180         185         190
Phe Val Asn Glu Ile Val Ala Met Thr Glu Gly Leu Ala Ser Val Met
      195         200         205
Ala Pro Phe Val Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Ala
      210         215         220
Val Leu Lys Ile Pro Ser Ala Ala Gly Lys His Lys Ala Phe Ser Thr
      225         230         235         240
Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Ile Ser

```

245 250 255  
 Tyr Val Tyr Leu Gln Pro Leu Ser Ser Tyr Thr Val Lys Asp Arg Ile  
 260 265 270  
 Ala Thr Ile Asn Tyr Thr Val Leu Thr Ser Val Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Gln Lys Leu Ile  
 290 295 300  
 Asn Lys Ile Lys Ser Gln Met Ser Arg Phe Ser Thr Lys  
 305 310 315

&lt;210&gt; 1893

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g811 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1893

Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr  
 1 5 10 15  
 Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile  
 20 25 30  
 Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile  
 35 40 45  
 Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu  
 50 55 60  
 Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu  
 65 70 75 80  
 Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile  
 85 90 95  
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu  
 100 105 110  
 Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile  
 130 135 140  
 Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met  
 145 150 155 160  
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe  
 165 170 175  
 Cys Asp Val Lys Pro Leu Leu Lys Leu Ser Leu Ile Ser Gly Trp Leu  
 180 185 190  
 Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu  
 195 200 205  
 Leu Ser Tyr Phe Tyr Ile Ile Thr His Leu Phe Phe Lys Thr His Ser  
 210 215 220  
 Phe Ser Met Leu Arg Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met  
 225 230 235 240  
 Val Val Ile Leu Leu Tyr Ala Pro Val Leu Phe Thr Tyr Ile His His  
 245 250 255  
 Ala Ser Gly Thr Ser Met Asp Gln Asp Arg Ile Thr Ala Ile Met Tyr  
 260 265 270  
 Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn  
 275 280 285  
 Lys Glu Val Lys Gly Ala Phe Asn Arg Ala Met Lys Arg Trp Leu Trp  
 290 295 300  
 Pro Lys Glu Ile Leu  
 305

&lt;210&gt; 1894

<211> 328  
 <212> PRT  
 <213> Unknown (H38g812 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(328)  
 <223> Xaa = Any Amino Acid

<400> 1894

Ser	Val	Asp	Gln	Val	Asn	Asp	Ser	Leu	Val	Thr	Glu	Phe	Val	Leu	Leu
1				5					10					15	
Gly	Leu	Ala	Gln	Ser	Leu	Glu	Met	Gln	Phe	Phe	Leu	Phe	Leu	Phe	Phe
		20						25					30		
Ser	Leu	Phe	Tyr	Val	Gly	Ile	Ile	Leu	Gly	Asn	Leu	Phe	Ile	Val	Phe
	35					40					45				
Thr	Val	Ile	Phe	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Ile	Leu	Leu
	50					55					60				
Ala	Asn	Leu	Ser	Leu	Ile	Asp	Leu	Ser	Leu	Ser	Ser	Thr	Thr	Val	Pro
65					70					75					80
Arg	Leu	Ile	Tyr	Asp	Leu	Phe	Thr	Asp	Cys	Lys	Val	Ile	Ser	Phe	His
			85						90					95	
Asn	Cys	Met	Ile	Gln	Lys	Phe	Phe	Ile	His	Val	Thr	Gly	Gly	Val	Glu
		100						105					110		
Met	Val	Leu	Leu	Ile	Val	Met	Glu	Tyr	Asp	Arg	Tyr	Thr	Ala	Ile	Cys
	115					120						125			
Lys	Pro	Leu	His	Tyr	Pro	Thr	Ile	Met	Asn	Pro	Lys	Met	Cys	Met	Phe
	130					135					140				
Leu	Val	Ala	Ala	Ala	Trp	Val	Ile	Gly	Val	Ile	His	Ala	Met	Ser	Gln
145					150					155					160
Phe	Val	Phe	Val	Ile	Asn	Xaa	Pro	Phe	Cys	Gly	Pro	Asn	Asn	Val	Gly
			165						170					175	
Ser	Phe	Tyr	Cys	Asp	Phe	Pro	Arg	Val	Ile	Lys	Leu	Ala	Cys	Met	Asp
		180					185					190			
Thr	Tyr	Gly	Leu	Glu	Phe	Val	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile	Ser
	195					200						205			
Met	Gly	Thr	Phe	Phe	Phe	Leu	Ile	Val	Ser	Tyr	Ile	Phe	Ile	Leu	Val
	210					215					220				
Thr	Val	Gln	Arg	His	Ser	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe	Thr
225					230					235					240
Ser	Xaa	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Ala	Pro	Cys	Met
			245						250				255		
Phe	Leu	Tyr	Val	Trp	Pro	Phe	Pro	Thr	Lys	Ser	Leu	Asp	Lys	Phe	Phe
		260						265					270		
Ala	Ile	Met	Asn	Phe	Val	Val	Thr	Pro	Val	Leu	Asn	Pro	Ala	Ile	Tyr
	275						280					285			
Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys	Phe	Ala	Met	Arg	Arg	Leu	Asn	Gln
	290					295					300				
His	Ile	Leu	Asn	Ser	Met	Glu	Thr	Thr	Xaa	His	Ile	Trp	Leu	Met	Arg
305					310					315					320
Ala	Gln	Asp	Lys	Cys	His	Gly	Pro								
				325											

<210> 1895  
 <211> 272  
 <212> PRT  
 <213> Unknown (H38g813 protein)

<220>

&lt;223&gt; Synthetic construct

&lt;400&gt; 1895

```

Met Trp Ile Asn Asn Gln Ser S r Leu Asp Asp Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
      20           25           30
Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
 35           40           45
His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
 50           55           60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
65           70           75           80
Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
      85           90           95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
      100           105           110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
 115           120           125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
 130           135           140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
145           150           155           160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
      165           170           175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
      180           185           190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Leu Met
 195           200           205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
 210           215           220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
225           230           235           240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
      245           250           255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
      260           265           270

```

&lt;210&gt; 1896

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g814 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1896

```

Met Asn Val Ser Glu Pro Asn Ser Ser Phe Ala Phe Val Asn Glu Phe
 1           5           10           15
Ile Leu Gln Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe
      20           25           30
Ser Leu Phe Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala
 35           40           45
Ile Ala Phe Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr
 50           55           60
Met Phe Leu Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser
65           70           75           80
Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile
      85           90           95
Ser Phe Ala Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
      100           105           110

```



```

Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu
    115                      120                      125
Ala Ile Cys Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu
    130                      135                      140
Tyr Ala Lys Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe
    145                      150                      155                      160
Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn
    165                      170                      175
Ile Ile Asp His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp
    180                      185                      190
Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser
    195                      200                      205
Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu
    210                      215                      220
Val Leu Lys Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys
    225                      230                      235                      240
Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr
    245                      250                      255
Ser Ser Leu Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr
    260                      265                      270
Gly Met Gln Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu
    275                      280                      285
Phe Asn Pro Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala
    290                      295                      300
Leu Arg Lys Val Leu Gly Ser Ser Asn Ile Ile
    305                      310                      315

```

&lt;210&gt; 1897

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g815 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1897

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
    1      5      10      15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
    20      25      30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
    35      40      45
His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
    50      55      60
Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
    65      70      75      80
Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
    85      90      95
Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
    100     105     110
Tyr Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu Asn Tyr Thr Thr Ile
    115     120     125
Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
    130     135     140
Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
    145     150     155                      160
Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
    165     170     175
Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
    180     185     190
Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile

```

```

      195              200              205
Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210              215              220
Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225              230              235              240
Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
      245              250              255
Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
      260              265              270
Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
      275              280              285
Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
      290              295              300
Phe
305

```

&lt;210&gt; 1898

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g816 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1898

```

Met Thr Leu Pro Ser Asp Asp Ser Thr Val Pro Val Ser Glu Phe Leu
 1              5              10              15
Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Leu Leu Ser Leu
      20              25              30
Pro Leu Ser Leu Met Phe Leu Leu Ala Met Gly Thr Asn Thr Thr Pro
      35              40              45
Pro Ile Thr Ile His Leu Glu Ala Ser Leu His Leu Pro Leu Tyr Tyr
      50              55              60
Leu Pro Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val
      65              70              75              80
Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Gly
      85              90              95
Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Pro
      100              105              110
Met Glu Ser Cys Thr Phe Met Val Lys Asp Tyr Asp His Tyr Val Ala
      115              120              125
Ile Cys His Pro Leu Gln Tyr Leu Ser Ile Ile Thr His Gln Phe Val
      130              135              140
Ala Lys Ala Ser Val Phe Ile Val Val Gln Asn Ala Leu Leu Leu Ser
      145              150              155              160
Pro Val Pro Ile Leu Ser Ala Gln Leu His Tyr Cys Arg Lys Asn Val
      165              170              175
Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser Arg Leu Ser Cys
      180              185              190
Asp Asn Phe Thr Leu Asn Arg Leu Tyr Gln Phe Val Ala Gly Trp Thr
      195              200              205
Phe Leu Gly Ser Asp Phe Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile
      210              215              220
Leu Arg Ala Val Leu Arg Phe Lys Val Glu Gly Val Ala Val Lys Ala
      225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Ile
      245              250              255

```

Leu Leu Val Val Val Leu Thr Asn Val Ala Arg Lys Lys Val Pro Met  
                   260                  265                  270  
 Asp Ile Leu Ile Leu Phe Asn Val Leu His Pro Phe Ser Pro Pro Ala  
                   275                  280                  285  
 Leu Asn Pro Ile Ile Cys Gly Phe Gln Thr Lys Glu Leu Lys Lys Glu  
                   290                  295                  300  
 Phe Xaa Lys Leu Leu Gln Arg Gly Leu Xaa Lys His Gly Arg  
 305                  310                  315

<210> 1899

<211> 317

<212> PRT

<213> Unknown (H38g817 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1899

Lys His Asn His Thr Ala Val Thr Lys Val Thr Glu Phe Ile Leu Met  
   1                  5                  10                  15  
 Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro Leu Phe Gly Leu Phe  
                   20                  25                  30  
 Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn Leu Gly Met Val Ile  
                   35                  40                  45  
 Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Lys His Leu Ala Ile Thr Asp Leu Gly Tyr Ser Thr Val Ile Gly Pro  
   65                  70                  75                  80  
 Gln Met Met Phe Ser Glu Thr Ser Tyr Val His Lys Glu His Asn Phe  
                   85                  90                  95  
 Phe Tyr Asn Trp Tyr Ala Asn His Arg Ala Arg Phe Glu Arg Asn Ile  
                   100                  105                  110  
 Ile Ser His Arg Gly Ile Leu Ser Ala Thr Asn Asn Glu Pro Tyr Lys  
                   115                  120                  125  
 Pro Ile Thr Lys Gln Leu Leu Asn Pro Ile Ile Met Pro Glu Lys Ile  
                   130                  135                  140  
 Arg Glu Glu Gln Ile Thr Val Pro Glu Leu Asp Lys Thr Cys Ala Pro  
   145                  150                  155                  160  
 Leu Phe Leu Lys Arg Lys Xaa Val Lys Thr Val Ser Thr Asn Pro Asp  
                   165                  170                  175  
 Thr Thr Asn Asn Cys His Gly Glu Gly Thr Ala Lys Met Xaa Ile Leu  
                   180                  185                  190  
 Arg Ser Glu Lys Lys Lys Ile Thr Ile Ile Lys Ala Met Thr Ala Gly  
                   195                  200                  205  
 Thr Asn Met Leu Ile Ser Leu Ser Ile Val Leu Ile Ser Tyr Met Phe  
                   210                  215                  220  
 Ile Leu Val Ala Asn Leu Arg Met Asn Ser Arg Lys Gly Arg Tyr Lys  
   225                  230                  235                  240  
 Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met Phe Tyr  
                   245                  250                  255  
 Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His Thr Leu  
                   260                  265                  270  
 Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile Pro Met  
                   275                  280                  285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala  
                   290                  295                  300  
 Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile

305

310

315

&lt;210&gt; 1900

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g818 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(220)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1900

```

Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro
 1           5           10          15
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro Tyr Ala
      20           25           30
Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 35           40           45
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 50           55           60
Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
 65           70           75           80
Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      85           90           95
Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Ser Asn Val Glu Ile Ala
      100          105          110
Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu Asp Cys Ser Asp
 115          120          125
Thr Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Met Phe Gly Phe
 130          135          140
Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val Pro Ser
 145          150          155          160
Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ala Thr
      165          170          175
Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr Gly Ile
      180          185          190
Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val
      195          200          205
Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
      210          215          220

```

&lt;210&gt; 1901

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g819 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1901

```

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1           5           10          15
Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
      20           25           30
Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
      35           40           45
Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
 50           55           60

```

Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met  
 65 70 75 80  
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met  
 85 90 95  
 Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile  
 100 105 110  
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile  
 130 135 140  
 Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu  
 145 150 155 160  
 Thr Ile Phe Val Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe  
 165 170 175  
 Cys Asp Val Tyr Pro Leu Leu Lys Leu Ala Cys Ser Asn Ile His Met  
 180 185 190  
 Ile Gly Leu Leu Val Ile Ala Asn Ser Gly Leu Ile Ala Leu Val Thr  
 195 200 205  
 Phe Val Val Leu Leu Leu Ser Tyr Val Phe Ile Leu Tyr Thr Ile Arg  
 210 215 220  
 Ala Tyr Ser Ala Glu Arg Ser Lys Ala Leu Ala Thr Cys Ser Ser  
 225 230 235 240  
 His Val Ile Val Val Val Leu Phe Phe Ala Pro Ala Leu Phe Ile Tyr  
 245 250 255  
 Ile Arg Pro Val Thr Thr Phe Ser Glu Asp Lys Val Phe Ala Leu Phe  
 260 265 270  
 Tyr Thr Ile Ala Pro Met Phe Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Thr Glu Met Lys Asn Ala Met Arg Lys Val Trp Cys Cys Gln Ile  
 290 295 300  
 Leu Leu Lys Arg Asn Gln Leu  
 305 310

&lt;210&gt; 1902

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g820 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1902

Arg Asn Phe Ser Phe Leu Glu Ile Ser Phe Thr Thr Val Cys Ile Pro  
 1 5 10 15  
 Arg Phe Leu Gly Ala Ile Ile Thr Arg Asn Lys Thr Ile Ser Tyr Asn  
 20 25 30  
 Asn Cys Ala Ala Gln Leu Phe Phe Ile Phe Met Gly Val Thr Glu  
 35 40 45  
 Phe Tyr Ile Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys  
 50 55 60  
 Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys Leu Cys Thr Leu  
 65 70 75 80  
 Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Pro Thr Ile Phe Pro Pro  
 85 90 95  
 Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser Asn Val Ile Asp  
 100 105 110  
 His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu Ser Cys Ser Asp  
 115 120 125  
 Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala Leu Val Thr Leu  
 130 135 140  
 Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met Tyr Ile Ile Arg

```

145          150          155          160
Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys Lys Ala Phe Ser
          165          170          175
Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser Tyr Gly Ser Cys
          180          185          190
Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys Ala Ser Leu Thr
          195          200          205
Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro Met Leu
          210          215          220

```

&lt;210&gt; 1903

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g821 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1903

```

Ile Ile Leu Cys Phe Phe Ile Ile Gly Asn Ser Gln Asp Asn Ser Gln
 1          5          10          15
Met Thr Leu Met Asp Asn Ile Ser Glu Val Thr Glu Phe Val Leu Val
          20          25          30
Gly Leu Thr Asp Val Leu Glu Leu Gln Val Pro Leu Phe Ile Ile Phe
          35          40          45
Thr Val Ile Tyr Leu Thr Thr Leu Val Gly Asn Phe Gly Met Ile Met
          50          55          60
Leu Ile Leu Leu Asp Ser Arg Leu His Ile Pro Met Tyr Phe Phe Leu
          65          70          75          80
Gly Lys Leu Ser Leu Val Asp Ser Val Cys Ala Cys Leu Val Thr Gly
          85          90          95
Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His Val Ala Phe Thr
          100          105          110
Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn His Phe Phe Cys
          115          120          125
Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Ile Tyr Ala His
          130          135          140
Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile Phe Phe Thr Leu
145          150          155          160
Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile Ala Ile Leu Arg
          165          170          175
Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser Thr Cys Ala Tyr
          180          185          190
His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile Thr Phe Met Tyr
          195          200          205
Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Ile Ser Ser
          210          215          220
Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr Ser
225          230          235          240
Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val Val Ile Gly Lys
          245          250          255
Ala Lys Ser Ser Leu Gly Leu Ala Tyr Tyr Leu
          260          265

```

&lt;210&gt; 1904

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g822 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1904

```

Trp Xaa Pro Val Phe Asn Gln Ser Ala Pro Leu Gln Phe Val Phe Arg
 1          5          10          15
Val Phe Thr Thr Val Pro Glu Phe Gln Val Leu Leu Phe Leu Leu Phe
      20          25          30
Leu Leu Phe Tyr Leu Met Ile Leu Cys Gly Asn Thr Ala Ile Ile Trp
      35          40          45
Val Val Cys Thr Tyr Ser Val Leu Arg Thr Pro Met Tyr Phe Phe Leu
      50          55          60
Ser Asn Leu Ser Phe Val Glu Ile Cys Tyr Thr Thr Val Val Val Pro
65          70          75          80
Leu Met Leu Ser Asn Ile Phe Gly Ala Gln Lys Pro Ile Pro Leu Ala
      85          90          95
Gly Cys Gly Ala Gln Met Phe Phe Phe Leu Thr Leu Gly Gly Ala Asp
      100          105          110
Cys Phe Leu Leu Ala Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Arg Leu Ile Met Thr Cys Asn Leu Cys Val Gln
      130          135          140
Met Leu Gly Gly Ala Val Gly Leu Ala Leu Phe Leu Ser Leu Gln Leu
145          150          155          160
Thr Ala Leu Ile Phe Thr Leu Pro Phe Cys Gly Tyr Arg Gln Glu Ile
      165          170          175
Asn His Phe Leu Cys Asp Val Pro Pro Val Leu Arg Leu Ala Cys Ala
      180          185          190
Ala Ile Arg Val His Gln Ala Val Leu Tyr Val Val Ser Ile Leu Val
      195          200          205
Leu Thr Val Pro Phe Leu Leu Ile Cys Val Ser Tyr Val Phe Ile Thr
      210          215          220
Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg His Gln Ala Phe
225          230          235          240
Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Leu Gln Tyr Gly Cys
      245          250          255
Cys Ala Leu Ala Tyr Leu His Pro Gln Ser Ser Ser Ser Ala Asp Glu
      260          265          270
Asp Arg Gln Phe Ala Leu Val Tyr Thr Phe Ile Thr Pro Leu Leu Asn
      275          280          285
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu
      290          295          300
Lys Ser Ala Gln Tyr Gln Arg Asp Thr Xaa Val Leu
305          310          315

```

&lt;210&gt; 1905

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g823 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1905

Met Xaa Asn Ser Arg Glu Ala Ser Gln Phe Ile Phe Leu Gly Leu Ser

```

1           5           10           15
Asn Val Pro Glu Leu Gln Val Pro Phe Ile Met Phe Val Leu Ile
20           25           30
Tyr Leu Ile Asn Val Val Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
35           40           45
Trp Tyr Ser Gln Leu His Asn Pro Met Tyr Phe Phe Phe Ser Asn Leu
50           55           60
Ser Leu Val Asp Phe Phe Tyr Ser Ser Val Val Thr Pro Lys Val Met
65           70           75           80
Thr Gly Leu Leu Arg Glu Asp Lys Ile Ile Ser Tyr Thr Val Trp Ala
85           90           95
Thr Gln Thr Phe Phe Ser Asp Ser Phe Ala Ser Val Val Asn Leu Leu
100          105          110
Leu Ala Leu Met Ala Ser Gly His Tyr Ala Ala Val Cys Lys Pro Leu
115          120          125
His Tyr Thr Thr Thr Met Met Thr Ser Val Cys Thr Cys Leu Ala Ile
130          135          140
Gly Xaa Tyr Val Gly Gly Phe Leu Asn Ala Ser Ile His Thr Gly Glu
145          150          155          160
Thr Phe Ser Leu Phe Cys Met Ser Ser Glu Val His His Phe Phe Cys
165          170          175
Glu Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Arg His Val Asn
180          185          190
Val Val Val Leu Val Tyr Val Thr Ser Phe Asn Ile Leu Phe Ala Leu
195          200          205
Leu Val Ile Leu Ile Ser Tyr Leu Leu Met Phe Ile Thr Ile Leu Lys
210          215          220
Met His Ser Thr Ala Gly Tyr Gln Lys Ala Leu Ala Ile Cys Ala Ser
225          230          235          240
His Leu Thr Ala Val Ala Ile Phe Tyr Gly Thr Ile Ile Phe Met His
245          250          255
Ile Gln Pro Ser Ser Ser His Ser Ile Asp Thr Asp Lys Ile Ala Ala
260          265          270
Val Phe Tyr Thr Ile Val Phe Pro Met Val Asn His Val Val Xaa Arg
275          280          285
Leu Lys Asn Lys Val Lys Ser Thr Phe Lys Lys Ile Val Glu Lys Val
290          295          300
Lys Leu Ser Leu Gly Leu Xaa Val
305          310

```

&lt;210&gt; 1906

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g824 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1906

```

Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
1           5           10           15
Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
20           25           30
Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu
35           40           45
Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
50           55           60
Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
65           70           75           80
Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
85           90           95

```



Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu  
 100 105 110  
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala  
 130 135 140  
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His  
 145 150 155 160  
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro  
 165 170 175  
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly  
 180 185 190  
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile  
 195 200 205  
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly  
 210 215 220  
 Ala Asn Leu Ala Met Gly Leu Thr Gln Ser Arg Arg Lys Val Phe Ser  
 225 230 235 240  
 Thr Cys Ser Ser His Arg Leu Val Val Ser Leu Phe Phe Gly Thr Ala  
 245 250 255  
 Ser Ile Thr Asn Asn Arg Pro Gln Ala Gly Ser Ser Glu Thr Thr Asp  
 260 265 270  
 Arg Val Ile Ser Leu Phe Asn Thr Val Ile Thr Pro Met Leu Asn Pro  
 275 280 285  
 Ile Ile Asn Thr His Gly Asn Lys Asp Val Arg Arg Ala Leu Arg Tyr  
 290 295 300  
 Leu Val Lys Arg Arg Arg Pro Ser Pro Gly Arg Gly Ser Gly  
 305 310 315

&lt;210&gt; 1907

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g825 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1907

Met Glu Thr Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu  
 1 5 10 15  
 Gly Leu Ser Ser Asn Pro Lys Leu Gln Lys Pro Leu Phe Ala Ile Phe  
 20 25 30  
 Leu Ile Met Tyr Leu Leu Thr Ala Val Gly Asn Val Leu Ile Ile Leu  
 35 40 45  
 Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro  
 65 70 75 80  
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser Tyr Val  
 85 90 95  
 Gly Cys Leu Ile Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp  
 100 105 110  
 Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Trp His Cys Leu Leu  
 130 135 140  
 Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg  
 145 150 155 160  
 Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys  
 165 170 175  
 His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp

```

      180      185      190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195      200      205
Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val
      210      215      220
Thr Val Leu Arg Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser
225      230      235      240
Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val
      245      250      255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
      290      295      300
Leu Arg His Arg Ile Tyr Ser
305      310

```

<210> 1908  
 <211> 131  
 <212> PRT  
 <213> Unknown (H38g826 protein)

<220>  
 <223> Synthetic construct

```

<400> 1908
Met Lys Asn Lys Thr Val Leu Thr Glu Phe Ile Leu Leu Gly Leu Thr
  1      5      10      15
Asp Val Pro Glu Leu Gln Val Ala Val Phe Thr Phe Leu Phe Leu Ala
      20      25      30
Tyr Leu Leu Ser Ile Leu Gly Asn Leu Thr Ile Leu Ile Leu Thr Leu
      35      40      45
Leu Asp Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
      50      55      60
Ser Phe Leu Glu Ile Ser Phe Thr Asn Ile Phe Ile Pro Arg Val Leu
      65      70      75      80
Ile Ser Ile Thr Thr Gly Asn Lys Ser Ile Ser Phe Ala Gly Cys Phe
      85      90      95
Thr Gln Tyr Phe Phe Ala Met Phe Leu Gly Ala Thr Glu Phe Tyr Leu
      100      105      110
Leu Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Leu Met
      115      120      125
Thr Met His
      130

```

<210> 1909  
 <211> 311  
 <212> PRT  
 <213> Unknown (H38g827 protein)

<220>  
 <223> Synthetic construct

```

<400> 1909
Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
  1      5      10      15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
      20      25      30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
      35      40      45

```

Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro  
 65 70 75 80  
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val  
 85 90 95  
 Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp  
 100 105 110  
 Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys  
 115 120 125  
 Asn Pro Leu His Tyr Asp Val Met Lys Pro Arg His Cys Leu Leu  
 130 135 140  
 Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg  
 145 150 155 160  
 Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys  
 165 170 175  
 His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp  
 180 185 190  
 Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile  
 195 200 205  
 Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val  
 210 215 220  
 Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile  
 245 250 255  
 Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp  
 260 265 270  
 Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275 280 285  
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys  
 290 295 300  
 Leu Gln Asp Arg Ile Tyr Arg  
 305 310

&lt;210&gt; 1910

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g828 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1910

Met Pro Asn Lys Ile Val Val Thr Glu Phe Phe Leu Thr Arg Pro Asp  
 1 5 10 15  
 Gly Leu Gln Lys Ser Phe Gln Val Ala Val Phe Leu Leu Pro Asp Ala  
 20 25 30  
 Cys His Thr Leu Xaa Leu Ser Leu Gly Thr Xaa Ile Ile Ile Thr Met  
 35 40 45  
 Thr Leu Leu Asp Thr Arg Met Gln Thr Ser Met Tyr Leu Phe Leu Gln  
 50 55 60  
 Asn Leu Ser Cys Leu Glu Ile Trp Phe Gln Thr Val Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Leu Asn Ile Ala Met Gly Thr Lys Thr Val Ser Phe Ala Gly  
 85 90 95  
 Cys Ile Thr Gln Asp Phe Phe His Ile Phe Leu Gly Ala Thr Glu Phe

```

      100      105      110
Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Tyr Ile Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Pro Met Leu Ile Ser Ser Arg Val Cys Thr Gln Leu
      130      135      140
Ile Leu Thr Cys Trp Leu Leu Gly Phe Ser Phe Ile Ile Met Pro Val
      145      150      155      160
Ile Leu Thr Ser Gln Leu Pro Phe Cys Asp Thr His Ile Lys His Phe
      165      170      175
Phe Cys Asp Tyr Thr Pro Leu Met Glu Val Val Cys Ser Gly Pro Lys
      180      185      190
Val Leu Glu Met Val Asp Phe Thr Leu Ala Leu Val Ala Leu Phe Gly
      195      200      205
Thr Leu Val Leu Ile Thr Leu Ser Tyr Val Gln Ile Ile Gln Thr Ile
      210      215      220
Val Arg Ile Pro Ala Val Gln Glu Arg Lys Lys Ala Phe Ser Thr Cys
      225      230      235      240
Ser Ser His Val Ile Met Val Thr Met Cys Tyr Asp Ser Cys Phe Phe
      245      250      255
Met Tyr Val Lys Pro Ser Pro Gly Lys Trp Val Asp Val Asn Lys Gly
      260      265      270
Val Ser Leu Ile Asn Thr Ile Ile Ala Pro Leu Leu Asn Pro Phe Ile
      275      280      285
Cys Thr Leu Arg Asn Gln Gln Val Lys Gln Val Met Lys Asp Leu Val
      290      295      300
Arg Lys Met Thr Leu Ser Glu Asn Lys
      305      310

```

&lt;210&gt; 1911

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g829 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1911

```

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
  1      5      10      15
Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
      20      25      30
Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
      35      40      45
Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
      50      55      60
Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala
      65      70      75      80
Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
      85      90      95
Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
      100      105      110
Asp Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      115      120      125
Ala Ile Arg Asn Pro Leu Leu Tyr Thr Thr Ala Met Ser Gln Arg Leu
      130      135      140
Cys Leu Ala Leu Leu Gly Ala Ser Gly Leu Gly Gly Ala Val Ser Ala
      145      150      155      160
Phe Val His Thr Thr Leu Thr Phe Arg Leu Ser Phe Cys Arg Ser Arg
      165      170      175
Lys Ile Asn Ser Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Ile Ser
      180      185      190

```

Cys Ser Asp Thr Ser Leu Asn Glu Leu Leu Leu Phe Ala Ile Cys Gly  
           195                  200                  205  
 Phe Ile Gln Thr Ala Thr Val Leu Ala Ile Thr Val Ser Tyr Gly Phe  
           210                  215                  220  
 Ile Ala Gly Ala Val Ile His Met Arg Ser Val Glu Gly Ser Arg Arg  
 225                  230                  235                  240  
 Ala Ala Ser Thr Gly Gly Ser His Leu Thr Ala Val Ala Met Met Tyr  
                   245                  250                  255  
 Gly Thr Leu Ile Phe Met Tyr Leu Arg Pro Ser Ser Ser Tyr Ala Leu  
                   260                  265                  270  
 Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Ser  
           275                  280                  285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala  
           290                  295                  300  
 Leu Arg Gln Thr Trp Ser Arg Phe His Cys Pro Gly Gln  
 305                  310                  315

&lt;210&gt; 1912

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g830 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1912

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val  
   1                  5                  10                  15  
 Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met  
           20                  25                  30  
 Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile  
           35                  40                  45  
 Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe  
           50                  55                  60  
 Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile  
 65                  70                  75                  80  
 Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser  
           85                  90                  95  
 Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala  
           100                  105                  110  
 Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala  
           115                  120                  125  
 Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys  
           130                  135                  140  
 Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala  
 145                  150                  155                  160  
 Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu  
           165                  170                  175  
 Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys  
           180                  185                  190  
 Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala  
           195                  200                  205  
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val  
           210                  215                  220  
 Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala  
 225                  230                  235                  240  
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly

<400> 1913																
Glu 1	Xaa	Met	Gly	Thr 5	Ser	Asn	Asn	Val	Thr 10	Glu	Phe	Val	Leu	Pro	Gly	15
Leu	Ser	Gln	Asp 20	Pro	Asp	Val	Gln	Lys 25	Ala	Leu	Phe	Val	Met 30	Phe	Leu	
Leu	Thr	Tyr	Asn 35	Val	Thr	Met	Val 40	Gly	Asn	Leu	Leu	Ile 45	Val	Val	Thr	
Ile 50	Ile	Ala	Ile	Ala	Ser	Leu 55	Asp	Ser	Pro	Val	Ser	Phe 60	Phe	Leu	Ala	
Cys 65	Leu	Ser	Phe	Ile	Asp 70	Ala	Val	Tyr	Ser	Thr 75	Ser	Phe	Ser	Pro	Lys	80
Leu	Met	Ile	Asp 85	Leu	Cys	Asp	Lys 90	Lys	Thr	Val	Ser	Phe 95	Leu	Ala		
Cys	Met	Gly	Gln 100	Leu	Phe	Ile	Asn 105	Tyr	Pro	Phe	Gly	Gly 110	Ile	Glu	Val	
Phe 115	Leu	Leu	Val	Gly	Met	Ala 120	Cys	Asp	His	Tyr	Val	Asp 125	Ile	Cys	Lys	
Leu 130	Leu	His	Tyr	Leu	Thr	Ile 135	Met	Asn	Trp	Gln	Val	Cys 140	Ile	Leu	Leu	
Phe 145	Met	Val	Ala	Val	Thr 150	Gly	Gly	Phe	Leu	His	Ser	Met 155	Phe	Gln	Ile	
Val	Val	Val	Tyr	Ser 165	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val 170	Ile	Asp	His	
Phe	Cys	Asp	Met 180	Tyr	Pro	Leu	Leu	Glu	Met	Val	Cys	Thr 190	Asp	Thr	Tyr	
Phe 195	Ile	Gly	Leu	Thr	Val	Ile 200	Ala	Asn	Gly	Gly	Ala	Val 205	Cys	Met	Val	
Ile 210	Phe	Ile	Leu	Leu	Leu	Ile 215	Ser	Tyr	Gly	Val	Ile	Leu 220	Asn	Ser	Leu	
Lys 225	Thr	Tyr	Ser	Gln	Glu	Gly 230	Gly	His	Lys	Ala	Leu	Ser 235	Thr	Cys	Ser	
Ser	Asn	Ile	Thr 245	Val	Ser	Leu	Phe	Phe	Asp	Pro	Cys	Ile 255	Phe	Ile		
Tyr	Val	Arg	Pro	Asp 260	Ser	Asn	Phe	Pro	Ile	Asp	Lys	Phe 270	Met	Thr	Val	
Phe	Tyr	Thr	Ile	Ile 275	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile 285	Tyr	Thr	Leu	
Arg	Asn	Leu	Glu	Val	Arg	Ile 295	Ala	Val	Lys	Asn	Leu	Trp 300	Cys	Lys	Asn	

Xaa Thr Ile Val Arg  
305

<210> 1914

<211> 318

<212> PRT

<213> Unknown (H38g832 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1914

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Pro Phe Leu Phe Trp Phe Phe Ser
          20          25          30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
          35          40          45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
 50          55          60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
65          70          75          80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
          85          90          95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
          100          105          110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
          115          120          125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
130          135          140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
145          150          155          160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
          165          170          175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
          180          185          190
Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
          195          200          205
Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
210          215          220
Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
225          230          235          240
Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu
          245          250          255
Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu Ser
          260          265          270
Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val Ser
          275          280          285
Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser Xaa
          290          295          300
Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro
305          310          315

```

<210> 1915

<211> 309

<212> PRT

<213> Unknown (H38g833 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1915

```

Met Glu Gly Ile Asn Lys Thr Ala Lys Met Gln Phe Phe Phe Arg Pro
 1           5           10           15
Phe Ser Pro Asp Pro Glu Val Gln Met Leu Ile Phe Val Val Phe Leu
          20           25           30
Met Met Tyr Leu Thr Ser Leu Gly Gly Asn Ala Thr Ile Ala Val Ile
          35           40           45
Val Gln Ile Asn His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50           55           60
Asn Leu Ala Val Leu Glu Ile Phe Tyr Thr Ser Ser Ile Thr Pro Leu
65           70           75           80
Ala Leu Ala Asn Leu Leu Ser Met Gly Lys Thr Pro Val Ser Ile Thr
          85           90           95
Gly Cys Gly Thr Gln Met Phe Phe Phe Val Phe Leu Gly Gly Ala Asp
          100          105          110
Cys Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys
          115          120          125
His Pro Leu Arg Tyr Arg Leu Ile Met Ser Trp Ser Leu Cys Val Glu
          130          135          140
Leu Leu Val Gly Ser Leu Val Leu Gly Phe Leu Leu Ser Leu Pro Leu
145          150          155          160
Thr Ile Leu Ile Phe His Leu Pro Phe Cys His Asn Asp Glu Ile Tyr
          165          170          175
His Phe Tyr Cys Asp Met Pro Ala Val Met Arg Leu Ala Cys Ala Asp
          180          185          190
Thr Arg Val His Lys Thr Ala Leu Tyr Ile Ile Ser Phe Ile Val Leu
          195          200          205
Ser Ile Pro Leu Ser Leu Ile Ser Ile Ser Tyr Val Phe Ile Val Val
          210          215          220
Ala Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Gln Ala Tyr Ser
225          230          235          240
Thr Cys Ser Ser His Ile Leu Val Val Leu Leu Gln Tyr Gly Cys Thr
          245          250          255
Ser Phe Ile Tyr Leu Ser Pro Ser Ser Ser Tyr Ser Pro Glu Met Gly
          260          265          270
Arg Val Val Ser Val Ala Tyr Thr Phe Ile Thr Pro Ile Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Leu Lys Asp Ala Leu Arg Lys
          290          295          300
Ala Leu Arg Lys Phe
305

```

&lt;210&gt; 1916

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g834 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1916

```

Asp Ser Val Asp Gln Val Asn Asp Ser Leu Val Thr Glu Phe Val Leu
 1           5           10           15

```



Leu Gly Leu Ala Gln Ser Leu Glu Met Gln Phe Phe Leu Phe Leu Phe  
                   20                  25                  30  
 Phe Ser Leu Phe Tyr Val Gly Ile Ile Leu Gly Asn Leu Phe Ile Val  
           35                  40                  45  
 Phe Thr Val Ile Phe Asp Pro His Leu His Ser Pro Met Tyr Ile Leu  
           50                  55                  60  
 Leu Ala Asn Leu Ser Leu Ile Asp Leu Ser Leu Ser Ser Thr Thr Val  
   65                  70                  75                  80  
 Pro Arg Leu Ile Tyr Asp Leu Phe Thr Asp Cys Lys Val Ile Ser Phe  
                   85                  90                  95  
 His Asn Cys Met Ile Gln Lys Phe Phe Ile His Val Thr Gly Gly Val  
           100                  105                  110  
 Glu Met Val Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile  
           115                  120                  125  
 Cys Lys Pro Leu His Tyr Pro Thr Ile Met Asn Pro Lys Met Cys Met  
           130                  135                  140  
 Phe Leu Val Ala Ala Ala Trp Val Ile Gly Val Ile His Ala Met Ser  
   145                  150                  155                  160  
 Gln Phe Val Phe Val Ile Asn Leu Pro Phe Cys Gly Pro Asn Asn Val  
                   165                  170                  175  
 Gly Ser Phe Tyr Cys Asp Phe Pro Arg Val Ile Lys Leu Ala Cys Met  
           180                  185                  190  
 Asp Thr Tyr Gly Leu Glu Phe Val Val Thr Ala Asn Ser Gly Phe Ile  
           195                  200                  205  
 Ser Met Gly Thr Phe Phe Phe Leu Ile Val Ser Tyr Ile Phe Ile Leu  
           210                  215                  220  
 Val Thr Val Gln Arg His Ser Ser Asn Asp Leu Ser Lys Ala Phe Phe  
   225                  230                  235                  240  
 Thr Ser Xaa Ala His Ile Thr Val Val Val Leu Phe Phe Ala Pro Cys  
                   245                  250                  255  
 Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe  
           260                  265                  270  
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile  
           275                  280                  285  
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn  
           290                  295                  300  
 Gln His Ile Leu Asn Ser Met Glu Met Thr Xaa His Ile Trp Leu Met  
   305                  310                  315                  320  
 Arg Ala Gln Asp Lys Cys His Gly Pro  
                   325

&lt;210&gt; 1917

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g835 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(257)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1917

Ser Met Tyr Phe Phe Leu Thr Asn Phe Ala Gly Leu Glu Ile Phe Tyr  
   1                  5                  10                  15  
 Phe Phe Thr Ile Ala Pro Leu Thr Leu Ala Asn Val Leu Pro Met Gly  
           20                  25                  30  
 Arg Asn Leu Ile Ser Leu Pro Gly Cys Gly Gly Gln Met Phe Phe Phe  
           35                  40                  45  
 Ile Phe Leu Gly Arg Ala Asp Cys Ile Leu Leu Ala Val Met Ala Phe

50	55	60
Asp Trp Phe Val Ala	Ile Cys Cys Pro Leu	Cys Tyr Gly Leu Ile Met
65	70	75
Ser Trp Arg Leu Cys	Val Gln Leu Thr Leu	Gly Ser Leu Leu Leu Gly
85	90	95
Phe Phe Leu Ala Met	Gln Leu Thr Val Leu	Ile Phe Gln Leu Pro Leu
100	105	110
Cys Ser Ser Lys Glu	Ile Ser Thr Phe Tyr	Cys Asp Val Leu Pro Val
115	120	125
Met Arg Leu Ala Cys	Ala Asp Thr Trp Val	His Glu Ala Thr Met Ser
130	135	140
Met Val Ser Thr Thr	Phe Leu Thr Val Pro	Phe Leu Leu Ile Thr Leu
145	150	155
Ser Tyr Val Ser Ile	Met Ala Ala Ile Leu	Lys Ile Cys Ser Ala Glu
165	170	175
Gly Arg His Lys Ala	Phe Ser Thr Cys Ser	Ser His Leu Thr Val Val
180	185	190
Leu Leu Gln Asp Xaa	Cys Thr Arg Leu Ala	Phe Leu Cys Pro Ser Ser
195	200	205
Ser Tyr Tyr Pro Glu	Arg Gly Gln Ala Val	Ser Val Val Tyr Thr Phe
210	215	220
Ile Thr Pro Val Leu	Asn Pro Leu Ile Tyr	Ser Met Arg Asn Thr Glu
225	230	235
Leu Lys Asp Ala Leu	Lys Arg Ala Met Thr	Arg Val Pro Leu Leu Xaa
245	250	255
Thr		

&lt;210&gt; 1918

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g836 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1918

Met Val Thr Glu Phe	Ile Phe Leu Gly Leu	Ser Asp Ser Gln Glu Leu
1	5	10
Gln Thr Phe Leu Phe	Met Leu Phe Phe	Val Phe Tyr Gly Gly Ile Val
20	25	30
Phe Gly Asn Leu Leu	Ile Val Ile Thr	Val Val Ser Asp Ser His Leu
35	40	45
His Ser Pro Met Tyr	Phe Leu Leu Ala	Asn Leu Ser Leu Ile Asp Leu
50	55	60
Ser Leu Ser Ser Val	Thr Ala Pro Lys	Met Ile Thr Asp Phe Phe Ser
65	70	75
Gln Arg Lys Val Ile	Ser Phe Lys Gly	Cys Leu Val Gln Ile Phe Leu
85	90	95
Leu His Phe Phe Gly	Gly Ser Glu Met	Val Ile Leu Ile Ala Met Gly
100	105	110
Phe Asp Arg Tyr Ile	Ala Ile Cys Lys	Pro Leu His Tyr Thr Thr Ile
115	120	125
Met Cys Gly Asn Ala	Cys Val Gly Ile	Met Ala Val Ala Trp Gly Ile
130	135	140
Gly Phe Leu His Ser	Val Ser Gln Leu	Ala Phe Ala Val His Leu Pro
145	150	155
Phe Cys Gly Pro Asn	Glu Val Asp Ser	Phe Tyr Cys Asp Leu Pro Arg
165	170	175
Val Ile Lys Leu Ala	Cys Thr Asp Thr	Tyr Arg Leu Asp Ile Met Val
180	185	190

Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
 195 200 205  
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Cys Pro Leu Asp  
 210 215 220  
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
 225 230 235 240  
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
 245 250 255  
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
 260 265 270  
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
 275 280 285  
 Thr Ala Ile Arg Arg Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
 290 295 300  
 Phe  
 305

&lt;210&gt; 1919

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g837 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1919

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly  
 1 5 10 15  
 Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser  
 20 25 30  
 Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr  
 35 40 45  
 Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala  
 50 55 60  
 Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe  
 65 70 75 80  
 Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe  
 85 90 95  
 Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met  
 100 105 110  
 Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr  
 115 120 125  
 Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile  
 130 135 140  
 Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu  
 145 150 155 160  
 Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro  
 165 170 175  
 Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val  
 180 185 190  
 Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu  
 195 200 205  
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser  
 210 215 220  
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val  
 225 230 235 240  
 Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu

245								250					255			
Pro	Lys	Thr	Thr	His	Asp	Xaa	Tyr	Leu	Phe	Ile	Val	Pro	Leu	Leu	Ser	
260								265					270			
Pro	Leu	Ser	Arg	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Asn	Val	Ser	
275								280					285			
Met	Glu	Arg	Leu	Gly	Lys	Trp	Ile	Ala	Gly	Ser	Ser	Arg	Met	Ser	Xaa	
290								295					300			
Xaa	Met	Val	Leu	Ser	Arg	Val	Gln	Asp	Asp	Ser	Val	Ser	Pro			
305								310					315			

**<210> 1920**

**<211> 328**

<212> PRT

<213> Unknown (H38g838 protein)

**<220>**

<223> Synthetic construct

## <221> VARIANT

<222> (1) . . . (328)

<223> Xaa = Any Amino Acid

**<400> 1920**

Leu 1	Ser	Ile	Cys	Phe 5	Phe	Leu	Cys	Ile	Phe 10	Ser	Ala	Asp	Ile	Xaa 15	Ser
Met	Leu	Ala	Met	Glu	Gln	Asn	Asn	Gly 25	Thr	Glu	Val	Thr	Glu	Phe	Ile
		20											30		
Leu	Leu	Gly	Phe	Ala	Gly	Gln	His	Lys	Ser	Trp	His	Ile	Leu	Ser	Ile
		35					40					45			
Ala	Phe	Leu	Ala	Ile	Tyr	Val	Val	Thr	Pro	Val	Gly	Asn	Ile	Gly	Met
	50					55				60					
Ile	Leu	Leu	Ile	Lys	Ile	Asp	Ala	Ser	Leu	His	Ile	Pro	Met	Xaa	Ile
65				70					75					80	
Phe	Leu	Gln	His	Leu	Ala	Phe	Val	Asp	Leu	Cys	Tyr	Thr	Ser	Ala	Ile
			85					90					95		
Thr	Pro	Lys	Met	Leu	Lys	Asn	Phe	Val	Glu	Thr	Lys	Lys	Ser	Ile	Ser
		100						105					110		
Cys	Ile	Gly	Cys	Met	Val	Gln	Leu	Leu	Val	Tyr	Gly	Thr	Phe	Ala	Thr
		115					120					125			
Ser	Asp	Cys	Tyr	Ile	Leu	Ala	Ala	Met	Ala	Val	Asp	Arg	Tyr	Val	Ala
	130					135					140				
Phe	Cys	Asn	Pro	Leu	His	Tyr	Pro	Gly	Val	Met	Ser	Gln	Arg	Leu	Cys
145				150						155				160	
Ile	Lys	Leu	Leu	Val	Ser	Ser	Tyr	Val	Met	Gly	Phe	Leu	Asn	Ala	Ser
			165					170					175		
Ile	Asn	Ile	Ser	Phe	Thr	Phe	Ser	Leu	Asn	Phe	Cys	Lys	Ser	Lys	Thr
		180						185					190		
Ile	Asn	His	Phe	Phe	Cys	Asp	Glu	Pro	Pro	Ile	Ile	Ala	Leu	Pro	Cys
	195						200					205			
Ser	Asn	Ile	Asp	Leu	Asn	Ile	Met	Leu	Leu	Thr	Val	Phe	Val	Gly	Leu
	210				215						220				
Asn	Leu	Met	Cys	Thr	Val	Met	Val	Val	Ile	Ile	Ser	Cys	Ile	Tyr	Val
225				230					235					240	
Leu	Val	Ala	Ile	Leu	Arg	Ile	Ser	Ser	Ala	Ala	Gly	Lys	Lys	Lys	Ser
			245					250					255		
Leu	Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Gly
		260						265					270		
Val	Leu	Ser	Tyr	Met	Tyr	Leu	Cys	His	Arg	Ile	Asn	Glu	Ser	Gln	Lys
	275						280					285			
Gln	Glu	Lys	Val	Ala	Ser	Val	Phe	Tyr	Gly	Ile	Ile	Ile	Pro	Met	Leu
	290					295					300				

Asn Pro Leu Ile Tyr Ser Gln Arg Asn Gln Asp Val Ile Glu Ala Ile  
 305 310 315 320  
 Lys L u Thr Glu Lys Lys Tyr Phe  
 325

<210> 1921  
 <211> 338  
 <212> PRT  
 <213> Unknown (H38g839 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(338)  
 <223> Xaa = Any Amino Acid

<400> 1921  
 Met Ile Ser Phe Leu Val Pro Gly Leu Met Glu Glu Glu Asn Gln Arg  
 1 5 10 15  
 Gly Val Val His Phe His Phe His Phe Phe Ser Thr Asp Leu Val Val  
 20 25 30  
 Ala Ser Phe Ile Ile Val Ala Leu Met Leu His Leu Arg Ser Leu Val  
 35 40 45  
 Gly His Phe Thr Phe Gly Pro Thr Val Trp Gln Asp Pro Phe Leu His  
 50 55 60  
 Ile Pro Met Tyr Leu Phe Leu Phe Ser Leu Ala Leu Thr Met Leu Glu  
 65 70 75 80  
 Ile Gly Tyr Ser Thr Asn Ile Ser Pro Pro Thr Leu Ala Thr Val Leu  
 85 90 95  
 Tyr Met Gly Lys Met Leu Ile Ser Leu Pro Gly Tyr Gly Thr Gln Met  
 100 105 110  
 Leu Phe Val Ile Leu Leu Arg Gly Ser Glu Cys Val Leu Leu Ala Val  
 115 120 125  
 Met Ala Tyr Asp Arg Tyr Ile Thr Ile Cys His Pro Phe Asn Tyr Asn  
 130 135 140  
 Leu Ile Met Ser Gly Xaa Leu Cys Gly Gln Met Thr Leu Gly Ser Leu  
 145 150 155 160  
 Arg Leu Gly Phe Leu Leu Ser Leu Phe Leu Thr Met Leu Ile Xaa His  
 165 170 175  
 Pro Pro Phe Cys Gly Leu Asp Glu Thr Tyr His Phe Phe Cys Asp Met  
 180 185 190  
 Pro Thr Ala Ser Arg Leu Val Cys Ala Asp Thr Thr Val His Glu Ser  
 195 200 205  
 Ala Leu Xaa Leu Pro Cys Gly His His His His Pro Leu Pro Ser Ser  
 210 215 220  
 Leu Ile Cys Leu Pro Tyr Gly Cys Leu Ala Ala Thr Ile Leu Arg Met  
 225 230 235 240  
 His Ser Ala Lys Arg Lys His Xaa Ala Phe Ser Thr Ser Ser Ser His  
 245 250 255  
 Leu Ile Val Val Leu Leu Lys Tyr Trp Cys Cys Ile Leu Ile Cys Leu  
 260 265 270  
 Cys Pro Ser Ser Tyr Ser Pro Glu Glu Gly Trp Glu Val Ser Leu  
 275 280 285  
 Val His Met Phe Ile Leu Pro Val Trp Asn Pro Leu Ile Tyr Ser Val  
 290 295 300  
 Trp Asn Gln Asp Val Thr Asp Ala Val Glu Arg Leu Val Ala Arg Met  
 305 310 315 320  
 Ser Leu Val Leu Thr Ala Arg Asn Ile Pro Ser Xaa Lys Ile Phe Pro  
 325 330 335  
 Xaa Leu

<210> 1922  
 <211> 329  
 <212> PRT  
 <213> Unknown (H38g840 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(329)  
 <223> Xaa = Any Amino Acid

<400> 1922  
 Asp Ser Val Asp Gln Val Asn Asp Ser Leu Val Thr Glu Phe Val Leu  
 1 5 10 15  
 Leu Gly Leu Ala Gln Ser Leu Glu Met Gln Phe Phe Leu Phe Leu Phe  
 20 25 30  
 Phe Ser Leu Phe Tyr Val Gly Ile Leu Gly Asn Leu Phe Ile Val  
 35 40 45  
 Phe Thr Val Ile Phe Asp Pro His Leu His Ser Pro Met Tyr Ile Leu  
 50 55 60  
 Leu Ala Asn Leu Ser Leu Ile Asp Leu Ser Leu Ser Ser Thr Thr Val  
 65 70 75 80  
 Pro Arg Leu Ile Tyr Asp Leu Phe Thr Asp Cys Lys Val Ile Ser Phe  
 85 90 95  
 His Asn Cys Met Ile Gln Lys Phe Phe Ile His Val Thr Gly Gly Val  
 100 105 110  
 Glu Met Val Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile  
 115 120 125  
 Cys Lys Pro Leu His Tyr Pro Thr Ile Met Asn Pro Lys Met Cys Met  
 130 135 140  
 Phe Leu Val Ala Ala Ala Trp Val Ile Gly Val Ile His Ala Met Ser  
 145 150 155 160  
 Gln Phe Val Phe Val Ile Asn Leu Pro Phe Cys Gly Pro Asn Asn Val  
 165 170 175  
 Gly Ser Phe Tyr Cys Asp Phe Pro Arg Val Ile Lys Leu Ala Cys Met  
 180 185 190  
 Asp Thr Tyr Gly Leu Glu Phe Val Val Thr Ala Asn Ser Gly Phe Ile  
 195 200 205  
 Ser Met Gly Thr Phe Phe Phe Leu Ile Val Ser Tyr Ile Phe Ile Leu  
 210 215 220  
 Val Thr Val Gln Arg His Ser Ser Asn Asp Leu Ser Lys Ala Phe Phe  
 225 230 235 240  
 Thr Ser Xaa Ala His Ile Thr Val Val Val Leu Phe Phe Ala Pro Cys  
 245 250 255  
 Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe  
 260 265 270  
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn  
 290 295 300  
 Gln His Ile Leu Asn Ser Met Glu Met Thr Xaa His Ile Trp Leu Met  
 305 310 315 320  
 Arg Ala Gln Asp Lys Cys His Gly Pro  
 325

<210> 1923  
 <211> 245  
 <212> PRT

<213> Unknown (H38g841 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(245)

<223> Xaa = Any Amino Acid

<400> 1923

```

Met Gln Ser Glu His Leu Ala Glu Phe Ser Glu Phe Leu Ile Leu Ser
 1              5              10              15
Leu Ser Glu Ile Gln Asn Cys Ser Pro Phe Phe Gly Leu Phe Leu Ser
      20              25              30
Met Asn Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
      35              40              45
Ser Ser Asp Ser His Leu His Lys Pro Met Tyr Phe Leu Leu Ser Lys
 50              55              60
Leu Ser Met Ala Ala Ile Cys Phe Val Phe Thr Met Ile Gln Lys Met
65              70              75              80
Met Val Asn Leu Arg Ala Gln Ser Lys Asp Ile Phe Thr Gln Pro Ser
      85              90              95
Gly Ser Pro Ile Pro Phe Xaa Met Cys Ser Leu Ile Arg Phe Leu Leu
      100             105             110
Ile Gln Gln Lys Ser Val Val Leu Ile Phe Glu Tyr Ser Arg Phe Xaa
      115             120             125
Phe Ser Tyr Leu Asn Leu Lys Met Xaa Thr Asn Tyr Ser Phe Val Xaa
      130             135             140
Ala Phe Gln Asn Asn Xaa Arg Gln Leu Cys Pro Phe Leu Asp Asn His
      145             150             155             160
His Thr Phe Phe Thr Leu Ile Asp Thr Gln Leu Leu Ile Ser His Gly
      165             170             175
Phe Ser Thr Gln Thr Thr Phe Ile Leu Ser Ser Tyr Ala Ser Gly Tyr
      180             185             190
Ala Thr Val Asp Ser Gln Cys Phe Ile Tyr Phe Leu Asn Met Met Ile
      195             200             205
Thr Ile Asn Leu Phe Val Arg Phe Lys Asn Ile Phe Met His Ser Ser
      210             215             220
Ile Ser Ile Asn Tyr Asn Tyr Tyr Phe Lys Lys Xaa Asn Lys Gly Gly
      225             230             235             240
Ile Tyr Glu Ile Tyr
              245

```

<210> 1924

<211> 305

<212> PRT

<213> Unknown (H38g842 protein)

<220>

<223> Synthetic construct

<400> 1924

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1              5              10              15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20              25              30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
      35              40              45
His Ser Pro Met Tyr Phe Leu Ala Asn Leu Ser Leu Ile Asp Leu
      50              55              60
Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser

```

65					70					75				80	
Gln	Arg	Lys	Val	Ile	Ser	Phe	Lys	Gly	Cys	Leu	Val	Gln	Ile	Phe	Leu
				85					90					95	
Leu	His	Phe	Phe	Gly	Gly	Ser	Glu	Met	Val	Ile	Leu	Ile	Ala	Met	Gly
			100					105					110		
Phe	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Thr	Thr	Ile
	115						120					125			
Met	Cys	Gly	Asn	Ala	Cys	Val	Gly	Ile	Met	Ala	Val	Ala	Trp	Gly	Ile
	130					135					140				
Gly	Phe	Leu	His	Ser	Val	Ser	Gln	Leu	Ala	Phe	Ala	Val	His	Leu	Pro
145					150					155					160
Phe	Cys	Gly	Pro	Asn	Glu	Val	Asp	Ser	Phe	Tyr	Cys	Asp	Leu	Pro	Arg
			165					170					175		
Val	Ile	Lys	Leu	Ala	Cys	Thr	Asp	Thr	Tyr	Arg	Leu	Asp	Ile	Met	Val
		180					185						190		
Ile	Ala	Asn	Ser	Gly	Val	Leu	Thr	Val	Cys	Ser	Phe	Val	Leu	Leu	Ile
	195						200					205			
Ile	Ser	Tyr	Thr	Ile	Ile	Leu	Met	Thr	Ile	Gln	His	Arg	Pro	Leu	Asp
	210					215					220				
Lys	Ser	Ser	Lys	Ala	Leu	Ser	Thr	Leu	Thr	Ala	His	Ile	Thr	Val	Val
225					230					235					240
Leu	Leu	Phe	Phe	Gly	Pro	Cys	Val	Phe	Ile	Tyr	Ala	Trp	Pro	Phe	Pro
				245					250					255	
Ile	Lys	Ser	Leu	Asp	Lys	Phe	Leu	Ala	Val	Phe	Tyr	Ser	Val	Ile	Thr
		260					265					270			
Pro	Leu	Leu	Asn	Pro	Ile	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys
	275						280					285			
Thr	Ala	Ile	Arg	Arg	Leu	Arg	Lys	Trp	Asp	Ala	His	Ser	Ser	Val	Lys
	290					295					300				

Phe  
305

<210> 1925

<211> 309

<212> PRT

<213> Unknown (H38g843 protein)

<220>

<223> Synthetic construct

<400> 1925

Met	Ala	Ala	Gly	Asn	His	Ser	Thr	Val	Thr	Glu	Phe	Ile	Leu	Lys	Gly
1				5					10					15	
Leu	Thr	Lys	Arg	Ala	Asp	Leu	Gln	Leu	Pro	Leu	Phe	Leu	Leu	Phe	Leu
		20					25					30			
Gly	Ile	Tyr	Leu	Val	Thr	Ile	Val	Gly	Asn	Leu	Gly	Met	Ile	Thr	Leu
	35					40					45				
Ile	Cys	Leu	Asn	Ser	Gln	Leu	His	Thr	Pro	Met	Tyr	Tyr	Phe	Leu	Ser
	50					55				60					
Asn	Leu	Ser	Leu	Met	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Ile	Thr	Pro	Lys
65					70					75				80	
Met	Leu	Val	Asn	Phe	Val	Ser	Glu	Lys	Asn	Ile	Ile	Ser	Tyr	Ala	Gly
			85						90					95	
Cys	Met	Ser	Gln	Leu	Tyr	Phe	Phe	Leu	Val	Phe	Val	Ile	Ala	Glu	Cys
		100						105					110		
Tyr	Met	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
	115					120						125			
Pro	Leu	Leu	Tyr	Asn	Ile	Ile	Met	Ser	His	His	Thr	Cys	Leu	Leu	Leu
	130					135					140				
Val	Ala	Val	Val	Tyr	Ala	Ile	Gly	Leu	Ile	Gly	Ser	Thr	Ile	Glu	Thr
145					150					155					160



Gly Leu M t Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr  
 165 170 175  
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr  
 180 185 190  
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val  
 195 200 205  
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile  
 210 215 220  
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe  
 245 250 255  
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val  
 260 265 270  
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu  
 290 295 300  
 Arg Gly Lys Leu Phe  
 305

<210> 1926

<211> 310

<212> PRT

<213> Unknown (H38g844 protein)

<220>

<223> Synthetic construct

<400> 1926

Met Ala Ala Lys Asn Ser Ser Val Thr Glu Phe Ile Leu Glu Gly Leu  
 1 5 10 15  
 Thr His Gln Pro Gly Leu Arg Ile Pro Leu Phe Phe Leu Phe Leu Gly  
 20 25 30  
 Phe Tyr Thr Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu Ile  
 35 40 45  
 Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn  
 50 55 60  
 Leu Ser Leu Ile Asp Phe Cys Phe Ser Thr Thr Ile Thr Pro Lys Met  
 65 70 75 80  
 Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly Cys  
 85 90 95  
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Val Ser Glu Ser Phe  
 100 105 110  
 Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 115 120 125  
 Leu Leu Tyr Thr Val Thr Met Ser Cys Gln Val Cys Leu Leu Leu Leu  
 130 135 140  
 Leu Gly Ala Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr Gly  
 145 150 155 160  
 Ser Ile Met Asn Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His Phe  
 165 170 175  
 Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr  
 180 185 190  
 Met Asn Glu Leu Val Val Phe Ile Val Val Ala Val Asp Val Gly Met  
 195 200 205  
 Pro Ile Val Thr Val Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser Ile  
 210 215 220  
 Leu His Asn Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe

[illegible]

<210> 1927  
<211> 157  
<212> PRT  
<213> Unknown (H38g845 protein)

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(157)
<223> Xaa = Any Amino Acid
```

<400> 1927																
Met	Gly	Glu	Ala	Arg	Asn	Arg	Thr	Val	Val	Gln	Glu	Phe	Ile	Leu	Glu	
1				5					10					15		
Gly	Phe	Pro	Ala	Val	Gln	His	Leu	Gly	Asn	Val	Leu	Phe	Leu	Val	His	
			20					25					30			
Leu	Leu	Ala	Tyr	Leu	Ala	Ser	Ile	Met	Ala	Asn	Met	Leu	Ile	Ile	Thr	
			35				40					45				
Ile	Thr	Trp	Ala	Asp	His	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	
	50					55					60					
Ser	Ser	Phe	Ser	Phe	Cys	Glu	Cys	Cys	Phe	Ile	Thr	Thr	Val	Ile	Pro	
65					70					75					80	
Lys	Leu	Leu	Val	Ile	Leu	Leu	Ser	Gly	Arg	Ala	Lys	Ile	Pro	Leu	Ser	
				85					90					95		
Thr	Thr	Leu	Ser	His	Ala	Val	Pro	Phe	Ser	Phe	Leu	Tyr	Ser	Trp	Val	
				100				105					110			
Asn	Ser	Phe	Ser	Ser	Leu	Asn	Gly	Cys	Asp	Val	Pro	Leu	Asp	Xaa	Tyr	
		115					120					125				
Leu	Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Leu	Arg	
	130					135					140					
Thr	Ser	Phe	His	Lys	Val	Thr	Ala	Trp	Leu	Cys	Pro	Gly				
145					150					155						

<210> 1928  
<211> 333  
<212> PRT  
<213> Unknown (H38g846 protein)

<220>  
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(333)
<223> Xaa = Any Amino Acid
```

<400> 1928

Thr	Asp	Pro	Gln	Asn	Leu	Thr	Thr	Asp	Val	Ser	Ile	Phe	Leu	Val	Leu
1				5				10						15	
Glu	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		

Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Leu Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 100 105 110  
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Leu Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys Gly  
 130 135 140  
 Phe Leu Val Leu Leu Ser Cys Cys Leu Ser Leu Leu Asp Ser Gln Leu  
 145 150 155 160  
 His Asn Leu Ile Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile  
 165 170 175  
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His His Ala Cys Cys  
 180 185 190  
 Asp Thr Phe Thr Asn Asn Ile Val Met Tyr Phe Pro Ala Ala Ile Phe  
 195 200 205  
 Gly Phe Leu Pro Thr Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val  
 210 215 220  
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala Leu  
 225 230 235 240  
 Ser Ala Cys Gly Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr  
 245 250 255  
 Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys  
 260 265 270  
 Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn  
 275 280 285  
 Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg  
 290 295 300  
 Arg Leu His Gly Arg Thr Val Xaa Ser Gln Tyr Leu Ile Ile Cys Ser  
 305 310 315 320  
 Ile Pro Phe Val Val Trp Val Xaa Lys Gly Ser Lys Val  
 325 330

&lt;210&gt; 1929

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g847 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1929

Ser Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Leu Pro  
 1 5 10 15  
 Lys Met Ile Phe Ser Tyr Leu Ser Gly Lys Lys Ser Ile Ser Leu Ala  
 20 25 30  
 Gly Cys Gly Thr Gln Ile Phe Phe Tyr Val Ser Leu Leu Gly Ala Glu  
 35 40 45  
 Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 50 55 60  
 His Pro Leu Gln Tyr Thr Ile Leu Met Asn Pro Glu Leu Cys Val Phe  
 65 70 75 80  
 Met Thr Val Ala Ser Trp Thr Leu Gly Ser Leu Asp Gly Ile Ile Val  
 85 90 95  
 Leu Ala Ala Val Leu Ser Phe Ser Tyr Cys Ser Ser Leu Glu Ile His

```

      100      105      110
His Phe Phe Cys Asp Val Ala Ala Leu Leu Pro Leu Ser Cys Thr Glu
      115      120      125
Thr Ser Ala Phe Glu Arg Leu Leu Val Ile Cys Cys Val Val Met Leu
      130      135      140
Ile Phe Pro Val Ser Val Ile Ile Leu Ser Tyr Ser His Val Leu Arg
      145      150      155      160
Ala Val Ile His Met Gly Ser Gly Glu Ser Arg Arg Lys Ala Phe Thr
      165      170      175
Thr Cys Ser Ser His Pro Ser Val Val Gly Leu Tyr Tyr Gly Ala Ala
      180      185      190
Met Phe Met Tyr Met Arg Pro Ala Ser Lys His Thr Pro Asp Gln Asp
      195      200      205
Lys Met Val Ser Ala Phe Tyr Thr Asn Leu Thr Pro Met Leu
      210      215      220

```

&lt;210&gt; 1930

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g848 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(114)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1930

```

Leu Ala Cys Ile Val Gly Xaa Lys Phe Ala Phe Ile Ile Ser Pro Asn
 1      5      10      15
His His Phe Met Ile Met Val Thr Phe Ile Leu Val Asn Ile Xaa Lys
      20      25      30
His Ser Ser Gly Asn Leu Ser Ser Ala Leu Ile Ile Leu Phe Ile Phe
      35      40      45
Ile Pro Val Val Ser Leu Phe Phe Thr Pro Cys Val Val Leu Tyr Val
      50      55      60
Trp Pro Thr Leu Pro Pro Ser Leu Asp Lys Asn Met Phe Ile Val Asp
      65      70      75      80
Phe Val Val Asn Pro Val Leu Lys Pro Ala Thr Tyr Ile Leu Gln Asn
      85      90      95
Lys Asp Ile Lys Val Ala Leu Xaa Asn Leu His Glu Lys Arg Thr Tyr
      100      105      110
Ser Ser

```

&lt;210&gt; 1931

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g849 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1931

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
 1      5      10      15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20      25      30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
      35      40      45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu  
 50 55 60  
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser  
 65 70 75 80  
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu  
 85 90 95  
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly  
 100 105 110  
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile  
 115 120 125  
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile  
 130 135 140  
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro  
 145 150 155 160  
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
 165 170 175  
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val  
 180 185 190  
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
 195 200 205  
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp  
 210 215 220  
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
 225 230 235 240  
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
 245 250 255  
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
 260 265 270  
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
 275 280 285  
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
 290 295 300  
 Phe  
 305

&lt;210&gt; 1932

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g850 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1) ... (223)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1932

Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro  
 1 5 10 15  
 Lys Met Val Val Asp Ile Gln Ser His Ser Arg Ser Phe Ser Tyr Ala  
 20 25 30  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 35 40 45  
 Glu Thr Leu Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile  
 50 55 60  
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly  
 65 70 75 80  
 Phe Leu Leu Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln  
 85 90 95  
 Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu

	100		105		110										
Ile	Pro	Asn	Phe	Leu	Cys	Asp	Pro	Ser	Pro	Leu	Pro	His	Leu	Ala	Cys
	115						120					125			
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile
	130					135					140				
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	Ile
145					150					155				160	
Val	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala
			165						170					175	
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	Gly
			180					185					190		
Thr	Gly	Val	Gly	Gly	Tyr	Leu	Gly	Ser	Asp	Val	Ser	Ser	Ser	Pro	Arg
		195				200						205			
Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	
	210					215						220			

&lt;210&gt; 1933

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g851 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1933

Asp	Ser	Val	Asp	Gln	Val	Asn	Asp	Ser	Leu	Val	Thr	Glu	Phe	Val	Leu
1				5					10					15	
Leu	Gly	Leu	Ala	Gln	Ser	Leu	Glu	Met	Gln	Phe	Phe	Leu	Phe	Leu	Phe
			20					25					30		
Phe	Ser	Leu	Phe	Tyr	Val	Gly	Ile	Ile	Leu	Gly	Asn	Leu	Phe	Ile	Val
		35				40					45				
Phe	Thr	Val	Ile	Phe	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Ile	Leu
		50				55					60				
Leu	Ala	Asn	Leu	Ser	Leu	Ile	Asp	Leu	Ser	Leu	Ser	Ser	Thr	Thr	Val
65					70					75				80	
Pro	Arg	Leu	Ile	Tyr	Asp	Leu	Phe	Thr	Asp	Cys	Lys	Val	Ile	Ser	Phe
				85					90					95	
His	Asn	Cys	Met	Ile	Gln	Lys	Phe	Phe	Ile	His	Val	Thr	Gly	Gly	Val
		100						105					110		
Glu	Met	Val	Leu	Leu	Ile	Val	Met	Glu	Tyr	Asp	Arg	Tyr	Thr	Ala	Ile
		115				120						125			
Cys	Lys	Pro	Leu	His	Tyr	Pro	Thr	Ile	Met	Asn	Pro	Lys	Met	Cys	Met
		130				135					140				
Phe	Leu	Val	Ala	Ala	Ala	Trp	Val	Ile	Gly	Val	Ile	His	Ala	Met	Ser
145					150					155				160	
Gln	Phe	Val	Phe	Val	Ile	Asn	Xaa	Pro	Phe	Cys	Gly	Pro	Asn	Asn	Val
				165					170					175	
Gly	Ser	Phe	Tyr	Cys	Asp	Phe	Pro	Arg	Val	Ile	Lys	Leu	Ala	Cys	Met
			180					185					190		
Asp	Thr	Tyr	Gly	Leu	Glu	Phe	Val	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile
		195					200					205			
Ser	Met	Gly	Thr	Phe	Phe	Phe	Leu	Ile	Val	Ser	Tyr	Ile	Phe	Ile	Leu
		210				215						220			
Val	Thr	Val	Gln	Arg	His	Ser	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe
225					230					235				240	
Thr	Ser	Xaa	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Ala	Pro	Cys
				245					250					255	

Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe  
                   260                                  265                                  270  
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile  
                   275                                  280                                  285  
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn  
                   290                                  295                                  300  
 Gln His Ile Leu Asn Ser Met Glu Thr Thr Xaa His Ile Trp Leu Met  
 305                                  310                                  315                                  320  
 Arg Ala Gln Asp Lys Cys His Gly Pro  
                                   325

<210> 1934  
 <211> 220  
 <212> PRT  
 <213> Unknown (H38g852 protein)

<220>  
 <223> Synthetic construct

<400> 1934  
 Ser Val Leu Ser Ile Ser Glu Thr Tyr Tyr Thr Val Ala Ile Asn Pro  
   1                                  5                                  10                                  15  
 Gln Met Leu Ser Gly Leu Leu Ser Pro Gln Gln Thr Ile Ser Ile Pro  
                   20                                  25                                  30  
 Gly Cys Ala Ala Gln Leu Phe Phe Tyr Leu Thr Phe Gly Val Asn Lys  
                   35                                  40                                  45  
 Cys Phe Leu Leu Thr Ala Met Gly Tyr Asp His Tyr Val Ala Ile Cys  
   50                                  55                                  60  
 Asn Pro Leu Gln Tyr Ser Val Ile Met Gly Lys Lys Ala Cys Ile Gln  
 65                                  70                                  75                                  80  
 Leu Val Ser Gly Ser Trp Asn Ile Gly Leu Ser Thr Ala Ile Ile Gln  
                   85                                  90                                  95  
 Val Ser Ser Val Phe Ser Leu Pro Phe Cys Asp Ala Asn Leu Ile Ser  
                   100                                  105                                  110  
 His Phe Phe Cys Asp Ile Arg Pro Ile Met Lys Leu Ala Cys Ala Asp  
                   115                                  120                                  125  
 Thr Thr Ile Lys Glu Phe Ile Thr Leu Leu Ile Ser Leu Cys Val Leu  
   130                                  135                                  140  
 Val Leu Pro Met Val Leu Ile Phe Ile Ser Tyr Val Leu Ile Val Thr  
 145                                  150                                  155                                  160  
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala  
                   165                                  170                                  175  
 Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Arg Thr  
                   180                                  185                                  190  
 Ser Phe Ile Tyr Leu Lys Pro Lys Ser Gln Asn Ser Leu Gln Asp Arg  
                   195                                  200                                  205  
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu  
                   210                                  215                                  220

<210> 1935  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g853 protein)

<220>  
 <223> Synthetic construct

<400> 1935  
 Met Ser Thr Ser Asn His Thr Gln Phe His Pro Ser Ser Phe Leu Leu  
   1                                  5                                  10                                  15  
 Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Val Pro

```
<210> 1936
<211> 295
<212> PRT
<213> Unknown (H38g854 protein)
```

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(295)  
<223> Xaa = Any Amino Acid

```

<400> 1936
Tyr Met Ile Thr Ile Leu Trp Glu Ile Ser Lys Pro Val Asn Asn Ile
  1             5             10             15
Phe Leu Thr Leu Ser Val Arg Tyr Gln Met Leu Ile Thr Thr Val Ser
      20             25             30
Xaa Leu Xaa Met Lys Ser Ile Ile Xaa Ile Tyr Xaa Ser Phe Ser Glu
      35             40             45
Tyr Leu Met Ser Xaa Lys Ile Trp Glu His Met Xaa Tyr Cys Ala Cys
      50             55             60
Ile Asn Met Asp Lys Val Ser Glu Val Phe Ser Glu His Leu Phe Gly
65             70             75             80

```



Ala Ala Glu Ile Ile Pro Leu Met Gly Met Val His Gly Cys Tyr Val  
85 90 95  
Thr Ile Cys Thr Ala Xaa Asn Ile Met Thr Gln Tyr Arg Cys Gly His  
100 105 110  
Leu Ala Gly Met Ala Cys Thr Gly Arg Phe Ile His Gly Thr Val Xaa  
115 120 125  
Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr Asn Ser Asn Val Thr Ile  
130 135 140  
Xaa Ile Ala His Phe Ile Cys Asp Leu Asn Thr Leu Leu Lys Leu Leu  
145 150 155 160  
Cys Ile Gly Ser His Asp Thr Leu Gly Leu Phe Val Ala Ala Asn Asp  
165 170 175  
Gly Phe Asn Cys Leu Leu Asn Ile Ile Phe Leu Met Val Ser Xaa Val  
180 185 190  
Ala Ile Leu Tyr Thr Leu Lys Ser His Ser Leu Glu Glu Arg Tyr Lys  
195 200 205  
Ala Leu Ser Thr Cys Val Ser His Thr Thr Val Ala Ile Xaa Phe Phe  
210 215 220  
Val Phe Cys Ile Leu Val Tyr Leu Cys Pro Val Thr Leu Leu Pro Val  
225 230 235 240  
Ser Lys Ala Val Ala Val Leu Tyr Thr Met Ile Thr Pro Thr Leu Asn  
245 250 255  
Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Val Glu Lys  
260 265 270  
Leu Leu Gly Gln Lys Met Thr Xaa Arg Glu Lys Xaa Ser Lys His Lys  
275 280 285  
Met Ile Leu Leu Phe Gln Trp  
290 295

&lt;210&gt; 1937

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g855 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1937

Met Glu Lys Lys Lys Asn Val Thr Glu Phe Ile Leu Ile Gly Leu Thr  
1 5 10 15  
Gln Asn Pro Ile Met Glu Lys Val Thr Phe Val Val Phe Leu Val Leu  
20 25 30  
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Ile Val Val Thr Ile Thr  
35 40 45  
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Thr His Leu  
50 55 60  
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ala Pro Lys Leu Ile  
65 70 75 80  
Val Asp Ser Phe Gln Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met  
85 90 95  
Ala Gln Ala Tyr Ala Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu  
100 105 110  
Leu Thr Val Met Ala Cys Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu  
115 120 125  
Asn Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Ala  
130 135 140  
Val Ala Trp Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe  
145 150 155 160  
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Gly His Phe Met  
165 170 175  
Cys Asp Leu Tyr Pro Leu Leu Lys Leu Val Cys Ile Asp Thr His Thr

```

      180      185      190
Leu Gly Leu Phe Val Ala Val Asn Ser Gly Phe Ile Cys Leu Leu Asn
      195      200      205
Phe Leu Ile Leu Val Val Ser Tyr Val Ile Ile Leu Arg Ser Leu Lys
      210      215      220
Asn Asn Ser Leu Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ile Ser
      225      230      235      240
His Ile Ile Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
      245      250      255
Leu Arg Ser Val Thr Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
      260      265      270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Val Val Tyr Thr Leu Arg
      275      280      285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
      290      295      300
Thr Ser Asp Asn Asp
305

```

&lt;210&gt; 1938

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g856 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(246)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1938

```

Cys Ile Gln Gln His Xaa Ser Pro Leu Cys Leu Cys Met Phe Ser Phe
  1           5           10           15
Tyr Phe Asn Leu Tyr His Phe Phe Pro Lys Xaa Lys Tyr Leu His Ser
      20      25      30
Leu Arg Asp Ala Glu Ile Asn Xaa Leu Val Xaa Ser Lys Val Leu Ile
      35      40      45
Asn Gln Ile Tyr Thr Lys Ala Asn Trp Pro Phe His Gly Leu Xaa His
      50      55      60
Tyr Ala Gln Pro Leu His Thr Gln Thr Cys Ile Ser Phe Ser Asn Val
      65      70      75      80
Ile Xaa Cys Ser Thr Xaa Leu Phe Thr Gly His Phe Phe Leu Gly Gly
      85      90      95
Ser Gln Ile Phe Leu Leu Leu Val Met Ala Tyr Gly His Tyr Arg Ala
      100     105     110
Ile Cys Lys Ser Leu Gln Tyr Leu Val Val Met Lys Gln Trp Leu Cys
      115     120     125
Val Val Leu Leu Val Val Ser Trp Ala Gly Gly Phe Leu His Ile Val
      130     135     140
Ile Gln Leu Gly Leu Ile Tyr Gly Leu Pro Ser Tyr Asp Pro Asn Val
      145     150     155     160
Ile Gly His Phe Ile Cys Asp Met Asp Pro Leu Met Lys Leu Val Cys
      165     170     175
Asp Tyr Thr Leu Asn Arg Phe Ala Tyr Phe Ala Gly His Asp Xaa Ile
      180     185     190
Leu Gly Phe Met Tyr Phe Thr Tyr Ala Gln Thr Gly Leu Phe Pro Phe
      195     200     205
Gly Asp Ser Thr Ser Leu Phe Phe Cys His Phe Phe Pro Arg Gly Leu
      210     215     220
Gly Ser Ile Asn Leu Ala Ile His Ser Tyr Tyr Pro Cys Gly Ile Ser
      225     230     235     240

```

Arg Asp Thr Glu Pro Thr  
245

<210> 1939  
<211> 262  
<212> PRT  
<213> Unknown (H38g857 protein)

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(262)  
<223> Xaa = Any Amino Acid

<400> 1939  
Leu Ile Val Val Thr Val Thr Val Ser Glu Thr Leu Gly Ser Pro Met  
1 5 10 15  
Tyr Phe Phe Leu Ala Gly Leu Ser Phe Ile Asp Ile Ile Tyr Ser Ser  
20 25 30  
Ser Ile Ser His Arg Leu Ile Ser Asp Leu Phe Phe Gly Asn Asn Ser  
35 40 45  
Ile Ser Phe Pro Ser Cys Leu Ala Gln Leu Phe Thr Glu His Leu Phe  
50 55 60  
Gly Gly Ser Glu Val Phe Leu Leu Leu Val Met Ala Tyr Asp Leu His  
65 70 75 80  
Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Val Ala  
85 90 95  
Ser Trp Val Gly Gly Phe Leu His Ser Val Phe Gln Leu Ser Val Ile  
100 105 110  
Tyr Gly Leu Pro Phe Cys Asp Leu Asn Val Ile Asp His Phe Phe Cys  
115 120 125  
Asp Met His Pro Leu Leu Lys Leu Val Cys Thr Asp Thr His Val Ile  
130 135 140  
Gly Leu Leu Val Val Ala Asn Gly Gly Leu Gly Cys Thr Ile Val Phe  
145 150 155 160  
Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys Asn  
165 170 175  
Leu Ser Gln Lys Gly Arg Xaa Lys Ala Leu Ser Thr Cys Ser Ser His  
180 185 190  
Ile Thr Val Val Val Phe Phe Phe Val Pro Cys Ile Phe Met Tyr Ala  
195 200 205  
Arg Pro Ala Arg Thr Phe Pro Ile Asp Lys Ser Val Ser Val Phe Tyr  
210 215 220  
Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn  
225 230 235 240  
Ser Glu Met Thr Ser Ala Met Lys Lys Leu Trp Arg Arg Asp Phe Ile  
245 250 255  
Ser Ser Ser Thr Xaa Val  
260

<210> 1940  
<211> 309  
<212> PRT  
<213> Unknown (H38g858 protein)

<220>  
<223> Synthetic construct

<221> VARIANT  
<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1940

```

M t Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1           5           10           15
Gln Asp Leu Asp Val Gln Lys Ala Leu Phe Val Ile Phe Leu Leu Thr
 20           25           30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
 35           40           45
Ala Ser Pro Ser Leu Gly Ser Ser Met Tyr Phe Phe Leu Ala Cys Leu
 50           55           60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
 65           70           75           80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
 85           90           95
Gly Gln Leu Phe Ile Asp His Leu Asp Gly Gly Ala Glu Val Val Leu
 100          105          110
Leu Val Val Lys Ala Cys Asp His Val Asp Ile Trp Lys Pro Leu
 115          120          125
Arg Tyr Leu Thr Ile Met Asn Arg Gln Gly Xaa Met Arg Leu Leu Val
 130          135          140
Ala Val Val Thr Gly Gly Val Leu His Ser Leu Ser His Ile Val Ser
 145          150          155          160
Val Val Tyr Ser Leu Ala Tyr Cys Gly Pro Asn Val Ile Asp Tyr Phe
 165          170          175
Val Cys Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr
 180          185          190
Phe Ile Gly Leu Thr Val Phe Val Asn Gly Gly Thr Ile Cys Ile Val
 195          200          205
Val Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu
 210          215          220
Lys Thr Tyr Ser Gln Glu Gly Arg His Lys Val Leu Phe Thr Cys Ser
 225          230          235          240
Ser His Ile Ile Val Phe Ala Leu Phe Phe Val Pro Cys Ile Phe Met
 245          250          255
Tyr Val Arg Pro Val Ser Asn Tyr Pro Phe Asp Lys Phe Leu Thr Val
 260          265          270
Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu
 275          280          285
Arg Asn Ser Glu Met Arg Asn Ser Val Glu Thr Leu Leu Cys Lys Lys
 290          295          300
Leu Thr Val Leu Glu
 305

```

<210> 1941

<211> 305

<212> PRT

<213> Unknown (H38g859 protein)

<220>

<223> Synthetic construct

<400> 1941

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
 35           40           45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Val Gly Asn
 50           55           60

```

Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile  
 65 70 75 80  
 Leu Val Ile Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys  
 85 90 95  
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Cys  
 100 105 110  
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro  
 115 120 125  
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val  
 130 135 140  
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys  
 145 150 155 160  
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe  
 165 170 175  
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly  
 180 185 190  
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys  
 195 200 205  
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val  
 210 215 220  
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr  
 245 250 255  
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile  
 260 265 270  
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu  
 290 295 300  
 Pro  
 305

&lt;210&gt; 1942

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g860 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1942

Met Ile Cys Glu Asn His Thr Arg Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Thr Asn Asn Pro Glu Met Gln Val Ser Leu Phe Ile Phe Phe Leu  
 20 25 30  
 Ala Ile Tyr Thr Val Thr Leu Leu Gly Asn Phe Leu Ile Val Thr Val  
 35 40 45  
 Thr Ser Val Asp Leu Ala Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln  
 50 55 60  
 Asn Leu Ser Leu Leu Glu Val Cys Phe Thr Leu Val Met Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Leu Val Ser Pro Arg Lys Ile Ile Ser Phe Val Gly  
 85 90 95  
 Cys Gly Thr Gln Met Tyr Phe Phe Phe Phe Gly Ser Ser Glu Cys  
 100 105 110  
 Phe Leu Leu Ser Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu His Tyr Ser Val Ile Met Asn Arg Ser Leu Cys Leu Trp Met  
 130 135 140  
 Ala Ile Gly Ser Trp Met Ser Gly Val Pro Val Ser Met Leu Gln Thr

```

145          150          155          160
Ala Trp Met Met Ala Leu Pro Phe Cys Gly Pro Asn Ala Val Asp His
          165          170          175
Phe Phe Cys Asp Gly Pro Pro Val Leu Lys Leu Val Thr Val Asp Thr
          180          185          190
Thr Met Tyr Glu Met Gln Ala Leu Ala Ser Thr Leu Leu Phe Ile Met
          195          200          205
Phe Pro Phe Cys Leu Ile Leu Val Ser Tyr Thr Arg Ile Ile Ile Thr
          210          215          220
Ile Leu Arg Met Ser Ser Ala Thr Gly Arg Gln Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ser
          245          250          255
Leu Thr Tyr Leu Arg Pro Lys Ser Asn Gln Ser Pro Glu Ser Lys Lys
          260          265          270
Leu Val Ser Leu Ser Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile
          275          280          285
Ile Tyr Gly Leu Arg Asn Asn Glu Val Lys Gly Ala Val Lys Arg Thr
          290          295          300
Ile Thr Gln Lys Val Leu Gln Lys Leu Asp Val Phe
305          310          315

```

&lt;210&gt; 1943

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g861 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1943

```

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Ser Val Ile
          20          25          30
Tyr Ile Asn Ala Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr
          35          40          45
Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Ala Tyr Leu
          50          55          60
Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
65          70          75          80
Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Phe Asn Gly Cys Met
          85          90          95
Thr Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu
          100          105          110
Leu Thr Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Lys Pro Leu
          115          120          125
His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly
          130          135          140
Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
145          150          155          160
Ile Cys Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
          165          170          175
Cys Asp Leu Tyr Thr Leu Ile Asn Leu Ala Cys Thr Asn Thr His Thr
          180          185          190
Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
          195          200          205
Cys Leu Leu Leu Val Ser Cys Val Val Ile Leu Tyr Ser Leu Lys
          210          215          220
Thr His Ser Leu Glu Ala Arg His Glu Ala Leu Ser Thr Cys Val Ser
225          230          235          240

```

His Ile Thr Val Val Ile Leu Ser Phe Ile Pro Cys Ile Phe Val Tyr  
                                   245                                  250                                  255  
 Met Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe  
                                   260                                  265                                  270  
 Tyr Thr Met Ile Thr Ser Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
                                   275                                  280                                  285  
 Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala  
                                   290                                  295                                  300  
 Ile Ser Ser Val Lys  
 305

&lt;210&gt; 1944

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g862 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(164)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1944

Trp Lys Asn His Phe Thr Ser Val Asn Cys Gly Phe Ala Ile Cys Arg  
   1                                  5                                  10                                  15  
 Ala Glu Cys Xaa Pro Xaa Pro Lys Ile Leu Ser Ile Ile Gly Leu Lys  
                                   20                                  25                                  30  
 Xaa Asn Ile Asn Glu Thr Leu Xaa Met Leu Asn Tyr Asn Thr Asn His  
                                   35                                  40                                  45  
 Met Val Ser Val Asp Val Leu Ile Val Pro Asn Ser Leu Ile Thr Leu  
                                   50                                  55                                  60  
 Ser Tyr Phe Phe Ile Val Ala Ala Ile Leu His Ile Arg Ser Ala Glu  
   65                                  70                                  75                                  80  
 Gly Arg His Lys Ala Phe Pro Thr Cys Ser Phe His Leu Val Val Ile  
                                   85                                  90                                  95  
 Leu Leu Gln His Asn Ala Thr Ser Leu Thr Tyr Leu Cys Pro Ser Ser  
                                   100                                  105                                  110  
 Ile Phe Ser Tyr Glu Arg Gly Lys Val Val Ser Thr Val Tyr Thr Cys  
                                   115                                  120                                  125  
 Ile Thr Pro Val Pro Asn Pro Leu Ile Cys Ser Met Arg Lys Lys Glu  
                                   130                                  135                                  140  
 Leu Lys His Ala Leu Lys Lys Lys Glu Glu Ile Ala Arg Phe Leu Leu  
   145                                  150                                  155                                  160  
 Leu Arg Thr His

&lt;210&gt; 1945

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g863 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1945

Met Phe Ser Ser Glu Pro Thr Ile Asp Gly Asn Gln Ser Leu Cys Ala  
   1                                  5                                  10                                  15  
 Lys Phe Thr Phe Val Ala Phe Ser Ser Ile Glu Glu Leu Gln Leu Val  
                                   20                                  25                                  30  
 Leu Phe Ile Val Phe Leu Ile Ile Tyr Leu Cys Thr Ile Gly Gly Asn

```

      35              40              45
Ile Ile Ile Ile Ser Leu Ile Trp Ile Thr Pro Ala Leu His Thr Pro
 50              55              60
Met Tyr Phe Phe Leu Val Asn Leu Ser Phe Leu Glu Met Cys Tyr Thr
65              70              75              80
Thr Ser Val Val Pro Leu Leu Val His Leu Leu Val Glu Thr Lys Thr
      85              90              95
Ile Ser Val Gly Gly Cys Ala Thr Gln Met Tyr Ile Phe Ala Ile Leu
 100              105              110
Gly Leu Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe
 115              120              125
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Leu Phe Met Gly Pro Arg
 130              135              140
Val Cys Leu Lys Leu Ala Ala Ala Ser Trp Phe Thr Gly Val Val Val
 145              150              155              160
Glu Ser Ala Gln Ile Thr Leu Ile Phe Thr Leu Pro Phe Cys Gly Thr
      165              170              175
Gly Lys Ile Pro Thr Leu Phe Cys Asp Ile Met Pro Val Leu Lys Leu
 180              185              190
Ala Cys Ile Asp Thr Ser Gln Ile Glu Ile Val Met Phe Ser Leu Ser
 195              200              205
Val Leu Phe Ile Val Ser Pro Cys Phe Leu Ile Leu Cys Ser His Met
 210              215              220
His Ile Pro Val Thr Ile Leu Arg Ile Pro Ser Ala Ala Gly Arg His
 225              230              235              240
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Leu Val Val Ser Leu Phe
      245              250              255
Tyr Gly Thr Ala Leu Phe Thr Tyr Leu Gln Pro Lys Thr Ala His Thr
 260              265              270
Pro Glu Thr Asp Lys Ala Thr Ala Leu Met Tyr Thr Met Val Thr Pro
 275              280              285
Ala Leu Asn Pro Val Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu
 290              295              300
Ala Phe Gln Arg Ile Thr Gln Arg Asn Ser Leu Arg Gln Thr
 305              310              315

```

&lt;210&gt; 1946

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g864 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(291)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1946

```

Ser Met Tyr Leu Val Thr Met Leu Arg Asn Leu Phe Ile Ile Leu Ala
 1              5              10              15
Gly Ser Ser Asp Pro His Phe His Thr Pro Met Tyr Phe Phe Leu Ser
      20              25              30
Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys
 35              40              45
Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
 50              55              60
Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp
65              70              75              80
Met Leu Leu Thr Leu Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      85              90              95

```



Ile Cys His Pro Leu His Tyr Arg Val Ile Met Asn Pro His Leu Cys  
 100 105 110  
 Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Asp Ser Gln  
 115 120 125  
 Leu His Ser Trp Ile Val Leu His Asn Ser Pro Phe Gln Glu Cys Gly  
 130 135 140  
 Asn Leu Xaa Phe Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala  
 145 150 155 160  
 Cys Ser Asp Ser Ile Ile Asn Asn Ile Leu Cys Ile Leu Asp Ile Pro  
 165 170 175  
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys  
 180 185 190  
 Ile Val Ser Ser Ile Pro Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys  
 195 200 205  
 Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr  
 210 215 220  
 Glu Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro  
 225 230 235 240  
 Arg Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Ile Pro Met  
 245 250 255  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Ser Ala  
 260 265 270  
 Leu Trp Arg Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His  
 275 280 285  
 Pro Phe Ser  
 290

&lt;210&gt; 1947

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g865 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1947

Met Asp Val Ser Ile Phe Leu Leu Leu Gly Thr Thr Glu Asp Pro Glu  
 1 5 10 15  
 Arg Gln Pro Val Leu Thr Gly Leu Phe Leu Ser Met Cys Leu Val Thr  
 20 25 30  
 Val Leu Gly Lys Leu Leu Ile Met Leu Ala Phe Ser Pro Asp Ser His  
 35 40 45  
 Leu His Thr His Met Tyr Phe Phe Leu Ser Asn Leu Ser Leu Pro Asp  
 50 55 60  
 Ile Gly Phe Thr Ser Thr Ile Val Pro Lys Met Ile Ala Asp Ile Gln  
 65 70 75 80  
 Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr Gln Met Ser  
 85 90 95  
 Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asp Met Leu Leu Ser Val  
 100 105 110  
 Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Tyr His Ser  
 115 120 125  
 Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu Phe Phe  
 130 135 140  
 Phe Phe Leu Ser Leu Leu Asp Thr Gln Leu His Asn Leu Ile Ala Leu  
 145 150 155 160  
 Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Asp

										165			170				175			
Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr	Asn	Asn					
				180			185			190										
Ile	Ile	Val	Tyr	Phe	Pro	Ala	Val	Ile	Phe	Val	Phe	Leu	Pro	Ile	Ser					
				195			200			205										
Gly	Thr	Leu	Phe	Ser	Tyr	Lys	Thr	Val	Ser	Ser	Ile	Leu	Arg	Val	Ser					
				210			215			220										
Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Thr	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu					
				225			230			235			240							
Ser	Val	Ile	Cys	Xaa	Phe	Tyr	Gly	Thr	Gly	Val	Gly	Gly	Tyr	Leu	Ser					
				245			250			255										
Ser	Asp	Val	Ser	Ser	Ser	Leu	Arg	Lys	Ala	Ala	Val	Ala	Ser	Val	Met					
				260			265			270										
Tyr	Lys	Met	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg					
				275			280			285										
Asn	Arg	Asp	Met	Lys	Ser	Val	Leu	Arg	Arg	Pro	His	Gly	Ser	Thr	Val					
				290			295			300										
Xaa	Ser	Gln	Tyr	Leu	Leu	Ile	Cys	Ser	Ile	Pro	Phe	Val	Gly	Trp	Val					
				305			310			315			320							
Lys	Lys	Gly	Ser	Lys	Val	Lys														
				325																

&lt;210&gt; 1948

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g866 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1948

Met	Gly	Asp	Lys	Gly	Thr	Gly	Asn	His	Ser	Asp	Val	Thr	Asp	Phe	Ile				
1				5				10				15							
Leu	Glu	Gly	Phe	Arg	Val	Arg	Pro	Glu	Phe	Tyr	Ile	Leu	Leu	Phe	Phe				
				20			25			30									
Leu	Phe	Leu	Leu	Ile	Tyr	Ser	Met	Val	Leu	Leu	Gly	Asn	Ile	Ser	Val				
				35			40			45									
Met	Thr	Ile	Ile	Val	Thr	Asp	Ser	Gln	Leu	Asn	Thr	Pro	Met	Tyr	Phe				
				50			55			60									
Phe	Leu	Gly	Asn	Leu	Ser	Phe	Ile	Asp	Val	Ser	Tyr	Ser	Thr	Val	Ile				
				65			70			75			80						
Ala	Pro	Lys	Ala	Met	Ala	His	Phe	Leu	Ser	Glu	Lys	Lys	Thr	Val	Ser				
				85			90			95									
Phe	Ala	Gly	Cys	Val	Ala	Gln	Leu	Phe	Leu	Phe	Ala	Leu	Phe	Ile	Val				
				100			105			110									
Thr	Glu	Gly	Phe	Val	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Ser	Ala				
				115			120			125									
Ile	Cys	Asn	Pro	Leu	Leu	His	Ser	Val	His	Met	Ser	Arg	Arg	Leu	Cys				
				130			135			140									
Thr	Gln	Leu	Val	Ala	Gly	Ser	Tyr	Phe	Cys	Gly	Trp	Ala	Ser	Ser	Ile				
				145			150			155			160						
Leu	Gln	Val	Ser	Val	Thr	Phe	Ser	Val	Ser	Phe	Cys	Ala	Ser	Arg	Val				
				165			170			175									
Ile	Ala	His	Phe	Tyr	Cys	Asp	Ser	Tyr	Gln	Ile	Glu	Lys	Ile	Ser	Cys				
				180			185			190									
Ser	Asn	Leu	Phe	Val	Asn	Lys	Met	Val	Ser	Leu	Ser	Leu	Ser	Val	Ile				
				195			200			205									
Ile	Ile	Leu	Pro	Thr	Ile	Val	Val	Ile	Ile	Val	Ser	Tyr	Leu	Tyr	Ile				
				210			215			220									
Val	Ser	Ser	Val	Leu	Lys	Ile	Pro	Ser	Ser	Glu	Gly	Arg	Lys	Lys	Asp				
				225			230			235			240						

Phe Ser Thr Cys Ser Ser His Arg Gly Val Val Ser Leu Leu  
 245 250

<210> 1949

<211> 335

<212> PRT

<213> Unknown (H38g867 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1949

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Ala Ser Lys Tyr Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Lys Leu Gln Leu Ala Leu Ser Gly Arg Glu  
 20 25 30  
 Pro Cys Thr Cys Thr Xaa Ser Leu Val Leu Glu Asn Leu Leu Ile Ile  
 35 40 45  
 Leu Ala Val Ser Ser Asp Phe His Leu His Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val  
 65 70 75 80  
 Pro Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr  
 85 90 95  
 Ala Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met  
 100 105 110  
 Glu Glu Asn Met Leu Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala  
 115 120 125  
 Ile Cys His Pro Leu Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys  
 130 135 140  
 Gly Phe Leu Val Leu Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser Gln  
 145 150 155 160  
 Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu  
 165 170 175  
 Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys  
 180 185 190  
 Cys Asp Thr Phe Thr Asn Asn Ile Val Met Tyr Phe Leu Ala Ala Ile  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Arg Ile Ile Phe Ser Tyr Tyr Lys Ile  
 210 215 220  
 Val Ser Ser Met Leu Ser Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Gly Ser Pro Leu Ser Val Val Cys Leu Phe Tyr Gly  
 245 250 255  
 Lys Val Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg  
 260 265 270  
 Lys Gly Ala Val Ala Ser Met Met Tyr Thr Val Ile Thr Pro Met Leu  
 275 280 285  
 Asn Pro Phe Ile Tyr Arg Leu Arg Asn Arg Asp Ile Lys Arg Val Leu  
 290 295 300  
 Trp Trp Leu His Gly Arg Thr Val Xaa Ser His Tyr Phe Ile Ile Cys  
 305 310 315 320  
 Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys  
 325 330 335

<210> 1950

<211> 317

<212> PRT  
 <213> Unknown (H38g868 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(317)  
 <223> Xaa = Any Amino Acid

<400> 1950  
 Thr Gly Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu  
 1 5 10 15  
 Leu Gln Pro Ala Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu  
 20 25 30  
 Val Thr Val Leu Arg Asn Leu Phe Ser Ile Leu Ala Val Ser Ser Asp  
 35 40 45  
 Cys Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp  
 50 55 60  
 Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp  
 65 70 75 80  
 Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln  
 85 90 95  
 Met Ser Phe Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr  
 100 105 110  
 Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr  
 115 120 125  
 Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser  
 130 135 140  
 Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu  
 145 150 155 160  
 Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp  
 165 170 175  
 Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn  
 180 185 190  
 Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser  
 195 200 205  
 Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile  
 210 215 220  
 Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His  
 225 230 235 240  
 Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu  
 245 250 255  
 Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val  
 260 265 270  
 Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu  
 275 280 285  
 Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Gly Ser Arg Ala  
 290 295 300  
 Phe Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys  
 305 310 315

<210> 1951  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g869 protein)

<220>  
 <223> Synthetic construct

<400> 1951

```

Met Gly Asp Arg Gly Thr Ser Asn His Ser Glu Met Thr Asp Phe Ile
 1      5      10      15
Leu Ala Gly Phe Arg Val Arg Pro Glu Leu His Ile Leu Leu Phe Leu
 20      25      30
Leu Phe Leu Phe Val Tyr Ala Met Ile Leu Leu Gly Asn Val Gly Met
 35      40      45
Met Thr Ile Ile Met Thr Asp Pro Arg Leu Asn Thr Pro Met Tyr Phe
 50      55      60
Phe Leu Gly Asn Leu Ser Phe Ile Asp Leu Phe Tyr Ser Ser Val Ile
 65      70      75      80
Glu Pro Lys Ala Met Ile Asn Phe Trp Ser Glu Asn Lys Ser Ile Ser
 85      90      95
Phe Ala Gly Cys Val Ala Gln Leu Phe Leu Phe Ala Leu Leu Ile Val
 100     105     110
Thr Glu Gly Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala
 115     120     125
Ile Cys Asn Pro Leu Leu Tyr Ser Val Gln Met Ser Thr Arg Leu Cys
 130     135     140
Thr Gln Leu Val Ala Gly Ser Tyr Phe Cys Gly Cys Ile Ser Ser Val
 145     150     155     160
Ile Gln Thr Ser Met Thr Phe Thr Leu Ser Phe Cys Ala Ser Arg Ala
 165     170     175
Val Asp His Phe Tyr Cys Asp Ser Arg Pro Leu Gln Arg Leu Ser Cys
 180     185     190
Ser Asp Leu Phe Ile His Arg Met Ile Ser Phe Ser Leu Ser Cys Ile
 195     200     205
Ile Ile Leu Pro Thr Ile Ile Val Ile Ile Val Ser Tyr Met Tyr Ile
 210     215     220
Val Ser Thr Val Leu Lys Ile His Ser Thr Glu Gly His Lys Lys Ala
 225     230     235     240
Phe Ser Thr Cys Ser Ser His Leu Gly Val Val Ser Val Leu Tyr Gly
 245     250     255
Ala Val Phe Phe Met Tyr Leu Thr Pro Asp Arg Phe Pro Glu Leu Ser
 260     265     270
Lys Val Ala Ser Leu Cys Tyr Ser Leu Val Thr Pro Met Leu Asn Pro
 275     280     285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Gln Glu Ala Leu Lys Lys
 290     295     300
Phe Leu Glu Lys Lys Asn Ile Ile Leu
305      310

```

&lt;210&gt; 1952

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g870 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(277)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1952

```

His Ser Phe Leu Arg Tyr Ile Phe Ala Lys Leu Thr Gly Glu Pro Glu
 1      5      10      15
Leu Gln Pro Ser Leu Tyr Ser Val Phe Trp Ser Pro Xaa Leu Gly Xaa
 20      25      30
Pro His His Thr Ser Met Tyr Pro Leu His Thr Ser Met Tyr Leu Tyr
 35      40      45
Ile Phe Ser Phe Ser Phe Ile Gly Phe Phe Tyr Ser Ser Val Ile Ser

```

```

      50      55      60
Pro Gln Met Thr Ile Ser Phe Val Thr Glu Lys Asn Ile Ile Thr Tyr
65      70      75      80
Val Thr Ser Asn Thr Gln Pro Phe Pro Leu Cys Phe Phe Val Ile Ser
      85      90      95
Asp Tyr Ser Ile Phe Ile Pro Leu Ala Leu Asp His Tyr Glu Ala Met
      100      105      110
Thr Leu Pro Val Ser Phe Ile Ser Phe Ile Ser Val Asp Gly Ser Xaa
      115      120      125
Val Ile Glu Phe Ala Asp Ala Val Val His Gln Gly Ser Met Asp Gln
      130      135      140
Phe Leu Phe Cys Asp His Ser Cys Met Ser Leu Asn Leu Cys Asn Ile
145      150      155      160
Gly Pro Leu Gln Ala Ala Xaa Ile Ser Thr Tyr Val Ser Lys Gln Val
      165      170      175
Asp Leu Tyr Ser Xaa Glu Pro Ala Val Tyr His Ala Val Leu Ser Phe
      180      185      190
Ser Tyr Phe Val Phe Ile Leu Phe Asn Ile Phe His Xaa Pro Ser Gly
      195      200      205
Pro Asn Leu Gln Pro Asp Ser Ile Asn Leu Phe Ile Ser Phe Phe Gly
      210      215      220
Leu Gly Thr Phe Met Tyr Leu Arg Ser Pro Glu Ala Met Gly Xaa Cys
225      230      235      240
Lys Phe Thr Val Ser Phe Thr Lys Met Gly Pro Val Met Asn Gly Leu
      245      250      255
Phe Asn Thr Leu Arg Asn Lys Thr Ile Xaa Leu Ala Ala Met Lys Pro
      260      265      270
Leu Ser Phe Ser Ser
      275

```

&lt;210&gt; 1953

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g871 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1953

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Arg Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
      115      120      125
Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
      130      135      140

```

Phe Leu Asp Leu Leu Ser Leu Phe Phe Phe Phe Phe Phe Phe Ser  
 145 150 155 160  
 Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met  
 165 170 175  
 Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Cys  
 180 185 190  
 Cys Asp Thr Phe Thr Arg Asn Ile Asn Met Tyr Phe Pro Ala Ala Val  
 195 200 205  
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Ile  
 210 215 220  
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Thr Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly  
 245 250 255  
 Thr Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg  
 260 265 270  
 Lys Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val Leu  
 290 295 300  
 Arg Arg Pro His Ser Ser Ala Val Xaa Ser Gln Tyr Leu Leu Ile Cys  
 305 310 315 320  
 Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys  
 325 330 335

&lt;210&gt; 1954

&lt;211&gt; 342

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g872 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(342)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1954

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Ala Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Ser Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala  
 85 90 95  
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu  
 100 105 110  
 Lys Arg His Ala Pro Glu Val Met Ala Tyr Asp Leu Phe Val Pro Ile  
 115 120 125  
 Cys His Leu Leu Tyr Arg Ser Thr Ile Leu Asn Pro Phe Val Arg Gly  
 130 135 140  
 Phe Leu Asn Leu Leu Ser Leu Phe Val Gly Phe Phe Phe Phe Ser Leu  
 145 150 155 160  
 Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr  
 165 170 175  
 Tyr Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln

```

      180      185      190
Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Asn Asn Met
      195      200      205
Tyr Phe Pro Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu
      210      215      220
Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser
      225      230      235      240
Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
      245      250      255
Val Cys Xaa Phe Tyr Gly Ala Gly Val Gly Gly Tyr Leu Gly Ser Asp
      260      265      270
Val Ser Ser Ser Pro Arg Lys Gly Ala Val Ala Ser Val Thr Tyr Tyr
      275      280      285
Thr Val Val Thr Pro Met Leu Asn Ser Phe Ile Tyr Ser Leu Arg Asn
      290      295      300
Gly Asp Ile Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
      305      310      315      320
Ser Gln Tyr Val Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Asn
      325      330      335
Lys Asp Ser Lys Val Lys
      340

```

&lt;210&gt; 1955

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g873 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1955

```

Met Asp Leu Gly Asn Ser Gly Asn Asp Ser Val Val Thr Lys Phe Val
  1      5      10      15
Leu Leu Gly Leu Thr Glu Thr Ala Ala Leu Gln Pro Ile Leu Phe Val
      20      25      30
Ile Phe Leu Leu Ala Tyr Val Thr Thr Ile Gly Gly Thr Leu Ser Ile
      35      40      45
Leu Ala Ala Ile Leu Met Glu Thr Lys Leu His Ser Pro Met Tyr Phe
      50      55      60
Phe Leu Gly Asn Leu Ser Leu Pro Asp Val Gly Cys Val Ser Val Thr
      65      70      75      80
Val Pro Ala Met Leu Ser His Phe Ile Ser Asn Asp Arg Ser Ile Pro
      85      90      95
Tyr Lys Ala Cys Leu Ser Glu Leu Phe Phe His Leu Leu Ala Gly
      100      105      110
Ala Asp Cys Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Leu Ala
      115      120      125
Ile Cys Gln Ser Leu Thr Tyr Ser Ser Arg Met Ser Trp Gly Ile Gln
      130      135      140
Gln Ala Leu Val Gly Met Ser Trp Val Phe Ser Phe Thr Asn Ala Leu
      145      150      155      160
Thr Gln Thr Val Ala Leu Ser Pro Leu Asn Phe Cys Gly Pro Asn Val
      165      170      175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Pro Phe Gln Leu Ser Cys
      180      185      190
Ala Ser Val His Leu Asn Gly Gln Leu Leu Phe Val Ala Ala Ala Phe
      195      200      205
Met Gly Val Ala Pro Leu Val Leu Ile Thr Val Ser Tyr Ala His Val
      210      215      220
Ala Ala Ala Val Leu Arg Ile Arg Ser Ala Glu Gly Lys Lys Lys Ala
      225      230      235      240

```



Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Thr	Val	Val	Gly	Ile	Phe	Tyr	Gly
				245					250					255	
Thr	Gly	Val	Phe	Ser	Tyr	Thr	Arg	Leu	Gly	Ser	Val	Glu	Ser	Ser	Asp
			260					265					270		
Lys	Asp	Lys	Gly	Ile	Gly	Ile	Leu	Asn	Thr	Val	Ile	Ser	Pro	Met	Leu
		275					280					285			
Asn	Pro	Leu	Ile	Tyr	Trp	Thr	Ser	Leu	Leu	Asp	Val	Gly	Cys	Ile	Ser
	290					295					300				
His	Cys	Ser	Ser	Asp	Ala	Gly	Val	Ser	Pro	Gly	Pro	Pro	Val	Gln	Ser
305					310					315					320
Ser	Leu	Cys	Cys	Leu	Gln	Phe	Thr	Ala	Leu	Leu	Ser	Pro	Pro	Pro	Gly
				325					330					335	
Trp	Gly	Gly	Leu	Ser	Pro	Leu	Asn	Ser	His	Gly	Leu				
			340					345							

<210> 1956

<211> 230

<212> PRT

<213> Unknown (H38g874 protein)

**<220>**

<223> Synthetic construct

## <221> VARIANT

**<222> (1) . . . (230)**

<223> Xaa = Any Amino Acid

<400> 1956

[illegible]

<210> 1957

<211> 331

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g875 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1957

```

His Thr Glu Pro Arg Asn Leu Thr Ser Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Leu Leu Ser
      20           25           30
Leu Ser Leu Ser Met His Leu Val Met Val Leu Arg Asn Leu Leu Asn
      35           40           45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
      50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65           70           75           80
Val Pro Asn Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85           90           95
His Ala Asp Cys Leu Thr Gln Ile Ser Phe Leu Leu Leu Phe Ala Cys
      100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Thr Tyr Asp Cys Phe Val Ala
      115          120          125
Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165          170          175
Ile Ser Asn Ser Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Met His Phe His Asn Thr Met
      195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Val Ser Tyr Tyr Lys Ile
      210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
      245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg
      260          265          270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
      275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290          295          300
Trp Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
      305          310          315          320
Phe Ser Cys Val Gly Lys Gly Asn His Ile Lys
      325          330

```

&lt;210&gt; 1958

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g876 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1958

```

His Arg Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Thr Pro Ile Tyr Phe
          50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
          65           70           75           80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
          85           90           95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
          145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Phe Ala Cys
          180          185          190
Ser Asp Ser Ile Ile Asn Ser Ile Phe Ile Tyr Phe His Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
          210          215          220
Ile Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
          225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Asp Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
          260          265          270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Trp Gly Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
          305          310          315          320
Phe Ser

```

&lt;210&gt; 1959

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g877 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1959

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val

```

<210> 1960  
<211> 323  
<212> PRT  
<213> Unknown (H38g878 protein)

400> 1960															
Met	Thr	Asp	Tyr	Asn	Glu	Pro	Met	Glu	Pro	Met	Glu	Asp	Lys	Asn	Gln
1				5					10					15	
Thr	Val	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Leu	Thr	Asp	His	Pro	Tyr
			20					25					30		
Gln	Lys	Ile	Val	Leu	Phe	Phe	Met	Phe	Leu	Phe	Val	Tyr	Leu	Ile	Thr
	35						40					45			
Leu	Gly	Gly	Asn	Leu	Gly	Met	Ile	Thr	Leu	Ile	Trp	Ile	Asp	Pro	Arg
	50					55					60				
Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg	His	Leu	Ser	Phe	Val	Asp
65					70					75					80
Ile	Cys	Ser	Ser	Ser	Ser	Val	Val	Pro	Lys	Met	Leu	Cys	Asn	Ile	Phe
				85					90				95		
Ala	Glu	Lys	Lys	Asp	Ile	Thr	Phe	Leu	Gly	Cys	Ala	Ala	Gln	Met	Trp
			100					105					110		

Phe Phe Gly Leu Phe Glu Ala Ala Glu Cys Phe Leu Leu Ala Ala Met  
 115 120 125  
 Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Thr Leu  
 130 135 140  
 Ile Met Ser Gln Gln Val Cys Met Gln Leu Val Val Gly Pro Tyr Ala  
 145 150 155 160  
 Met Ala Leu Ile Ser Thr Met Thr His Thr Ile Phe Thr Phe Cys Leu  
 165 170 175  
 Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ile Phe  
 180 185 190  
 Pro Leu Leu Ser Leu Ala Cys Ala Asp Thr Trp Val Asn Lys Phe Val  
 195 200 205  
 Leu Phe Val Leu Ala Gly Ala Ile Gly Val Leu Ser Gly Leu Ile Ile  
 210 215 220  
 Met Val Ser Tyr Ile Cys Ile Leu Met Thr Ile Leu Lys Ile Gln Thr  
 225 230 235 240  
 Ala Asp Gly Lys Gln Lys Ala Phe Phe Thr Cys Phe Ser His Leu Ala  
 245 250 255  
 Ala Val Ser Ile Leu Tyr Gly Thr Leu Phe Leu Ile Tyr Val Arg Pro  
 260 265 270  
 Ser Ser Ser Ser Ser Leu Gly Ile Tyr Lys Val Ile Ser Leu Phe Tyr  
 275 280 285  
 Thr Val Val Ile Pro Met Val Asn Pro Leu Ile Tyr Ser Leu Arg Asn  
 290 295 300  
 Lys Glu Val Lys Asp Ala Phe Arg Arg Lys Ile Glu Arg Lys Lys Phe  
 305 310 315 320  
 Ile Ile Gly

&lt;210&gt; 1961

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g879 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(229)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1961

Phe Phe Ser Leu Asp Leu Ile Arg Ser Gln Ala Asn Thr Met Ser Lys  
 1 5 10 15  
 Lys His Trp Thr Ala Ile Ala Glu Phe Ile Pro Leu Gly Pro Thr Asp  
 20 25 30  
 Gln Ala Glu Leu Gln Leu Val Leu Phe Phe Phe Thr Phe Leu Val Ile  
 35 40 45  
 Tyr Leu Ile Met Val Met Gly Asn Leu Ser Met Ile Leu Ile Ile Arg  
 50 55 60  
 Ser Asp Xaa Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser His Leu  
 65 70 75 80  
 Ser Phe Ala Val Leu Cys Tyr Thr Leu Asn Val Thr Pro Gln Ile Leu  
 85 90 95  
 Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Phe Phe Ile Gly Cys Val  
 100 105 110  
 Ser Val Leu Xaa Phe Tyr Phe Phe Ile Val Leu Ile Ile Arg Asp Tyr  
 115 120 125  
 His Met Leu Thr Val Met Ala Asn Asp Cys Tyr Met Ala Ile Cys Lys  
 130 135 140  
 Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Phe Val Cys Leu Ser Leu

145                      150                      155                      160  
 Ala Ser Val Ser Xaa Ile Tyr Gly Phe Ala Asn Tyr Leu Ala Gln Thr  
                                  165                      170                      175  
 Ile Arg Met Leu Leu Leu Ser Phe Xaa Gly Ser Asn Glu Ile Asn His  
                                  180                      185                      190  
 Phe Asp Cys Ala Asp Pro Pro Leu Leu Val Leu Pro Cys Ala Gly Thr  
                                  195                      200                      205  
 Cys Val Lys Xaa Ile Ile Met Leu Met Glu Pro His Cys Leu Leu Lys  
                                  210                      215                      220  
 Pro Gly Tyr Ile Leu  
 225

<210> 1962

<211> 286

<212> PRT

<213> Unknown (H38g880 protein)

<220>

<223> Synthetic construct

<400> 1962

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val  
 1                      5                      10                      15  
 Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn  
                                  20                      25                      30  
 Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met  
                                  35                      40                      45  
 Ile Val Asp Met Gly Ser His Ser Arg Val Ile Ser Tyr Gly Gly Cys  
                                  50                      55                      60  
 Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met  
 65                      70                      75                      80  
 Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro  
                                  85                      90                      95  
 Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val  
                                  100                      105                      110  
 Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp  
                                  115                      120                      125  
 Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe  
                                  130                      135                      140  
 Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val  
 145                      150                      155                      160  
 Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu  
                                  165                      170                      175  
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile  
                                  180                      185                      190  
 Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys  
                                  195                      200                      205  
 Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly  
                                  210                      215                      220  
 Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val  
 225                      230                      235                      240  
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile  
                                  245                      250                      255  
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys  
                                  260                      265                      270  
 Asn Lys Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser  
                                  275                      280                      285

<210> 1963

<211> 325

<212> PRT

<213> Unknown (H38g881 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1963

```

Met Ala Asn Glu Asn Tyr Thr Lys Val Thr Xaa Phe Ile Phe Thr Gly
 1           5           10           15
Leu Asn Tyr Asn Pro Gln Leu Arg Val Phe Leu Phe Leu Leu Phe Leu
      20           25           30
Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
 35           40           45
Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50           55           60
Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
 65           70           75           80
Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
      85           90           95
Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
      100           105           110
Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
      115           120           125
Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
      130           135           140
Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
      145           150           155           160
Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn
      165           170           175
Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
      180           185           190
Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
      195           200           205
Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
      210           215           220
Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
      225           230           235           240
Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr Leu
      245           250           255
Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
      260           265           270
Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
      275           280           285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His Arg
      290           295           300
Thr Val Thr Gln Arg Lys Phe Cys Lys Ala Xaa Ile Leu Ile Gln Lys
      305           310           315           320
Glu Leu Gly Arg Lys
                        325

```

<210> 1964

<211> 314

<212> PRT

<213> Unknown (H38g882 protein)

<220>

<223> Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1964

```

Met Glu Thr Glu Asn Asn Thr Thr Val Thr Glu Phe Ile Ile Leu Gly
 1              5              10              15
Leu Thr Asp Asn Pro Met Leu Cys Ala Ile Phe Phe Val Phe Phe Leu
      20              25              30
Ala Val Tyr Ile Val Thr Ile Pro Gly Asn Ile Ser Ile Ile Leu Leu
      35              40              45
Ile Gln Ser Ser Pro Gln Leu His Thr Leu Met Tyr Leu Phe Leu Ser
      50              55              60
His Leu Ala Ser Val Asp Ile Gly Tyr Ser Ile Ser Val Thr Pro Ile
      65              70              75              80
Ile Leu Ile Asn Phe Leu Arg Glu Lys Thr Thr Ile Pro Val Thr Gly
      85              90              95
Cys Ile Ala Gln Leu Gly Ser Asp Val Met Phe Gly Thr Thr Glu Cys
      100             105             110
Phe Leu Leu Asp His Tyr Val Ala Ile Cys Ser Pro Leu Leu Tyr Ser
      115             120             125
Ile Gln Met Pro Pro Val Val Cys Phe Leu Leu Leu Gly Ala Ser Tyr
      130             135             140
Leu Gly Gly Cys Leu Asn Ala Ser Ser Phe Thr Gly Cys Leu Met Asn
      145             150             155             160
Leu Ser Phe Cys Gly Pro Asn Lys Ile Asn His Phe Phe Cys Asp Leu
      165             170             175
Phe Pro Leu Leu Lys Leu Ser Cys Gly His Val Tyr Ile Ala Glu Ile
      180             185             190
Ser Pro Ala Ile Ser Ser Ala Ser Val Leu Ile Ser Thr Leu Phe Thr
      195             200             205
Ile Ile Val Ser Tyr Ile Tyr Ile Leu His Ser Ile Leu Lys Val Cys
      210             215             220
Ser Thr Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu
      225             230             235             240
Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Leu Phe Val Tyr Val Met
      245             250             255
Pro Lys Ser Ser Tyr Ser Ala Asp Gln Val Lys Val Ala Phe Val Ile
      260             265             270
Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
      275             280             285
Asn Lys Glu Val Lys Glu Ala Met Arg Lys Leu Met Ala Arg Thr His
      290             295             300
Trp Phe Ser Xaa Ile Lys Ser Val Xaa Ser
      305             310

```

&lt;210&gt; 1965

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g883 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1965

```

Ile Phe Ala Ile Leu Thr Thr Ile Asp Cys Cys Val Phe Val Trp Glu
 1              5              10              15

```



Phe Leu Glu Cys Thr Val Phe Val Asn Lys Arg Ala Cys Ala Gln Leu  
                   20                  25                  30  
 Ala Cys Gly Ala Phe Cys Ile Gly Leu Ile Met Thr Val Val Xaa Ile  
                   35                  40                  45  
 Thr Thr Val Ser Gln Arg Tyr Lys Arg Ser Thr Tyr Ala Ile Val Asp  
                   50                  55                  60  
 Cys Phe Leu Phe Asp Thr Leu Leu Val Met Lys Leu Ser Cys Ile Asp  
                   65                  70                  75                  80  
 Asn Thr Ile Tyr Glu Ile Ile Gln Tyr Phe Ile His His Thr Cys Val  
                   85                  90                  95  
 Gln Val Ser Met Gly Leu Val Cys Ile Ser Tyr Ile Asp Ile Pro Val  
                   100                  105                  110  
 Thr Ser Ile Val Leu Arg Ile Ser Xaa Ser Glu Val Phe Ala Thr Cys  
                   115                  120                  125  
 Val Pro Gln Pro Pro Pro His His Gly His Cys Leu Tyr Val Cys Ala  
                   130                  135                  140  
 Cys Thr Ala Tyr Leu Lys His Lys Pro Met Asn Ser Ile Glu Lys Gly  
                   145                  150                  155                  160  
 Leu Leu Xaa Glu Thr Tyr Ile Ile Ile Ile His Ser Ala Ser Gly Pro  
                   165                  170                  175  
 Val Val Tyr Thr Leu Arg Tyr Met Glu Ala Lys Asp Thr Met Tyr Arg  
                   180                  185                  190  
 Ala Val Asp Arg Asn Ile Ser Xaa Gln Ile  
                   195                  200

&lt;210&gt; 1966

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g884 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1966

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile  
   1                  5                  10                  15  
 Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val  
                   20                  25                  30  
 Leu Leu Leu Phe Ala Tyr Leu Val Thr Thr Gly Gly Asn Leu Ser Ile  
                   35                  40                  45  
 Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe  
                   50                  55                  60  
 Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr  
                   65                  70                  75                  80  
 Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser  
                   85                  90                  95  
 Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly  
                   100                  105                  110  
 Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala  
                   115                  120                  125  
 Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln  
                   130                  135                  140  
 Arg Met Leu Val Ala Ala Ser Leu Ala Cys Ala Phe Thr Asn Ala Leu  
                   145                  150                  155                  160  
 Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu  
                   165                  170                  175  
 Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys  
                   180                  185                  190  
 Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile  
                   195                  200                  205  
 Met Ala Gly Thr Pro Leu Val Leu Ile Ile Thr Ala Tyr Ser His Val

210 215 220  
 Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe Phe Gly  
 245 250 255  
 Arg Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Glu Glu Ala Ser Asp  
 260 265 270  
 Lys Asp Lys Gly Val Gly Val Phe Asn Thr Val Ile Asn Pro Met Leu  
 275 280 285  
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Pro Asp Val Gln Gly Ala Leu  
 290 295 300  
 Trp Gln Ile Phe Leu Gly Arg Arg Ser Leu Thr  
 305 310 315

<210> 1967  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g885 protein)

<220>  
 <223> Synthetic construct

<400> 1967  
 Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu  
 20 25 30  
 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile  
 35 40 45  
 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg  
 65 70 75 80  
 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly  
 85 90 95  
 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys  
 100 105 110  
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu  
 130 135 140  
 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val  
 145 150 155 160  
 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe  
 165 170 175  
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr  
 180 185 190  
 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val  
 195 200 205  
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile  
 210 215 220  
 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys  
 225 230 235 240  
 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile  
 245 250 255  
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val  
 260 265 270  
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Val  
 290 295 300

Gly Arg Asn Ile Ser  
305

<210> 1968

<211> 320

<212> PRT

<213> Unknown (H38g886 protein)

<220>

<223> Synthetic construct

<400> 1968

```

Met Leu Gln Arg Val Gly Glu Met Asp Gly Gly Asn Gln Ser Glu Gly
 1           5           10           15
Ser Glu Phe Leu Leu Gly Ile Ser Glu Ser Pro Glu Gln Gln Gln
      20           25           30
Met Leu Phe Trp Met Phe Leu Val Arg Tyr Leu Val Thr Val Leu Gly
 35           40           45
Asn Val Leu Ile Ile Leu Ala Ile Ser Ser Asp Ser Arg Leu His Thr
 50           55           60
Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Thr Asp Leu Phe Phe
 65           70           75           80
Val Thr Asn Thr Ile Pro Lys Met Leu Val Asn Leu Gln Ser Gln Asn
      85           90           95
Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr Gln Leu Tyr Phe Leu Val
      100           105           110
Ser Leu Val Ala Leu Asp Asn Leu Asn Leu Ala Val Met Ala Tyr Asp
      115           120           125
Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Val Thr Ala Met Ile
      130           135           140
Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu Cys Trp Val Phe Ser Ala
      145           150           155           160
Leu Tyr Gly Leu Ile His Ile Leu Leu Met Thr Arg Val Thr Phe Cys
      165           170           175
Gly Ser Gln Lys Ile His Tyr Leu Phe Cys Glu Met Tyr Phe Leu Leu
      180           185           190
Arg Leu Ala Cys Ser Asn Ile His Val Asn His Thr Val Leu Val Ala
      195           200           205
Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu Gly Phe Met Ile Thr Ser
      210           215           220
Tyr Ala Arg Ile Val Arg Ala Ile Leu Gln Ile Pro Ser Ala Thr Gly
      225           230           235           240
Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Ser
      245           250           255
Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr Leu Gln Pro Leu Gln Thr
      260           265           270
Tyr Ser Met Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr
      275           280           285
Pro Met Ile Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met His
      290           295           300
Gly Ala Leu Gly Arg Leu Arg Gln Gly Lys Ala Phe Gln Lys Leu Thr
      305           310           315           320

```

<210> 1969

<211> 276

<212> PRT

<213> Unknown (H38g887 protein)

<220>

<223> Synthetic construct

&lt;400&gt; 1969

```

Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly
 1           5           10           15
Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu
      20           25           30
Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
      35           40           45
Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
      65           70           75           80
Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
      85           90           95
Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
      100           105           110
Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
      115           120           125
Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
      130           135           140
Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
      145           150           155           160
Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
      165           170           175
Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
      180           185           190
Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
      195           200           205
Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
      210           215           220
Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
      225           230           235           240
Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
      245           250           255
Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
      260           265           270
Leu Ser Val Thr
      275

```

&lt;210&gt; 1970

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g888 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1970

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
      20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65           70           75           80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
      85           90           95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
      100           105           110

```

Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys  
 115 120 125  
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu  
 130 135 140  
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr  
 145 150 155 160  
 Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr  
 165 170 175  
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr  
 180 185 190  
 His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu  
 195 200 205  
 Thr Leu Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr  
 210 215 220  
 Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala  
 245 250 255  
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val  
 260 265 270  
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu  
 290 295 300  
 Trp Arg Pro Phe Gln Arg Pro Lys  
 305 310

&lt;210&gt; 1971

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g889 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(299)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1971

Met Ala Asp Gly Asn Tyr Lys Arg Ile Thr Glu Phe Ile Phe Val Gly  
 1 5 10 15  
 Leu Arg Tyr His Leu Gln Leu Gln Val Phe Leu Phe Leu Pro Phe Leu  
 20 25 30  
 Pro Phe Tyr Leu Ile Thr Met Thr Glu Asn Leu Gly Met Met Val Arg  
 35 40 45  
 Ile Trp Leu Asp Ser Cys Phe His Thr Pro Met Tyr Phe Val Leu Ser  
 50 55 60  
 Tyr Leu Ser Phe Val Asp Ile Cys Phe Ser Ser Val Val Gly His Lys  
 65 70 75 80  
 Leu Leu Thr Asp Leu Phe Ala Val Arg Lys Ala Ile Ser Phe Leu Gly  
 85 90 95  
 Cys Pro Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Val Ile Glu Tyr  
 100 105 110  
 Leu Leu Leu Ala Ser Met Ala Tyr Asp Asn Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Ser Val Ala Met Xaa Xaa Arg Leu Cys Ile Gln Leu  
 130 135 140  
 Val Val Val Arg Tyr Ala Ala Asp Phe Phe Asn Thr Ile Thr His Thr  
 145 150 155 160  
 Thr Ala Ala Phe His Phe Pro Phe Phe His Ser Asn Ile Ile Asn His

165 170 175  
 Phe Phe Cys Asp Met Ser Leu Leu Leu Ser Leu Val Cys Ala Asp Ala  
 180 185 190  
 Arg Ile Asn Lys Leu Leu Val Phe Ile Val Ala Gly Ala Val Leu Val  
 195 200 205  
 Val Ser Ser Leu Thr Ile Ile Ile Ser Tyr Phe Tyr Ile Leu Thr Asp  
 210 215 220  
 Ile Leu Arg Ile Cys Ser Ala Asn Gly Lys Asn Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Thr Ala Val Ser Ile Phe Tyr Gly Ser Leu Phe  
 245 250 255  
 Phe Ser Tyr Val Arg Pro Gly Ala Thr Phe Tyr Pro Glu Leu Asn Lys  
 260 265 270  
 Ile Val Leu Val Phe Cys Ile Ile Pro Met Leu Lys Pro Leu Ile Tyr  
 275 280 285  
 Ser Leu Ile Asn Lys Glu Val Ser Xaa Pro Leu  
 290 295

&lt;210&gt; 1972

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g890 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1972

Met Glu Lys Ile Asn Asn Val Thr Glu Phe Ile Phe Trp Gly Leu Ser  
 1 5 10 15  
 Gln Ser Pro Glu Ile Glu Lys Val Cys Phe Val Val Phe Ser Phe Phe  
 20 25 30  
 Tyr Ile Ile Ile Leu Leu Gly Asn Leu Leu Ile Met Leu Thr Val Cys  
 35 40 45  
 Leu Ser Asn Leu Phe Lys Ser Pro Met Tyr Phe Phe Leu Ser Phe Leu  
 50 55 60  
 Ser Phe Val Asp Ile Cys Tyr Ser Ser Val Thr Ala Pro Lys Met Ile  
 65 70 75 80  
 Val Asp Leu Leu Ala Lys Asp Lys Thr Ile Ser Tyr Val Gly Cys Met  
 85 90 95  
 Leu Gln Leu Leu Gly Val His Phe Phe Gly Cys Thr Glu Ile Phe Ile  
 100 105 110  
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Met Thr Ile Met Asn Arg Glu Thr Cys Asn Lys Met Leu Leu  
 130 135 140  
 Gly Thr Trp Val Gly Gly Phe Leu His Ser Ile Ile Gln Val Ala Leu  
 145 150 155 160  
 Val Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe  
 165 170 175  
 Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Thr Glu Thr Tyr Ile  
 180 185 190  
 Val Gly Val Val Val Thr Ala Asn Ser Gly Thr Ile Ala Leu Gly Ser  
 195 200 205  
 Phe Val Ile Leu Leu Ile Ser Tyr Ser Ile Ile Leu Val Ser Leu Arg  
 210 215 220  
 Lys Gln Ser Ala Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Gly Ser  
 225 230 235 240  
 His Ile Ala Met Val Ile Phe Phe Gly Pro Cys Thr Phe Met Tyr  
 245 250 255  
 Met Arg Pro Asp Thr Thr Phe Ser Glu Asp Lys Met Val Ala Val Phe  
 260 265 270

Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ala Glu Val Lys Asn Ala Met Lys Lys Leu Trp Gly Arg Asn Val  
 290 295 300  
 Phe Leu Glu Ala Lys Gly Lys  
 305 310

<210> 1973

<211> 318

<212> PRT

<213> Unknown (H38g891 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1973

Met Asp Tyr Arg Asn Gln Thr Leu Val Thr Glu Phe Phe Ser Val Gly  
 1 5 10 15  
 Leu Thr Asn Leu Phe Gln His Lys Ile Ala Leu Phe Leu Val Phe Leu  
 20 25 30  
 Phe Val Tyr Leu Val Thr Val Pro Gly Asn Leu Gly Met Ile Thr Leu  
 35 40 45  
 Ile Trp Met Asp Ser Arg Leu Gln Thr Pro Lys Tyr Phe Ser Leu Cys  
 50 55 60  
 His Leu Ser Phe Val Asp Val Cys Ser Ser Ser Ala Ile Gly Pro Lys  
 65 70 75 80  
 Met Leu Thr Asp Ile Phe Val Glu Lys Lys Val Ile Ser Phe Gly Cys  
 85 90 95  
 Val Ala Gln Leu Trp Phe Phe Gly His Phe Val Val Thr Glu Cys Phe  
 100 105 110  
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Met Ala Ile Tyr Lys Pro  
 115 120 125  
 Leu Leu Tyr Thr Leu Ile Met Ser Gln Gln Val Cys Val Gln Leu Val  
 130 135 140  
 Val Gly Pro Tyr Ala Val Gly Leu Ile Ser Thr Met Thr His Met Thr  
 145 150 155 160  
 Phe Thr Phe Arg Leu Leu Tyr Cys Gly Pro Asn Ile Ile Asn His Phe  
 165 170 175  
 Phe Cys Asp Leu Leu Pro Val Leu Ser Leu Ala Tyr Ala Asp Thr His  
 180 185 190  
 Ile Asn Lys Cys Leu Leu Phe Ile Leu Val Gly Ala Leu Gly Val Leu  
 195 200 205  
 Ser Gly Val Ile Ile Leu Val Ser Tyr Ile Tyr Ile Val Ile Ala Ile  
 210 215 220  
 Leu Arg Ile Arg Ser Ala Asp Ala Arg Arg Lys Asp Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Met Ala Val Ser Ile Leu Tyr Gly Thr Leu Phe Phe  
 245 250 255  
 Ile Cys Val Cys Pro Ser Ser Ser Phe Ser Ile Asn Ile Asn Lys Val  
 260 265 270  
 Val Ser Leu Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ser Phe Ser Lys Lys Phe  
 290 295 300  
 Glu Arg Lys Lys Phe Leu Ile Gly Arg Xaa Thr Arg Ile Pro  
 305 310 315

<210> 1974  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g892 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(310)  
 <223> Xaa = Any Amino Acid

<400> 1974  
 Met Val Asn Phe Thr His Val Ser Glu Phe Val Leu Leu Gly Phe Gln  
 1 5 10 15  
 Gly Gly Pro Gly Met Gln Ala Met Leu Phe Leu Ile Phe Leu Ile Leu  
 20 25 30  
 Tyr Gly Ile Ala Val Val Gly Asn Leu Gly Met Ile Val Ile Ile Trp  
 35 40 45  
 Val Asp Ala His Leu His Thr Pro Met Tyr Ala Phe Leu Gln Ser Leu  
 50 55 60  
 Ser Leu Leu Asp Ile Cys Tyr Ser Ser Thr Ile Ala Pro Arg Ala Leu  
 65 70 75 80  
 Ala Asn Ser Met Gln Glu Asp His Thr Ile Ser Phe Gly Gly Cys Ala  
 85 90 95  
 Ala Gln Phe Phe Phe Leu Ser Leu Phe Gly Ile Thr Glu Ala Phe Leu  
 100 105 110  
 Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu  
 115 120 125  
 Leu Tyr Ser Val Ser Met Ser His Gln Val Cys Val Leu Leu Ile Ser  
 130 135 140  
 Gly Ser Tyr Leu Trp Gly Val Val Asn Ala Ile Ala Gln Thr Thr Met  
 145 150 155 160  
 Thr Phe Arg Leu Pro Phe Cys Gly Ser Asn Glu Ile Asn Asp Phe Phe  
 165 170 175  
 Cys Asp Val Pro Pro Leu Leu Ser Leu Ser Cys Ser Asp Thr Phe Ile  
 180 185 190  
 Asn Gln Leu Val Leu Leu Gly Leu Cys Gly Ser Ile Ile Val Ser Thr  
 195 200 205  
 Phe Leu Ile Val Leu Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu  
 210 215 220  
 Arg Ile Pro Thr Met Gln Gly Arg Xaa Lys Ala Phe Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Leu Thr Gly Val Cys Leu Phe Phe Gly Thr Val Phe Phe Met  
 245 250 255  
 Tyr Ala Gln Pro Ser Ala Ile Phe Phe Met Glu Gln Ser Lys Ile Val  
 260 265 270  
 Ser Ile Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Glu Val Lys Gln Ala Leu Arg Arg Ser Met Gln  
 290 295 300  
 Lys Leu Ser Leu Xaa Ser  
 305 310

<210> 1975  
 <211> 309  
 <212> PRT  
 <213> Unknown (H38g893 protein)

<220>  
 <223> Synthetic construct



<400> 1975  
 Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu  
 20 25 30  
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala  
 35 40 45  
 Ile Cys Ser Asp Val Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser  
 100 105 110  
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser His  
 115 120 125  
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu  
 130 135 140  
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr  
 145 150 155 160  
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn  
 165 170 175  
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile  
 180 185 190  
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val  
 195 200 205  
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val  
 210 215 220  
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly  
 245 250 255  
 Thr Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile  
 260 265 270  
 Thr Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg Lys Leu Phe Asn  
 290 295 300  
 Lys Arg Ile Ser Ser  
 305

<210> 1976

<211> 309

<212> PRT

<213> Unknown (H38g894 protein)

<220>

<223> Synthetic construct

<400> 1976

Met Lys Lys Glu Asn Gln Ser Phe Asn Leu Asp Phe Ile Leu Leu Gly  
 1 5 10 15  
 Val Thr Ser Gln Gln Glu Gln Asn Asn Val Phe Phe Val Ile Phe Leu  
 20 25 30  
 Cys Ile Tyr Pro Ile Thr Leu Thr Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Cys Ala Asp Ile Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Val Asp Ile Ile Phe Ser Ser Val Thr Ile Pro Lys

```

65          70          75          80
Val Leu Ala Asn His Leu Leu Gly Ser Lys Phe Ile Ser Phe Gly Gly
          85          90          95
Cys Leu Met Gln Met Tyr Phe Met Ile Ala Leu Ala Lys Ala Asp Ser
          100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Cys
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Leu Leu
          130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Thr Ser Ala Leu Pro His Thr
145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
          165          170          175
Phe Tyr Cys Asp Ile Met Pro Leu Leu Lys Leu Ser Cys Ser Asp Val
          180          185          190
His Phe Asn Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Leu
          195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Val Gln Val Phe Ser Thr Val
          210          215          220
Phe Gln Val Pro Ser Thr Lys Ser Leu Phe Lys Ala Phe Cys Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Phe Leu Tyr Tyr Gly Thr Thr Met Gly
          245          250          255
Met Tyr Phe Arg Pro Leu Thr Ser Tyr Ser Pro Lys Asp Ala Val Ile
          260          265          270
Thr Val Met Tyr Val Ala Val Thr Pro Ala Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Trp Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Ser
          290          295          300
Lys Arg Ile Ser Ser
305

```

&lt;210&gt; 1977

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g895 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1977

```

Ala Leu Leu Phe His Ser Tyr Lys His Pro Thr Gln Arg Arg Met Thr
1          5          10          15
Val Lys Ser His Ser Ile Val Thr Glu Phe Ser Leu Arg Gly Leu Thr
          20          25          30
Lys Gln Pro Asp Leu Gln Leu Phe His Phe Leu Ile Phe Leu Asp Ile
          35          40          45
His Met Val Thr Met Val Gly Asn Leu Gly Met Ile Thr Leu Ile Cys
          50          55          60
Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Phe Ser Asn Leu
65          70          75          80
Ser Leu Leu Asp Leu Cys Tyr Ser Ser Ile Thr Asn Pro Lys Met Leu
          85          90          95
Val Asn Phe Val Leu Lys Lys Ser Ile Ile Ser Tyr Ala Gly Tyr Met
          100          105          110
Ser Xaa Phe Tyr Phe Phe Leu Val Phe Val Ile Ala Arg Cys Tyr Met
          115          120          125

```

```

Leu Met Val Lys Ala Cys Asp His Tyr Val Ala Ile Cys Cys Pro Leu
 130                135                140
Leu Cys Asn Val Ile Met Ser His Val Thr Cys Ser Leu Met Val Ala
145                150                155                160
Val Val Tyr Thr Met Gly Leu Val Val Ser Thr Ile Glu Thr Gly Leu
                165                170                175
Ile Leu Lys Leu Pro Tyr Cys Glu Leu Leu Thr Ser Arg Cys Phe Cys
                180                185                190
Asp Ile Leu Pro Leu Met Lys Leu Ser Xaa Ser Ser Ala Tyr Asp Val
                195                200                205
Glu Met Ala Val Phe Phe Phe Ala Arg Phe Asn Leu Arg Ile Met Ile
                210                215                220
Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Phe Ser Ile Leu His
225                230                235                240
Ile Ser Thr Thr Glu Gly Arg Ser Lys Val Phe Ser Thr Cys Ser Phe
                245                250                255
His Leu Ala Ala Ile Gly Met Phe His Gly Xaa Thr Ala Phe Arg Tyr
                260                265                270
Leu Lys Pro Ala Ile Thr Ser Ser Leu Ala Gln Glu Asn Val Ala Ser
                275                280                285
Val Phe Tyr Thr Thr Val Ile Tyr Val Pro Asn Pro Leu Met Tyr Ser
                290                295                300
Leu Lys Asn Lys Asp Val Lys Ala Ala Met Gln Lys Thr Leu Arg Ser
305                310                315                320
Lys Phe Cys Cys Arg Cys Asn Tyr Leu
                325

```

&lt;210&gt; 1978

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g896 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1978

```

Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu Leu Trp
 1                5                10                15
Gly Leu Ser Asp Gln Pro Gln Gln His Ile Phe Phe Leu Leu Phe
                20                25                30
Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile Val Leu
                35                40                45
Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu
                50                55                60
Ala Ser Leu Ser Cys Ala Asp Ile Phe Ser Thr Ser Thr Thr Val Pro
65                70                75                80
Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser Tyr Ala
                85                90                95
Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp
                100                105                110
Ile Phe Leu Pro Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
                115                120                125
His Leu Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys Ala Phe
                130                135                140
Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Leu Ala Met Thr Arg
145                150                155                160
Thr Phe Leu Ile Phe Arg Leu Ser Leu Cys Ser Xaa Ile Leu Pro Gly

```

<210> 1979  
<211> 336  
<212> PRT  
<213> Unknown (H38g897 protein)

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(336)
<223> Xaa = Any Amino Acid
```

<400> 1979															
Asp	Thr	Asp	Pro	Gln	Ser	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu
1				5					10					15	
Lys	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Val	Val	Ala	Gly	Leu	Phe	
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40						45		
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu
		50				55					60				
Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70					75					80
Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala
				85					90					95	
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
			100					105					110		
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile
		115					120					125			
Cys	His	Pro	Leu	Tyr	Cys	Ser	Ala	Ile	Phe	Asn	Pro	Cys	Phe	Cys	Gly
		130				135					140				
Phe	Leu	Asp	Leu	Leu	Ser	Phe	Ile	Phe	Phe	Phe	Leu	Ser	Leu	Ser	Asp
145					150					155					160
Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp
				165					170					175	
Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Ser	His	Leu
			180					185						190	
Ala	Cys	Cys	Asp	Thr	Phe	Thr	Arg	Asn	Ile	Met	Tyr	Phe	Pro	Ala	Ala
		195					200					205			
Ile	Phe	Gly	Phe	Leu	Pro	Ile	Leu	Gly	Thr	Leu	Phe	Ser	Tyr	Cys	Lys
		210				215					220				

```

Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
225          230          235          240
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr
          245          250          255
Gly Thr Gly Ile Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
          260          265          270
Arg Lys Gly Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
          275          280          285
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val
          290          295          300
Leu Arg Arg Pro His Gly Ser Thr Val Xaa Ser Gln His Leu Leu Ile
305          310          315          320
Cys Ser Ile Pro Phe Val Gly Trp Phe Lys Lys Gly Ala Lys Val Lys
          325          330          335

```

&lt;210&gt; 1980

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g898 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(309)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1980

```

Met Arg Gln Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
1          5          10          15
Gln Asp Leu Asp Val Gln Lys Ala Leu Phe Val Ile Phe Leu Leu Thr
          20          25          30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
          35          40          45
Thr Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
          50          55          60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
65          70          75          80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
          85          90          95
Gly Gln Leu Phe Ile Tyr His Leu Phe Gly Gly Ser Glu Val Phe Leu
          100          105          110
Leu Val Val Met Ala Cys Asp His Tyr Val Ala Ile Cys Lys Pro Leu
          115          120          125
His Tyr Leu Thr Ile Met Asn Arg Gln Val Xaa Ile Leu Leu Val
          130          135          140
Val Val Val Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Val Val
145          150          155          160
Val Tyr Ser Leu Ala Phe Cys Gly Pro Asn Val Ile Asp Tyr Phe Val
          165          170          175
Cys Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr Phe
          180          185          190
Ile Gly Leu Thr Val Phe Val Asn Gly Gly Thr Ile Cys Ile Val Val
          195          200          205
Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu Lys
          210          215          220
Thr Tyr Ser Gln Glu Gly Arg His Lys Val Leu Phe Thr Cys Ser Ser
225          230          235          240
His Ile Ile Val Phe Ala Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
          245          250          255
Val Arg Pro Val Ser Asn Tyr Pro Phe Asp Lys Phe Leu Thr Val Phe

```

260 265 270  
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Asn Ser Glu Met Arg Asn Ser Val Glu Thr Leu Leu Cys Lys Ser Xaa  
 290 295 300  
 Leu Tyr Xaa Ser Lys  
 305

<210> 1981  
 <211> 313  
 <212> PRT  
 <213> Unknown (H38g899 protein)

<220>  
 <223> Synthetic construct

<400> 1981  
 Met Glu Arg Ile Asn Ser Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly  
 1 5 10 15  
 Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe  
 20 25 30  
 Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr  
 35 40 45  
 Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu  
 50 55 60  
 Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro  
 65 70 75 80  
 Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly  
 85 90 95  
 Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln  
 100 105 110  
 Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys  
 115 120 125  
 Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu  
 130 135 140  
 Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln  
 145 150 155 160  
 Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp  
 165 170 175  
 Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala Cys Ala Asp  
 180 185 190  
 Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val  
 195 200 205  
 Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln  
 210 215 220  
 Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys  
 245 250 255  
 Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala  
 260 265 270  
 Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu  
 290 295 300  
 Arg Ser Pro Arg Thr Pro Ser Glu Val  
 305 310

<210> 1982  
 <211> 318  
 <212> PRT

<213> Unknown (H38g900 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1982

```

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Thr Val Val Arg Asp Phe
 1           5           10           15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Ile Arg Ser Leu Leu Phe
      20           25           30
Leu Val Phe Phe Val Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
 35           40           45
Ile Leu Leu Thr Val Trp Ala Asp Pro Lys Leu Arg Ala Arg Pro Met
 50           55           60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
 65           70           75           80
Val Ile Val Pro Xaa Ile Ile Leu Asn Phe Thr Pro Ala Asn Lys Ala
      85           90           95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
 100           105           110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
 115           120           125
Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
 130           135           140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
 145           150           155           160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
      165           170           175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
 180           185           190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
 195           200           205
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
 210           215           220
Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
 225           230           235           240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
      245           250           255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
 260           265           270
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
 275           280           285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
 290           295           300
Lys Arg Ile Thr Ala Gly Gln Gly Thr Glu Xaa Lys Xaa Val
 305           310           315

```

<210> 1983

<211> 310

<212> PRT

<213> Unknown (H38g901 protein)

<220>

<223> Synthetic construct

<400> 1983

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe

```

1           5           10           15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe
      20      25      30
Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
      35      40      45
Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met
      50      55      60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
65      70      75      80
Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala
      85      90      95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
      100     105     110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
      115     120     125
Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg
      130     135     140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
145     150     155     160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
      165     170     175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu
      180     185     190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
      195     200     205
Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
      210     215     220
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg
225     230     235     240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
      245     250     255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro
      260     265     270
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
      275     280     285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
      290     295     300
Lys Arg Ile Thr Ala Gly
305      310

```

&lt;210&gt; 1984

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g902 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1984

```

Met Phe Ile Leu Thr Gly Phe Thr Asp Asp Phe Glu Leu Gln Val Phe
1           5           10           15
Leu Phe Leu Leu Phe Phe Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn
      20      25      30
Leu Gly Leu Val Val Leu Val Ile Glu Asp Ser Trp Leu His Asn Pro
      35      40      45
Met Tyr Tyr Phe Leu Ser Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser
      50      55      60
Thr Val Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys
65      70      75      80
Ser Ile Ser Phe Ile Gly Cys Ala Thr Gln Met Leu Leu Phe Val Thr
      85      90      95

```



```

Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp His
      100      105      110
Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro
      115      120      125
Arg Val Tyr Val Pro Leu Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu
      130      135      140
His Ala Thr Ile His Ile Val Ala Thr Phe Ser Leu Ser Phe Cys Gly
      145      150      155      160
Ser Asn Glu Ile Arg His Val Phe Cys Asp Met Pro Pro Leu Leu Ala
      165      170      175
Ile Ser Cys Ser Asp Thr His Thr Asn Gln Leu Leu Leu Phe Tyr Phe
      180      185      190
Val Gly Ser Ile Glu Ile Val Thr Ile Leu Ile Val Leu Ile Ser Cys
      195      200      205
Asp Phe Ile Leu Leu Ser Ile Leu Lys Met His Ser Ala Lys Gly Arg
      210      215      220
Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Gly Val Thr Ile
      225      230      235      240
Tyr His Gly Thr Ile Leu Val Ser Tyr Met Arg Pro Ser Ser Ser Tyr
      245      250      255
Ala Ser Asp His Asp Ile Ile Val Ser Ile Phe Tyr Thr Ile Val Ile
      260      265      270
Pro Lys Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
      275      280      285
Lys Ala Val Lys Lys Met Leu Lys Leu Val Tyr Lys
      290      295      300

```

&lt;210&gt; 1985

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g903 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1985

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Leu Ala Val Arg Ser Glu Ser Pro Leu His Thr Thr Met Tyr Phe
      50      55      60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Lys Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu

```

```

      165      170      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180      185      190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
      195      200      205
Phe Gly Ph Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
      210      215      220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225      230      235      240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
      245      250      255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
      260      265      270
Asn Gly Val Val Val Ser Val Lys Xaa Ala Val Val Thr Pro Met Pro
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290      295      300
Arg Arg Leu Pro Asn Lys Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
      305      310      315      320
Phe Phe Trp Cys

```

<210> 1986  
 <211> 335  
 <212> PRT  
 <213> Unknown (H38g904 protein)

<220>  
 <223> Synthetic construct  
  
 <221> VARIANT  
 <222> (1)...(335)  
 <223> Xaa = Any Amino Acid

```

<400> 1986
Asp Thr Asp Pro Gln Ser Ile Thr Asp Val Ser Ile Phe Leu Leu Leu
 1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Lys Val Ile Tyr Ala Gly
      85      90      95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Lys
      100      105      110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Pro Ile Cys
      115      120      125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
      130      135      140
Leu Asn Leu Leu Ser Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
      165      170      175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
      180      185      190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
      195      200      205

```

Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met  
 210 215 220  
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala  
 225 230 235 240  
 Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly  
 245 250 255  
 Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg  
 260 265 270  
 Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu  
 275 280 285  
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu  
 290 295 300  
 Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys  
 305 310 315 320  
 Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys  
 325 330 335

&lt;210&gt; 1987

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g905 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1987

Met Glu Asn Arg Lys Asn Val Thr Xaa Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Gln Asn Pro Glu Gly Gln Lys Val Leu Phe Val Thr Phe Leu Leu Ile  
 20 25 30  
 Tyr Ile Val Thr Ile Met Gly Asn Leu Leu Ile Met Val Thr Ile Met  
 35 40 45  
 Ala Ser Gln Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu  
 50 55 60  
 Ser Phe Ile His Thr Val Tyr Tyr Thr Ala Ile Ala Pro Lys Met Ile  
 65 70 75 80  
 Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Gln Gly Cys Met  
 85 90 95  
 Ala Gln Leu Phe Met Asp His Leu Phe Ala Gly Ala Glu Val Ile Leu  
 100 105 110  
 Leu Val Val Met Ala Tyr Asp Gln Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Ile Ile Met Asn Arg Arg Val Cys Val Leu Met Leu Leu  
 130 135 140  
 Val Ala Trp Ile Gly Gly Phe Leu His Ser Leu Val Gln Phe Leu Phe  
 145 150 155 160  
 Ile Tyr Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Asn Phe Leu  
 165 170 175  
 Cys Asp Leu Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asn Thr Tyr Val  
 180 185 190  
 Thr Gly Leu Ser Met Ile Ala Asn Gly Gly Ala Ile Cys Thr Val Thr  
 195 200 205  
 Phe Phe Pro Leu Leu Leu Ser Tyr Gly Val Ile Leu Pro Ser Leu Lys  
 210 215 220  
 Thr Gln Ser Leu Glu Gly Lys Cys Lys Ala Phe Tyr Thr Cys Ala Ser  
 225 230 235 240  
 His Ile Thr Val Ile Thr Leu Phe Phe Val Pro Cys Ile Phe Leu Leu

245 250 255  
 Ala Arg Pro Asn Ser Thr Phe Pro Ile Asp Lys Ser Met Thr Val Val  
 260 265 270  
 Leu Thr Cys Ile Thr Pro Met Leu Lys Pro Leu Ile Tyr Ala Leu Arg  
 275 280 285  
 Asn Ala Glu Met Lys Ser Ala Met Arg Lys Leu Trp Ser Glu Lys Val  
 290 295 300  
 Ser Leu Ala Gly Lys Gly  
 305 310

<210> 1988

<211> 308

<212> PRT

<213> Unknown (H38g906 protein)

<220>

<223> Synthetic construct

<400> 1988

His Met Pro Pro Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Gln Asn Pro His Leu Gln Lys Ile Leu Phe Ile Val Phe Leu Phe Ile  
 20 25 30  
 Phe Leu Phe Thr Met Leu Ala Asn Leu Phe Ile Val Ile Thr Ile Ser  
 35 40 45  
 Cys Ser Pro Thr Leu Ser Ser Pro Met Tyr Phe Phe Leu Thr Tyr Leu  
 50 55 60  
 Ser Phe Ile Asp Ala Ser Tyr Thr Ser Val Thr Thr Pro Lys Met Ile  
 65 70 75 80  
 Thr Asp Leu Leu Tyr Gln Arg Arg Thr Ile Ser Leu Ala Gly Cys Leu  
 85 90 95  
 Thr Gln Leu Phe Val Glu His Leu Leu Gly Gly Ser Glu Ile Ile Leu  
 100 105 110  
 Leu Ile Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Thr Ile Met Gln Gln Gly Ile Cys His Leu Leu Val Val  
 130 135 140  
 Ile Ala Trp Ile Gly Gly Ile Leu His Ala Thr Val Gln Ile Leu Phe  
 145 150 155 160  
 Met Thr Asp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met  
 165 170 175  
 Cys Asp Leu Phe Pro Leu Leu Lys Leu Ala Cys Arg Asp Thr Tyr Arg  
 180 185 190  
 Leu Gly Met Leu Val Ala Ala Asn Ser Gly Ala Met Cys Leu Leu Ile  
 195 200 205  
 Phe Ser Leu Leu Val Ile Ser Tyr Ile Val Ile Leu Ser Ser Leu Lys  
 210 215 220  
 Ser Tyr Ser Ser Glu Gly Gln His Lys Ala Leu Ser Thr Cys Gly Ser  
 225 230 235 240  
 His Phe Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr  
 245 250 255  
 Met His Pro Val Val Thr Tyr Ser Val Asp Lys Leu Val Thr Val Phe  
 260 265 270  
 Phe Ala Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Val Arg  
 275 280 285  
 Asn Thr Glu Val Lys Asn Ala Val Arg Ser Leu Leu Arg Lys Arg Val  
 290 295 300  
 Thr Val Tyr Ala  
 305

<210> 1989

<211> 166  
 <212> PRT  
 <213> Unknown (H38g907 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(166)  
 <223> Xaa = Any Amino Acid

<400> 1989  
 Met Tyr Thr Thr Leu Leu Met Ala Arg Leu Cys Leu Cys Ala Asp Asn  
 1 5 10 15  
 Val Ile Pro His Ser Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala  
 20 25 30  
 Leu Ser Asp Thr Arg Val Asn Glu Xaa Val Ile Phe Ile Met Gly Gly  
 35 40 45  
 Leu Ile Leu Val Ile Pro Ser Ile Leu Ile Leu Gly Ser Tyr Ala Arg  
 50 55 60  
 Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Cys Ile Cys Lys  
 65 70 75 80  
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr  
 85 90 95  
 Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr  
 100 105 110  
 Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met  
 115 120 125  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala  
 130 135 140  
 Leu Ser Arg Val Ile His Gln Lys Lys Thr Phe Phe Ser Leu Xaa Xaa  
 145 150 155 160  
 Xaa His Leu Glu Leu Leu  
 165

<210> 1990  
 <211> 333  
 <212> PRT  
 <213> Unknown (H38g908 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(333)  
 <223> Xaa = Any Amino Acid

<400> 1990  
 Met Gly Pro Lys Asn Leu Thr Arg Val Leu Glu Phe Phe Leu Leu His  
 1 5 10 15  
 Phe Leu Asp Asp Leu Glu Leu Gln Pro Phe Leu Ser Gly Cys Pro Xaa  
 20 25 30  
 Thr Met His Leu Val Thr Val Leu Ala Asn Leu Leu Thr Ser Phe Xaa  
 35 40 45  
 Leu Ser Ala Leu Pro His Leu His Asn Pro Met Asn Phe Asn Leu Ser  
 50 55 60  
 Leu Ala Asp Ile Gly Phe Thr Pro Ala Thr Ile Ser Lys Ile Thr Val  
 65 70 75 80  
 Asp Leu Gln Thr His Ser Arg Ile Ile Leu Tyr Met Ser Cys Leu Lys  
 85 90 95  
 Xaa Met Ser Phe Lys Ile Ile Phe Gly Cys Leu His Asn Leu Leu Met

```

      100              105              110
Thr Val Met Ala Tyr Asp Pro Phe Val Ala Thr Cys His Leu Leu Tyr
      115              120              125
Tyr Thr Val Ile Arg Asn Pro His Leu Cys Gly Leu Leu Leu Leu Val
      130              135              140
Ser Leu Phe Ser Leu Ser Phe Phe Phe Leu Ile Ser Leu Leu Glu Thr
145              150              155              160
Gln Leu Tyr Ser Leu Met Val Ser Gln Val Leu Cys Met Gln Asp Val
      165              170              175
Asp Ile Pro His Phe Phe Cys Asp Pro Ser Gln Phe Leu His Leu Ser
      180              185              190
Cys Ser Asp Thr Ala Thr Asn Asn Thr Leu Met His Phe Ile Gly Ala
      195              200              205
Ile Phe Cys Gly Pro Phe Ser Gly Ile Leu Tyr Cys Tyr Thr Gln Ile
      210              215              220
Met Phe Ser Ile Leu Ile Thr Leu Xaa Asn Val Gly Ser Ile Lys Gln
225              230              235              240
Thr Phe Ser Thr His Arg Ser His Leu Ser Val Val Cys Leu Phe Tyr
      245              250              255
Gly Thr Gly Leu Gly Val Tyr Leu Ser Leu Ala Gly Ser Pro Ser Pro
      260              265              270
Arg Thr Gly Val Val Ala Ser Met Val Tyr Thr Thr Val Thr Leu Met
      275              280              285
Leu Asn Pro Val Ile His Ser Leu Arg Asn Arg Asp Ile Lys Asn Thr
      290              295              300
Trp Trp Trp Leu Leu Ser Ile Thr Ala Trp Tyr Gln Tyr Leu Cys Tyr
305              310              315              320
Pro Leu Trp Ser Val Val Arg Lys Asn Ser Lys Leu Lys
      325              330

```

&lt;210&gt; 1991

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g909 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1991

```

Met Gly Thr Ser Asn Asn Glu Thr Glu Phe Ile Leu Leu Gly Ile Thr
1      5      10      15
Lys Asn Pro Glu Leu Arg Lys Ile Phe Ser Ala Leu Phe Leu Ala Met
      20      25      30
Tyr Val Thr Thr Val Leu Gly Asn Leu Phe Ile Val Val Thr Leu Ala
      35      40      45
Ala Ser Trp Ser Leu Arg Ser Pro Met Tyr Phe Ser Leu Thr Ser Leu
      50      55      60
Ser Leu Met Gly Ala Thr Tyr Ser Ser Ile Thr Ala Pro Lys Met Thr
65      70      75      80
Val Asp Ser Leu Arg Ser Thr Thr Ile Ser Leu Glu Gly Cys Met Thr
      85      90      95
Gln Leu Phe Ala Glu His Phe Ser Asp Gly Val Ala Ile Ile Leu Leu
      100      105      110
Thr Val Met Val Cys Asp Cys Tyr Glu Ala Ile Ser Lys Pro Leu His
      115      120      125
Asp Thr Thr Ile Met Ser Pro Arg Val Cys Cys Leu Leu Val Val Glu
      130      135      140
Ala Trp Val Gly Gly Leu Thr His Ala Thr Ile Gln Leu Phe Phe Phe
145      150      155      160
Leu Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
      165      170      175

```

Cys Asp Leu Phe Pro Leu Leu Lys Leu Ala Tyr Met Asp Thr His Met  
 180 185 190  
 Leu Gly Leu Leu Val Ile Leu Asn Ser Gly Val Met Cys Met Ala Ile  
 195 200 205  
 Phe Leu Ile Leu Ile Ala Ser Tyr Ile Val Thr Leu Tyr Ser Leu Lys  
 210 215 220  
 Ser Cys Ser Ser Val Gly Arg Arg Asn Thr Leu Ser Thr Cys Gly Ser  
 225 230 235 240  
 His His Thr Val Val Ile Leu Phe Phe Val Glu Cys Ile Phe Leu Tyr  
 245 250 255  
 Ile Arg Pro Val Val Thr Tyr Pro Ile Asp Lys Asp Met Ala Ile Ser  
 260 265 270  
 Phe Thr Ile Val Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285  
 Gly Ile Lys Val Lys Asn Ala Ile Arg Lys Met Trp Met Lys Gln Gly  
 290 295 300  
 Thr Leu Gly Gly  
 305

&lt;210&gt; 1992

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g910 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1992

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Val Asp Gly Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys Leu  
 20 25 30  
 Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala Leu  
 35 40 45  
 Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu Gly  
 50 55 60  
 His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro Arg  
 65 70 75 80  
 Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln Ala  
 85 90 95  
 Cys Leu Ala Glu Met Tyr Phe Phe Val Thr Leu Gly Ile Thr Glu Ser  
 100 105 110  
 Tyr Leu Met Ala Ala Met Ser Xaa Arg Ala Arg Arg Val Pro Ala  
 115 120 125  
 Pro Leu Tyr Gly Ala Leu Val Thr Pro Ser Ala Cys Ala Ser Leu Val  
 130 135 140  
 Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His Thr Leu  
 145 150 155 160  
 Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg Pro Phe  
 165 170 175  
 Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp Thr Ser  
 180 185 190  
 Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val Leu Ala  
 195 200 205  
 Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val Ala Val  
 210 215 220  
 Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly Ala His

225                      230                      235                      240  
 Leu Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser Val Leu Ser Val  
                                  245                      250                      255  
 Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr Asp Arg Leu Ala  
                                  260                      265                      270  
 Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn Pro Phe Ile Asn  
                                  275                      280                      285  
 Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Arg Gly Leu Arg  
                                  290                      295                      300  
 Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala Asn Leu Ala  
 305                      310                      315

&lt;210&gt; 1993

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g911 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 1993

Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly  
 1                      5                      10                      15  
 Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu  
                                  20                      25                      30  
 Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu  
                                  35                      40                      45  
 Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys  
                                  50                      55                      60  
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln  
 65                      70                      75                      80  
 Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly  
                                  85                      90                      95  
 Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys  
                                  100                      105                      110  
 Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn  
                                  115                      120                      125  
 Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu  
                                  130                      135                      140  
 Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr  
 145                      150                      155                      160  
 Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His  
                                  165                      170                      175  
 Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr  
                                  180                      185                      190  
 Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu  
                                  195                      200                      205  
 Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr  
                                  210                      215                      220  
 Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr  
 225                      230                      235                      240  
 Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu  
                                  245                      250                      255  
 Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg  
                                  260                      265                      270  
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu  
                                  275                      280                      285  
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Val  
                                  290                      295                      300  
 Trp Gly Arg Lys Thr Met Glu  
 305                      310



<210> 1994  
 <211> 316  
 <212> PRT  
 <213> Unknown (H38g912 protein)

<220>  
 <223> Synthetic construct

<400> 1994

```

Met Gln Asn Gln Ser Phe Val Thr Glu Phe Val Leu Leu Gly Leu Ser
1           5           10           15
Gln Asn Pro Asn Val Gln Glu Ile Val Phe Val Val Phe Leu Phe Val
          20           25           30
Tyr Ile Ala Thr Val Gly Gly Asn Met Leu Ile Val Val Thr Ile Leu
          35           40           45
Ser Ser Pro Ala Leu Leu Val Ser Pro Met Tyr Phe Phe Leu Gly Phe
          50           55           60
Leu Ser Phe Leu Asp Ala Cys Phe Ser Ser Val Ile Thr Pro Lys Met
65           70           75           80
Ile Val Asp Ser Leu Tyr Val Thr Lys Thr Ile Ser Phe Glu Gly Cys
          85           90           95
Met Met Gln Leu Phe Ala Glu His Phe Phe Ala Gly Val Glu Val Ile
          100          105          110
Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
          115          120          125
Leu His Tyr Ser Ser Ile Met Asn Arg Arg Leu Cys Gly Ile Leu Met
          130          135          140
Gly Val Ala Trp Thr Gly Gly Leu Leu His Ser Met Ile Gln Ile Leu
145          150          155          160
Phe Thr Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe
          165          170          175
Met Cys Asp Leu Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr His
          180          185          190
Ile Phe Gly Leu Met Val Val Ile Asn Ser Gly Phe Ile Cys Ile Ile
          195          200          205
Asn Phe Ser Leu Leu Leu Val Ser Tyr Ala Val Ile Leu Leu Ser Leu
          210          215          220
Arg Thr His Ser Ser Glu Gly Arg Trp Lys Ala Leu Ser Thr Cys Gly
225          230          235          240
Ser His Ile Ala Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val
          245          250          255
Tyr Thr Arg Pro Pro Ser Ala Phe Ser Leu Asp Lys Met Ala Ala Ile
          260          265          270
Phe Tyr Ile Ile Leu Asn Pro Leu Leu Asn Pro Leu Ile Tyr Thr Phe
          275          280          285
Arg Asn Lys Glu Val Lys Gln Ala Met Arg Arg Ile Trp Asn Arg Leu
          290          295          300
Met Val Val Ser Asp Glu Lys Glu Asn Ile Lys Leu
305          310          315

```

<210> 1995  
 <211> 310  
 <212> PRT  
 <213> Unknown (H38g913 protein)

<220>  
 <223> Synthetic construct

<400> 1995

```

Met Gln Leu Asn Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr

```

```

1           5           10           15
Gln Asp Pro Phe Trp Lys Lys Ile Val Phe Val Ile Phe Leu Arg Leu
20           25           30
Tyr Leu Gly Thr Leu Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys
35           40           45
Ala Ser Gln Ala Leu Lys Asn Pro Met Phe Phe Phe Leu Phe Tyr Leu
50           55           60
Ser Leu Ser Asp Thr Cys Leu Ser Thr Ser Ile Ala Pro Arg Met Ile
65           70           75           80
Val Asp Ala Leu Leu Lys Lys Thr Thr Ile Ser Phe Ser Glu Cys Met
85           90           95
Ile Gln Val Phe Ser Ser His Val Phe Gly Cys Leu Glu Ile Phe Ile
100          105          110
Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
115          120          125
His Tyr Met Thr Ile Ile Ser Gln Trp Val Cys Gly Val Leu Met Ala
130          135          140
Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val Gln Ile Phe Leu
145          150          155          160
Ala Leu Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Cys Phe
165          170          175
Cys Asp Leu Gln Pro Leu Leu Lys Gln Ala Cys Ser Glu Thr Tyr Val
180          185          190
Val Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ala Val Ser
195          200          205
Tyr Val Met Leu Ile Phe Ser Tyr Val Ile Phe Leu His Ser Leu Arg
210          215          220
Asn His Ser Ala Glu Val Ile Lys Lys Ala Leu Ser Thr Cys Val Ser
225          230          235          240
His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Met Tyr
245          250          255
Thr Cys Pro Ala Thr Val Phe Pro Met Asp Lys Met Ile Ala Val Phe
260          265          270
Tyr Thr Val Gly Thr Ser Phe Leu Asn Pro Val Ile Tyr Thr Leu Lys
275          280          285
Asn Thr Glu Val Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Leu
290          295          300
Ile Thr Asp Asp Lys Arg
305          310

```

&lt;210&gt; 1996

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g914 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1996

```

Met Glu Thr Thr Asn His Ser Ala Val Thr Glu Phe Phe Leu Val Gly
1           5           10           15
Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Leu Cys Leu
20           25           30
Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Phe Leu Ile Ile Ile
35           40           45
Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
50           55           60

```

Asn Leu Ser Phe Leu Gly Ile Cys Tyr Thr Ser Ser Ser Ile Pro Pro  
 65 70 75 80  
 Met Leu Ile Ile Phe Val Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly  
 85 90 95  
 Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Ile Glu Cys  
 100 105 110  
 Ile Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Ser Ile Ile Met Asn Arg Val Leu Tyr Val Gln Met  
 130 135 140  
 Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Arg Thr  
 145 150 155 160  
 Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Ile Ile Asp His  
 165 170 175  
 Leu Thr Cys Glu Ile Leu Ala Leu Leu Lys Val Ile Cys Ser Asp Ile  
 180 185 190  
 Ser Ile Asn Val Phe Ile Met Thr Val Ser Ser Ile Val Leu Leu Val  
 195 200 205  
 Ile Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser Ile Leu  
 210 215 220  
 Arg Ile Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Phe Thr Cys Ser  
 225 230 235 240  
 Ala His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Val Leu Phe Met  
 245 250 255  
 His Met Lys Pro Lys Ser Lys Phe Thr Thr Ala Ser Asp Glu Ile Ile  
 260 265 270  
 Gly Leu Ser Tyr Glu Val Ile Thr Pro Met Asn Pro Ile Ile Tyr Ser  
 275 280 285  
 Leu Arg Asn Lys Glu Ile Lys Glu Ala Val Lys Lys Ile Leu Ser Arg  
 290 295 300  
 His Val His Leu Trp Lys Ile Xaa Lys Ala Leu Arg His Val Thr Phe  
 305 310 315 320  
 Ser

&lt;210&gt; 1997

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g915 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(177)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 1997

Ala Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Phe Phe  
 1 5 10 15  
 Leu Lys Asn Leu Ser Val Leu Asp Leu Cys Tyr Ile Ser Val Thr Val  
 20 25 30  
 Pro Lys Ser Ile Arg Asn Ser Leu Thr Arg Arg Ser Ser Ile Ser Tyr  
 35 40 45  
 Leu Gly Cys Val Ala Gln Ala Tyr Phe Phe Ser Ala Phe Ala Ser Ala  
 50 55 60  
 Glu Leu Ala Phe Leu Thr Val Met Ser Tyr Asp Arg Tyr Val Ala Ile  
 65 70 75 80  
 Cys His Pro Leu Gln Tyr Arg Ala Val Met Thr Ser Gly Gly Cys Tyr  
 85 90 95  
 Gln Met Ala Val Thr Thr Trp Leu Ser Cys Phe Ser Tyr Ala Ala Val

100 105 110  
 His Thr Gly Asn Met Phe Arg Glu His Val Cys Arg Ser Asn Val Ile  
 115 120 125  
 His Gln Phe Phe Arg Asp Ile Pro Gln Val Leu Ala Leu Val Ser Xaa  
 130 135 140  
 Glu Val Phe Phe Val Glu Leu Xaa Pro Ser Pro Glu Pro Gln Cys Leu  
 145 150 155 160  
 Asp Leu Gly Cys Phe Ile Pro Met Met Ile Ser Asn Phe Pro Asn Leu  
 165 170 175  
 Leu

<210> 1998  
 <211> 191  
 <212> PRT  
 <213> Unknown (H38g916 protein)

<220>  
 <223> Synthetic construct  
 <221> VARIANT  
 <222> (1)...(191)  
 <223> Xaa = Any Amino Acid

<400> 1998  
 Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Leu Phe Leu  
 1 5 10 15  
 Ser Asp Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro  
 20 25 30  
 Gln Met Leu Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu  
 35 40 45  
 Gly Cys Ser Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu  
 50 55 60  
 Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys  
 65 70 75 80  
 Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln  
 85 90 95  
 Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln  
 100 105 110  
 Thr Ser Ser Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp  
 115 120 125  
 Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Xaa Gly Asp  
 130 135 140  
 Thr Ser Tyr Asn Glu Ile Gln Leu Thr Val Ser Ser Val Ile Leu Val  
 145 150 155 160  
 Asp Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln  
 165 170 175  
 Ala Gly Leu Arg Ile Asn Phe Ala Lys Ala Trp Lys Lys Gly Leu  
 180 185 190

<210> 1999  
 <211> 134  
 <212> PRT  
 <213> Unknown (H38g921 protein)

<220>  
 <223> Synthetic construct

<400> 1999  
 Cys Tyr Pro Leu Gln Leu Arg Lys Pro Phe Met Ser Ser Leu Ala Leu  
 1 5 10 15

Gln Ala Gln Ala Trp Pro Trp Val Pro Gly Ser Gly Gly Phe Val Ala  
                   20                  25                  30  
 Ile Ala Val Pro Thr Ser Pro Ser Ser Ser Gly Leu Ser Phe Cys Gly  
                   35                  40                  45  
 Pro Pro Val Ala Ile Asn His Phe Leu Ser Cys Asp Ile Ala Pro Leu  
                   50                  55                  60  
 Ile Ala Leu Ala Cys Thr Gln His Thr Gly Ser Glu Ser Phe Val Ala  
 65                  70                  75                  80  
 Phe Val Ile Ala Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu  
                   85                  90                  95  
 Val Ser His Met Cys Thr Ser Ser Ser Thr Ile Leu Arg Ile Pro Ser  
                   100                  105                  110  
 Ala Ser Gly Arg Lys Gln Ser Leu Ser Pro Arg Ala Pro Arg His Leu  
                   115                  120                  125  
 Thr Val Val Leu Ile Leu  
                   130

&lt;210&gt; 2000

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g924 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(196)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2000

Thr Pro Pro Met Tyr Phe Leu Phe Leu Gly Glu Ala Glu Cys Phe Leu  
 1                  5                  10                  15  
 Leu Ala Thr Met Glu Tyr Asp Arg Tyr Glu Asp Ile Cys Ser Pro Leu  
                   20                  25                  30  
 Asn Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Gly  
                   35                  40                  45  
 Asp Ser Trp Val Pro Ser Phe Pro Glu Ala Thr Glu Gln Ala Thr Met  
                   50                  55                  60  
 Ala Leu Arg Phe Pro Phe Xaa Gly Thr Asn Lys Val Asn His Leu Phe  
 65                  70                  75                  80  
 Leu Arg Gln Pro Ala Val Leu Lys Ala Gly Leu Met Gln Asp Thr Ala  
                   85                  90                  95  
 Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Ala Met Asn  
                   100                  105                  110  
 Pro Cys Leu Leu Ile Leu Ser Ser Tyr Thr Arg Ile Gly Ala Ala Ile  
                   115                  120                  125  
 Pro Gln Glu Pro Ile Lys Leu Lys Gly Lys Gln Xaa Arg Pro Phe Ser  
                   130                  135                  140  
 Thr Cys Ser Xaa His Leu Pro Trp Trp Pro Leu Phe Ser Asn Ile Ile  
 145                  150                  155                  160  
 Ile Xaa Ala Ser Thr Tyr Phe Leu Gly Leu Lys Ser Asn Lys Phe Phe  
                   165                  170                  175  
 Trp Arg Gly Lys Lys Val Val Phe Ile Tyr Thr Thr Leu Val Glu Thr  
                   180                  185                  190  
 Pro Xaa Trp Asn  
                   195

&lt;210&gt; 2001

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g925 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(128)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2001

```

His Cys Met Phe Leu Ala His Gly Ser Pro Leu Pro Pro Thr Gln Leu
 1           5           10           15
Pro Ile Xaa Phe Cys Asp Tyr Ile Ser His Arg Tyr Leu Thr Cys His
      20           25           30
Leu Ser Leu Pro Asn Ser Phe Ser Ser Phe Pro Tyr Gln Xaa Ile
      35           40           45
Leu Pro Leu Ser Leu Leu Ala Gln Ala Arg Asn Pro Gly Ile Ile Phe
      50           55           60
Phe Leu Pro Thr Phe Asn Ala Leu Xaa Ser Pro Val His Ser Thr Ser
65           70           75           80
Xaa Arg Leu Ser Leu Ser Thr Tyr Tyr Tyr Ala Ser Gln Glu Thr Ile
      85           90           95
Ser Pro Arg Phe Asp Ser Thr Ala Val Ala Ser Tyr Leu Ile Phe Leu
      100          105          110
His Leu Leu Trp Pro Ile Phe Asn Pro Phe Ile Tyr Cys Leu Arg Asn
      115          120          125

```

&lt;210&gt; 2002

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Unknown (H38g926 protein)

&lt;220&gt;

&lt;223&gt; Synthetic construct

&lt;400&gt; 2002

```

Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala Leu Leu Leu Thr Ser Met
 1           5           10           15
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Leu Ile
      20           25           30
Arg Met Arg Lys Arg Val Cys Ala Leu Met Ile Thr Gly Ser Trp Met
      35           40           45
Ile Gly Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala Leu Arg Ile
      50           55           60
Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Cys Asp Val Pro
65           70           75           80
Ala Met Leu Thr Leu Ala Cys Thr Asp Thr Trp Val Tyr Glu Cys Thr
      85           90           95
Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile Cys Ile
      100          105          110
Ala Cys Ser Tyr Gly Arg Ile Leu Leu Ala Val Tyr His Met His Ser
      115          120          125
Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr His Leu Thr
130          135          140
Val Val Thr Phe Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro
145          150          155          160
Lys Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Phe
      165          170          175
Phe Ile Ser Ser Phe Ser Ser Asn Pro Phe Met Tyr Thr Leu Arg Asn
      180          185          190

```

&lt;210&gt; 2003

<211> 158  
 <212> PRT  
 <213> Unknown (H38g927 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(158)  
 <223> Xaa = Any Amino Acid

<400> 2003

```

Pro Met Tyr Phe Phe Leu Ser Met Leu Ser Ile Ser Glu Thr Cys Tyr
 1           5           10           15
Met Val Ala Ile Thr Pro His Met Leu Ser Arg Leu Leu Asn Pro His
          20           25           30
Xaa Leu Ile Val Met Gln Gly Cys Val Thr Gln Leu Phe Tyr Val Thr
          35           40           45
Phe Gly Ile Asn Asn Cys Phe Leu Leu Ile Ala Met Gly Tyr Asp Cys
          50           55           60
Tyr Val Val Phe Cys Asn Pro Leu Arg Tyr Ser Xaa Val Arg Gly Leu
65           70           75           80
Cys Val Xaa Leu Gly Ser Gly Ser Leu Arg Ile Gly Leu Gly Met Ala
          85           90           95
Ile Val Gln Val Thr Ser Met Phe Gly Leu Pro Phe Cys Asp Asp Phe
          100          105          110
Val Ile Ser His Phe Phe Cys Asp Val Arg Pro Leu Leu Lys Leu Ala
          115          120          125
Cys Thr Asp Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val
          130          135          140
Cys Val Leu Val Leu His Ile Ala Leu Ile Phe Ile Ser Tyr
145           150           155

```

<210> 2004  
 <211> 192  
 <212> PRT  
 <213> Unknown (H38g928 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(192)  
 <223> Xaa = Any Amino Acid

<400> 2004

```

Leu Leu Ala Thr Lys Ala Tyr Asp Xaa Tyr Val Pro Ile Arg His Pro
 1           5           10           15
Phe Pro Tyr Pro Thr Arg Met Ser Pro Ala Met Cys Ala Ala Leu Val
          20           25           30
Gly Met Ala Trp Leu Val Ser His Gly Asn Ser Leu Leu Tyr Ile Leu
          35           40           45
Leu Met Ala Arg Leu Ser Phe Leu Cys Phe Pro Thr Lys Cys Thr His
          50           55           60
Phe Phe Cys Asp Pro Pro Ser Leu Ser Xaa Arg Leu Ser Cys Ser Asp
65           70           75           80
Asn His Thr Ser Lys Leu Leu Ile Phe Thr Lys Gly Ala Ala Val Val
          85           90           95
Val Thr Pro Leu Leu Leu Ile Leu Ala Ser Leu Trp Asp His Asn Lys
          100          105          110
Leu Thr Val Leu Gln Leu Pro Ser Thr Ser Gly Arg Leu Arg Asp Leu

```

```

      115              120              125
Xaa Pro Thr Cys Gly Ser His Leu Asp Val Val Ser Leu Phe Tyr Arg
   130              135              140
Thr Val Ile Ala Val Tyr Phe Gln Ala Thr Ser Ser Thr Arg Ala Glu
  145              150              155              160
Trp Asp Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu
              165              170              175
Asn Pro Ile Ile Tyr Ser Leu Thr Xaa Pro Arg Gly Arg Thr Leu Arg
      180              185              190

```

<210> 2005  
 <211> 176  
 <212> PRT  
 <213> Unknown (H38g929 protein)

<220>  
 <223> Synthetic construct

```

<400> 2005
Arg Val Pro Pro Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Val Phe
  1              5              10              15
Asp Met Gly Phe Ser Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu
      20              25              30
Met Gly Leu Gly Arg Leu Ile Ser Tyr Lys Asp Cys Val Cys Gln Leu
      35              40              45
Phe Phe Phe His Phe Leu Gly Ser Ile Glu Cys Phe Leu Phe Thr Val
      50              55              60
Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys Tyr Pro Leu Arg Tyr Thr
      65              70              75              80
Val Ile Met Asn Pro Arg Ile Cys Val Ala Leu Ala Val Gly Thr Trp
      85              90              95
Leu Leu Gly Cys Ile His Ser Ser Ile Leu Thr Ser Leu Thr Phe Thr
      100              105              110
Leu Pro His Cys Gly Pro Asn Glu Val Asp His Phe Phe Cys Asp Ile
      115              120              125
Pro Ala Leu Leu Pro Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg
      130              135              140
Val Ser Phe Thr Asn Val Gly Leu Ile Ser Ala Gly Cys Phe Leu Leu
      145              150              155              160
Asn Leu Leu Ser Tyr Thr Arg Ile Thr Asn Ile Tyr Leu Lys His Ser
      165              170              175

```

<210> 2006  
 <211> 44  
 <212> PRT  
 <213> Unknown (H38g930 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(44)  
 <223> Xaa = Any Amino Acid

```

<400> 2006
Cys Ile Lys Leu Gly Thr Glu Leu Gly Ser Thr Ser Asn Gly Arg Gln
  1              5              10              15
Cys Ala Gly Ile Arg Pro Ser Tyr Val Phe Thr Leu His Leu Xaa Ala
      20              25              30
Asn Val Asn Pro Phe Ile Tyr Thr Leu Ser Asn Lys
      35              40

```



<210> 2007  
 <211> 187  
 <212> PRT  
 <213> Unknown (H38g931 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(187)  
 <223> Xaa = Any Amino Acid

<400> 2007  
 Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Leu Leu Leu  
 1 5 10 15  
 Ser Gln Leu Ser Leu Met Asp Leu Met Tyr Ile Ser Thr Thr Val Pro  
 20 25 30  
 Lys Met Ala Tyr Asn Phe Leu Ser Gly Gln Lys Gly Ile Ser Phe Leu  
 35 40 45  
 Gly Cys Gly Val Gln Ser Phe Phe Leu Thr Met Ala Cys Ser Glu  
 50 55 60  
 Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys  
 65 70 75 80  
 His Ser Leu Tyr Tyr Pro Ile Arg Met Ser Lys Met Met Cys Val Lys  
 85 90 95  
 Met Ile Gly Gly Ser Trp Thr Leu Gly Ser Ile Asn Ser Leu Ala His  
 100 105 110  
 Thr Val Phe Ala Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asp  
 115 120 125  
 His Phe Phe Cys Asp Val Pro Ala Met Leu Leu Leu Ser Cys Thr Asp  
 130 135 140  
 Thr Trp Val Tyr Glu Tyr Met Val Leu Xaa Gly Gln Ser Leu Phe Leu  
 145 150 155 160  
 Leu Leu Pro Phe Ile Gly Ile Thr Ser Ser Glu Gly Arg Val Leu Ile  
 165 170 175  
 Ala Gly Tyr Ile Met His Ser Lys Glu Gly Arg  
 180 185

<210> 2008  
 <211> 62  
 <212> PRT  
 <213> Unknown (H38g934 protein)

<220>  
 <223> Synthetic construct

<221> VARIANT  
 <222> (1)...(62)  
 <223> Xaa = Any Amino Acid

<400> 2008  
 Gly Gly Asn Arg Lys Lys Arg Glu Lys Glu Gly Arg Lys Lys Arg Lys  
 1 5 10 15  
 Val Arg Lys Lys Thr Gly Xaa Gly Arg Xaa Glu Val Gly Leu Leu Lys  
 20 25 30  
 Gly Ser Asn Ile Val Met Tyr Met Ala Pro Lys Tyr Arg His Pro Glu  
 35 40 45  
 Glu Gln Gln Lys Val Leu Phe Leu Phe Tyr Ser Ser Phe Asn  
 50 55 60

<210> 2009  
 <211> 103  
 <212> PRT  
 <213> Homo sapien (1000494-1-1-323)

<400> 2009

```

Pro Tyr Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Val Thr
1          5          10          15
Asp Thr Ser Cys Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val
          20          25          30
Ile Ala Thr Pro Phe Val Cys Ile Leu Ala Pro Tyr Ala Arg Ile Leu
          35          40          45
Val Ala Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe
          50          55          60
Ser Ala Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr
65          70          75          80
Thr Ile Gly Val Tyr Leu Cys Arg Ser Ser Val Leu Thr Thr Ala Lys
          85          90          95
Glu Lys Ala Ser Ala Val Met
          100

```

<210> 2010  
 <211> 314  
 <212> PRT  
 <213> Homo sapien (1336040-1-1-945)

<400> 2010

```

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
1          5          10          15
Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
          20          25          30
Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
          35          40          45
Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val
65          70          75          80
Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
          85          90          95
Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
          100          105          110
Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
          130          135          140
Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val
145          150          155          160
His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
          165          170          175
Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
          180          185          190
Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
          195          200          205
Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
          210          215          220
Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
          245          250          255
Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
          260          265          270

```

Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn  
 275 280 285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu  
 290 295 300  
 Lys Val Leu Arg Ser Lys Val Asp Ser Ser  
 305 310

<210> 2011

<211> 317

<212> PRT

<213> Homo sapien (1336042-1-1-954)

<400> 2011

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu  
 20 25 30  
 Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu  
 35 40 45  
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln  
 65 70 75 80  
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser  
 85 90 95  
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe  
 100 105 110  
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp  
 115 120 125  
 Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu  
 130 135 140  
 Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr  
 145 150 155 160  
 Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His  
 165 170 175  
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr  
 180 185 190  
 Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met  
 195 200 205  
 Thr Pro Leu Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile  
 245 250 255  
 Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys  
 260 265 270  
 Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu  
 290 295 300  
 Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr  
 305 310 315

<210> 2012

<211> 318

<212> PRT

<213> Homo sapien (1369835-1-20155-22741)

<220>

<221> VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2012

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
          20          25          30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
          35          40          45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
          50          55          60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
65          70          75          80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
          85          90          95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
          100          105          110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
          115          120          125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
          130          135          140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
          145          150          155          160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
          165          170          175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
          180          185          190
Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
          195          200          205
Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
          210          215          220
Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
          225          230          235          240
Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu
          245          250          255
Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu Ser
          260          265          270
Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val Ser
          275          280          285
Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser Xaa
          290          295          300
Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro
          305          310          315

```

&lt;210&gt; 2013

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (1857946-1-1-1049)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2013

```

Phe Ser Ser Val Asn Asn Ser Cys Pro Arg Asn Val Arg Pro Val Leu
 1          5          10          15
Ser Val Trp Ala Met Tyr Leu Val Met Ile Gly Ser Ile Val Met Thr
          20          25          30
Met Leu Gly Asn Met Ile Val Met Ile Ser Ile Ala His Phe Lys Gln

```

```

      35              40              45
Leu His Ser Pro Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp
  50              55              60
Phe Leu Leu Ser Cys Val Val Met Pro Phe Ser Val Ile Thr Ser Ile
  65              70              75              80
Glu Ser Cys Trp Tyr Phe Gly Asp Leu Phe Cys Lys Val His Ser Cys
      85              90              95
Cys Asp Ile Ile Leu Cys Thr Thr Ser Ile Phe His Leu Cys Phe Ile
      100              105              110
Ser Val Asp Arg Tyr Asp Ala Val Xaa Asp Pro Leu Gln Tyr Val Thr
      115              120              125
Arg Ile Thr Ile Pro Val Ile Glu Leu Phe Leu Leu Ile Ser Trp Ser
      130              135              140
Ile Pro Ile Leu Phe Ala Phe Gly Leu Val Phe Ser Lys Leu Asn Ile
      145              150              155              160
Ile Gly Ala Glu Glu Phe Val Ala Ala Ile Asp Cys Thr Gly Leu Cys
      165              170              175
Val Leu Ile Phe Asn Lys Pro Gly Gly Val Leu Ala Ser Phe Ile Ala
      180              185              190
Phe Phe Leu Pro Gly Thr Thr Thr Val Gly Ile Tyr Ile His Ile Phe
      195              200              205
Thr Val Ala Arg Lys His Ala Met Gln Ile Gly Thr Gly Ser Arg Thr
      210              215              220
Lys Gln Ala Gly Ser Glu Ser Lys Lys Lys Trp His Pro Leu Lys Arg
      225              230              235              240
Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe Val
      245              250              255
Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe Ile
      260              265              270
Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu Gly
      275              280              285
Tyr Phe Asn Ser Ala Phe Asn Ser Ile Leu Tyr Gly Met Leu Tyr Pro
      290              295              300
Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe
      305              310              315

```

&lt;210&gt; 2014

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (2358019-1-250070-250529)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(134)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2014

```

Leu Leu Phe Leu Met Phe Phe Ile Thr Ser Leu Gly His Lys Phe His
  1              5              10              15
Leu Ile Ser Phe Pro Phe Ser Gln Gln Thr Thr Xaa Gln Lys Tyr Phe
      20              25              30
Ile Ile Phe Glu Val Xaa Leu Cys Xaa Xaa His Thr Leu Thr Ala Leu
      35              40              45
Ile Tyr Cys Xaa Met Ser Leu Phe Xaa Gly Ile Asp Leu Phe Val Gly
      50              55              60
Tyr Asn Pro Cys Ser Pro Arg Val Leu Phe Leu Phe Leu Gly Arg Gly
      65              70              75              80
Pro Ser Gly Phe Ser Leu Glu Ser Leu Ser Phe Tyr Arg Thr Ser Phe
      85              90              95
Thr Trp Gln His Leu His Leu Lys Phe Tyr Cys Pro Ser Xaa Gly Xaa
      100              105              110

```

Leu Leu Lys Ser Phe Leu Ser Ala Ile Trp Leu Leu Phe Ser Thr Tyr  
 115 120 125  
 Phe Leu Arg Val Leu Ser  
 130

<210> 2015  
 <211> 127  
 <212> PRT  
 <213> Homo sapien (2447218-1-32642-33129)

<220>  
 <221> VARIANT  
 <222> (1)...(127)  
 <223> Xaa = Any Amino Acid

<400> 2015  
 Asn Leu Leu Pro Val Trp Thr Pro Gly Ser Arg Val Pro Ser Xaa Ser  
 1 5 10 15  
 Gln Ile Ser Val Ser Glu Lys Gln Gly Met Ser Phe Pro Lys Lys Leu  
 20 25 30  
 Phe Gln Asn His Lys Leu Phe Leu Phe Ala Gly Met Asn Val Phe  
 35 40 45  
 Leu Gln Thr Val Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro  
 50 55 60  
 Leu His Tyr Arg Val Ile Met Asn Pro Gly Ile Phe Gly Leu Trp Val  
 65 70 75 80  
 Leu Val Ser Trp Ser Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Arg  
 85 90 95  
 Met Val Leu Gln Leu Ser Phe Cys Thr Asn Leu Glu Ile Pro His Ile  
 100 105 110  
 Phe Phe Cys Glu Leu Asn Gln Leu Ile Leu Leu Ala Cys Ser Asn  
 115 120 125

<210> 2016  
 <211> 216  
 <212> PRT  
 <213> Homo sapien (2921627-1-1-649)

<400> 2016  
 Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met Leu Val  
 1 5 10 15  
 Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys Thr Ala  
 20 25 30  
 Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe Leu Leu  
 35 40 45  
 Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg  
 50 55 60  
 Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile Ala Gly  
 65 70 75 80  
 Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro Ile Thr  
 85 90 95  
 Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe Phe Cys  
 100 105 110  
 Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala Leu Tyr  
 115 120 125  
 Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile Pro Phe  
 130 135 140  
 Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val Gln Cys  
 145 150 155 160  
 Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser Ser  
 165 170 175

His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr Thr Tyr  
 180 185 190  
 Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val Leu Ser  
 195 200 205  
 Val Phe Tyr Thr Ile Leu Thr Pro  
 210 215

<210> 2017

<211> 216

<212> PRT

<213> Homo sapien (2921629-1-1-649)

<400> 2017

Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu Val  
 1 5 10 15  
 Asn Ile Gln Thr Arg His His Thr Ile Thr Tyr Thr Gly Cys Leu Thr  
 20 25 30  
 Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe Leu  
 35 40 45  
 Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Cys  
 50 55 60  
 Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala Leu  
 65 70 75 80  
 Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu Met  
 85 90 95  
 Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys  
 100 105 110  
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn  
 115 120 125  
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe  
 130 135 140  
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg  
 145 150 155 160  
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser  
 165 170 175  
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr  
 180 185 190  
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala  
 195 200 205  
 Ala Met Tyr Thr Ile Val Thr Pro  
 210 215

<210> 2018

<211> 212

<212> PRT

<213> Homo sapien (2921634-1-1-653)

<400> 2018

Cys His Ser Gln Val Ser Arg Leu Ala Gly Leu Gly Tyr Leu Glu Gly  
 1 5 10 15  
 Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys Ala Ala Gln Met Phe Phe  
 20 25 30  
 Phe Val Ala Leu Ala Thr Val Glu Asn Ile Leu Leu Thr Ser Met Ala  
 35 40 45  
 Tyr Asp His Tyr Ile Ala Val Cys Lys Pro Leu His Tyr Thr Thr Thr  
 50 55 60  
 Thr Ile Ala Ser Val Cys Ala His Leu Val Ile Gly Ser Tyr Val Cys  
 65 70 75 80  
 Gly Phe Leu Asn Ala Pro Leu Arg Ile Val Asp Ile Phe Ser Leu Ser  
 85 90 95  
 Phe Cys Lys Ser Asn Leu Val His His Leu Phe Cys Asp Val Pro Pro

```

      100      105      110
Val Met Ala Val Ser Cys Ser Gly Lys His Ile Ser Lys Lys Ile Leu
      115      120      125
Val Phe Met Ser Ser Phe Asn Val Phe Leu Ala Leu Leu Val Ile Leu
      130      135      140
Thr Ser Tyr Leu Val Ile Phe Ile Thr Ile Leu Lys Met His Ser Ala
      145      150      155      160
Gln Gly His Leu Lys Ala Trp Ser Thr Gly Ala Pro His Leu Ile Ala
      165      170      175
Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe Met Tyr Leu Gln Pro Ser
      180      185      190
Ser Ser His Ser Met Asp Thr Asp Glu Met Ala Ser Leu Phe Tyr Ala
      195      200      205
Val Phe Ile Ser
      210

```

&lt;210&gt; 2019

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (2921639-1-1-647)

&lt;400&gt; 2019

```

Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1          5          10          15
Asn Ile Arg Thr Gln Ser Lys Val Val Thr Tyr Ala Gly Cys Ile Thr
      20      25      30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
      35      40      45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
      50      55      60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65      70      75      80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
      85      90      95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
      100      105      110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
      115      120      125
Asp Met Val Met Tyr Met Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
      130      135      140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
      145      150      155      160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165      170      175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Gly Leu Gly Val Tyr
      180      185      190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
      195      200      205
Met Tyr Thr Val Val Thr Pro
      210      215

```

&lt;210&gt; 2020

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (2921641-1-1-636)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid



&lt;400&gt; 2020

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Ser Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr  
 20 25 30  
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu  
 35 40 45  
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg  
 50 55 60  
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu  
 65 70 75 80  
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr  
 85 90 95  
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys  
 100 105 110  
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val  
 115 120 125  
 Ser Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe  
 130 135 140  
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys  
 145 150 155 160  
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His  
 165 170 175  
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Thr Phe Ile Tyr Arg  
 180 185 190  
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr  
 195 200 205  
 Thr Ile Thr Pro  
 210

&lt;210&gt; 2021

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (2921661-1-1-649)

&lt;400&gt; 2021

Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Ala  
 1 5 10 15  
 Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly Cys Leu Leu  
 20 25 30  
 Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala Phe Leu Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His Pro Leu His  
 50 55 60  
 Tyr Ile Leu Ile Met Ser Pro Gly Leu Arg Ile Phe Leu Val Ser Ala  
 65 70 75 80  
 Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr Leu Leu Met  
 85 90 95  
 Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His Phe Leu Cys  
 100 105 110  
 Asp Ile Asn Pro Leu Leu Gly Leu Ser Cys Thr Asp Pro Phe Thr Asn  
 115 120 125  
 Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu Ile Cys Val  
 130 135 140  
 Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr Ile Leu Lys  
 145 150 155 160  
 Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe Cys Val Asp  
 180 185 190  
 Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr Val Ala Ser

195 200 205  
 Val Met Tyr Thr Val Val Thr Pro  
 210 215

<210> 2022  
 <211> 216  
 <212> PRT  
 <213> Homo sapien (2921667-1-1-649)

<400> 2022  
 Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly  
 1 5 10 15  
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser  
 20 25 30  
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu  
 35 40 45  
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala Ile Cys Gln Pro Leu Thr  
 50 55 60  
 Tyr Ser Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala  
 65 70 75 80  
 Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Ala Met  
 85 90 95  
 Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu Val Asn His Phe Tyr Cys  
 100 105 110  
 Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys Ser Ser Thr Gln Leu Asn  
 115 120 125  
 Glu Leu Leu Leu Phe Val Ala Ala Ala Phe Met Ala Val Ala Pro Leu  
 130 135 140  
 Val Phe Ile Ser Val Ser Tyr Ala His Val Val Ala Ala Val Pro Gln  
 145 150 155 160  
 Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Thr Val Val Gly Ile Phe Tyr Gly Thr Gly Val Phe Ser Tyr  
 180 185 190  
 Met Arg Leu Gly Ser Ala Glu Ser Ser Asp Lys Asp Lys Gly Val Gly  
 195 200 205  
 Val Phe Met Thr Val Ile Asn Pro  
 210 215

<210> 2023  
 <211> 215  
 <212> PRT  
 <213> Homo sapien (2921686-1-1-646)

<400> 2023  
 Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro Lys Met Ile Val  
 1 5 10 15  
 Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser Cys Leu Thr Gln  
 20 25 30  
 Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp Leu Leu Ile  
 35 40 45  
 Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Ser Pro His Tyr  
 50 55 60  
 Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe Val Leu Val Ser  
 65 70 75 80  
 Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Thr Val Leu  
 85 90 95  
 Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe Val Cys Asp  
 100 105 110  
 Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val Ile Asp Ser  
 115 120 125

```

Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe Leu Pro Ile Ser
 130          135          140
Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser Ile Leu Arg Ile
145          150          155          160
Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr Cys Arg Ser His
          165          170          175
Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Val Tyr Leu
          180          185          190
Thr Thr Ala Ala Gly Thr Thr Pro Arg Ser Gly Val Val Val Ser Val
          195          200          205
Met Tyr Thr Val Val Thr Pro
          210          215

```

&lt;210&gt; 2024

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (2921715-1-1-652)

&lt;400&gt; 2024

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1          5          10          15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
          20          25          30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
          35          40          45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
          50          55          60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
65          70          75          80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
          85          90          95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
          100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
          115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
          130          135          140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
145          150          155          160
Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
          165          170          175
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
          180          185          190
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
          195          200          205
Ser Leu Phe Tyr Ser Leu Phe Asn Pro
          210          215

```

&lt;210&gt; 2025

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3093312-1-33069-35776)

&lt;400&gt; 2025

```

Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
 1          5          10          15
Leu Val Gly Phe Ser Asn Trp Pro His Leu Glu Val Val Ile Phe Val
          20          25          30
Val Val Leu Ile Phe Tyr Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
          35          40          45
Ile Ile Leu Ser Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe

```

50                      55                      60  
 Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser  
 65                      70                      75                      80  
 Ile Pro Gln Leu Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser  
                     85                      90                      95  
 Tyr Ala Gly Cys Met Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr  
                     100                      105                      110  
 Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala  
                     115                      120                      125  
 Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys  
                     130                      135                      140  
 His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Ser Ala  
 145                      150                      155                      160  
 Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln  
                     165                      170                      175  
 Val Asp His Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys  
                     180                      185                      190  
 Val Asp Thr His Val Asn Glu Leu Thr Leu Met Ile Thr Ser Ser Ile  
                     195                      200                      205  
 Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile  
                     210                      215                      220  
 Val Arg Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val  
 225                      230                      235                      240  
 Phe Gly Thr Cys Gly Ala His Leu Met Ala Val Ser Leu Phe Phe Ile  
                     245                      250                      255  
 Pro Ala Met Cys Ile Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp  
                     260                      265                      270  
 Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu  
                     275                      280                      285  
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Val Val Arg Gly Ala Val  
                     290                      295                      300  
 Lys Arg Leu Met Gly Trp Glu  
 305                      310

&lt;210&gt; 2026

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3108020-1-23117-23433)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(330)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2026

Met Glu Pro Glu Asn Asp Thr Arg Ile Ser Glu Phe Arg Leu Leu Gly  
 1                      5                      10                      15  
 Phe Ser Glu Glu Pro Arg Leu Gln Arg Phe Arg Phe Leu Phe Gly Val  
                     20                      25                      30  
 Phe Leu Ser Met Tyr Leu Ile Ile Val Phe Gly Asn Leu Leu Ile Ile  
                     35                      40                      45  
 Leu Val Ile Ile Leu Cys Ser His Leu His Thr Ser Met Tyr Phe Phe  
                     50                      55                      60  
 Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Arg Val  
 65                      70                      75                      80  
 Pro Lys Met Leu Val Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Ser  
                     85                      90                      95  
 Ala Gly Cys Ile Thr Gln Met Tyr Phe Phe Ile His Phe Val Gly Leu  
                     100                      105                      110  
 Asp Ser Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
                     115                      120                      125

Cys His Pro Leu Tyr Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly  
 130 135 140  
 Leu Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu His Ser Leu Leu  
 145 150 155 160  
 His Ser Leu Met Val Leu Gln Leu Ser Leu Cys Arg Glu Leu Glu Ile  
 165 170 175  
 Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser  
 180 185 190  
 Asp Thr Phe Leu Asn Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu  
 195 200 205  
 Gly Gly Gly Ser Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val  
 210 215 220  
 Ser Ser Ile Cys Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Pro Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr  
 245 250 255  
 Ser Leu Gly Val Tyr Leu Ser Ser Ala Ala Ser His Asn Ser His Ser  
 260 265 270  
 Gly Ala Ile Ala Ser Val Arg Tyr Thr Val Val Thr Pro Met Leu Asn  
 275 280 285  
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys  
 290 295 300  
 Asn Ser Leu Gly Gly Lys Leu Glu Lys Gly Gln Leu Ser Xaa Gly Leu  
 305 310 315 320  
 Lys Leu Tyr Pro Xaa Leu Gln Gly Ser Lys  
 325 330

&lt;210&gt; 2027

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3108020-1-37593-38822)

&lt;400&gt; 2027

Met Glu Arg Gly Asn Gln Thr Glu Val Gly Asn Phe Leu Leu Leu Gly  
 1 5 10 15  
 Phe Ala Glu Asp Ser Asp Met Gln Leu Leu His Gly Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Ile Ile Gly Asn Leu Leu Ile Ile Leu Thr  
 35 40 45  
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Ile Phe Phe Phe Ile Ala Phe Gly Cys Leu Asp Asn  
 100 105 110  
 Leu Leu Leu Thr Met Thr Ala Tyr Asp Arg Phe Val Ala Ile Cys Tyr  
 115 120 125  
 Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu  
 130 135 140  
 Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr  
 145 150 155 160  
 Leu Thr Ile Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Pro Ser Glu Val Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Phe Ile Asn Asn Ile Val Met Tyr Phe Val Thr Ile Val Leu Gly Val  
 195 200 205  
 Phe Pro Leu Cys Gly Ile Leu Phe Ser Tyr Ser Gln Ile Phe Ser Ser  
 210 215 220

Val Leu Arg Val Ser Ala Arg Gly Gln His Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly  
 245 250 255  
 Val Tyr Leu Ser Ser Ala Val Thr Pro Pro Ser Arg Thr Ser Leu Ala  
 260 265 270  
 Ala Ser Val Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ser Leu Gly Arg Leu Leu  
 290 295 300  
 Leu Arg Ala Thr Ser Leu Lys Glu Gly Thr Ile Ala Lys Leu Ser  
 305 310 315

&lt;210&gt; 2028

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3184261-1-5713-7336)

&lt;400&gt; 2028

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly  
 1 5 10 15  
 Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu  
 20 25 30  
 Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
 50 55 60  
 Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His  
 115 120 125  
 Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu  
 130 135 140  
 Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr  
 145 150 155 160  
 Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His  
 165 170 175  
 Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr  
 180 185 190  
 His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr  
 195 200 205  
 Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr  
 210 215 220  
 Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe  
 245 250 255  
 Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys  
 260 265 270  
 Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu  
 290 295 300  
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro  
 305 310 315

&lt;210&gt; 2029

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3213020-1-101040-103030)

&lt;400&gt; 2029

```

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1           5           10           15
Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
          20           25           30
Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
          35           40           45
Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50           55           60
Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Thr Ile Leu Lys
65           70           75           80
Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
          85           90           95
Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
          130          135          140
Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
145          150          155          160
Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His
          165          170          175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
          180          185          190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu
          195          200          205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
          210          215          220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
          245          250          255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
          260          265          270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
          275          280          285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
          290          295          300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
305          310          315

```

&lt;210&gt; 2030

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (32504-1-1-343)

&lt;400&gt; 2030

```

Val Cys His Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys
 1           5           10           15
Gly Leu Leu Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu
          20           25           30
Leu His Ile Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu
          35           40           45
Ile Pro His Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys
          50           55           60
Ser Asp Thr Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val

```

<210> 2031  
<211> 114  
<212> PRT  
<213> Homo sapien (32508-1-1-343)

```
<210> 2032
<211> 112
<212> PRT
<213> Homo sapien (32509-1-1-338)
```

```
<210> 2033
<211> 114
<212> PRT
<213> Homo sapien (32513-1-1-343)
```

1186



```

      20      25      30
Ile Leu Thr Ser Leu Thr Phe Thr Leu Pro Tyr Cys Gly Pro Asn Glu
      35      40      45
Val Asp His Phe Phe Cys Asp Ile Pro Ala Leu Leu Pro Leu Ala Cys
      50      55      60
Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Thr Ser Val Gly Leu
      65      70      75      80
Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr Thr Arg Ile
      85      90      95
Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg Arg Arg Ala
      100      105      110
Phe Ser

```

&lt;210&gt; 2034

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (32518-1-1-343)

&lt;400&gt; 2034

```

Ile Cys Lys Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys
1      5      10      15
Ile Arg Leu Leu Ile Leu Ser Tyr Val Gly Gly Leu Leu His Ala Leu
      20      25      30
Ile His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile
      35      40      45
Val His His Ile Tyr Cys Asp Ile Ile Pro Leu Ser Lys Ile Ser Cys
      50      55      60
Thr Asp Ser Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ser Gly Ser
      65      70      75      80
Ile Gln Val Phe Ser Ile Val Thr Ile Leu Val Ser Tyr Thr Phe Val
      85      90      95
Leu Phe Ala Ile Leu Lys Arg Lys Ser Asp Lys Gly Val Arg Lys Ala
      100      105      110
Phe Ser

```

&lt;210&gt; 2035

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3289998-1-93404-94343)

&lt;400&gt; 2035

```

Met Val Leu Trp Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe
1      5      10      15
Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe
      20      25      30
Leu Asn Asp Met Gly Met Tyr Phe Ala Ala Gly Leu Leu Ala Gly Gly
      35      40      45
Pro Leu Val Gly Ile Leu Cys Ser Tyr Ser Lys Ile Val Ser Ser Ile
      50      55      60
Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys
      65      70      75      80
Ala Ser His Leu Ser Val Val Ser Leu Phe Cys Cys Thr Gly Leu Gly
      85      90      95
Val Tyr Leu Thr Ser Ala Ala Thr His Asn Ser His Thr Ser Ala Thr
      100      105      110
Ala Ser Val Met Tyr Thr Val Ala Thr Pro Met Leu Asn Pro Phe Ile
      115      120      125
Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys Met Ser Phe
      130      135      140

```

Arg Gly Lys Gln  
145

<210> 2036

<211> 312

<212> PRT

<213> Homo sapien (3402736-1-7079-10933)

<400> 2036

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
1      5      10      15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
20      25      30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
35      40      45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
50      55      60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
65      70      75      80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
85      90      95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
100     105     110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
115     120     125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
130     135     140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
145     150     155     160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
165     170     175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
180     185     190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
195     200     205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
210     215     220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
225     230     235     240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
245     250     255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
260     265     270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
275     280     285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
290     295     300
Gln Lys Thr Val Pro Met Glu Ile
305     310

```

<210> 2037

<211> 305

<212> PRT

<213> Homo sapien (3522966-1-8581-12533)

<400> 2037

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
1      5      10      15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
20      25      30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu

```

35 40 45  
 His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu  
 50 55 60  
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser  
 65 70 75 80  
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu  
 85 90 95  
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly  
 100 105 110  
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile  
 115 120 125  
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile  
 130 135 140  
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro  
 145 150 155 160  
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg  
 165 170 175  
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val  
 180 185 190  
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile  
 195 200 205  
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp  
 210 215 220  
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val  
 225 230 235 240  
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro  
 245 250 255  
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr  
 260 265 270  
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys  
 275 280 285  
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys  
 290 295 300  
 Phe  
 305

&lt;210&gt; 2038

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3738097-1-24383-25939)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(142)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2038

Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu  
 1 5 10 15  
 Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys  
 20 25 30  
 Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile  
 35 40 45  
 Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys  
 50 55 60  
 Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe  
 65 70 75 80  
 Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu  
 85 90 95  
 Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met  
 100 105 110

Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr  
 115 120 125  
 Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe  
 130 135 140

<210> 2039  
 <211> 297  
 <212> PRT  
 <213> Homo sapien (3738097-1-94180-96164)

<220>  
 <221> VARIANT  
 <222> (1)...(297)  
 <223> Xaa = Any Amino Acid

<400> 2039  
 Met Lys Xaa Met Ala Val Glu Asn Asn Ser Ser Val Thr Glu Phe Ile  
 1 5 10 15  
 Leu Val Arg Leu Thr Asn Ser Arg Cys Pro Ser Val Leu Phe Leu Met  
 20 25 30  
 Trp Ser Leu Trp Gly Glu Phe Glu His Asn Phe Met Ser Leu Asn Ser  
 35 40 45  
 His Leu His Thr Pro Thr His Phe Phe Leu Phe Thr Leu Ser Phe Ile  
 50 55 60  
 Asp Val Cys Tyr Ser Phe Val Cys Thr Thr Lys Ile Pro Met Gly Phe  
 65 70 75 80  
 Ile Ser Glu Arg Asn Ile Ile Ser Phe Val Gly Trp Pro Thr Xaa Leu  
 85 90 95  
 Tyr Phe Phe Cys Ile Phe Val Lys Glu Pro Lys Asn Gly Val Ile Val  
 100 105 110  
 Gly Ile Met Phe Ser Ala Lys Met Leu Val Cys Arg Glu Ile Met Asp  
 115 120 125  
 Xaa Ser Leu Met Xaa Asn Xaa Lys Met His Met Ala Leu Glu Arg Ser  
 130 135 140  
 Asp Phe Arg Met Gly Xaa Thr Gly Ser Ala Thr Lys Lys His Leu Ile  
 145 150 155 160  
 Ile Phe Leu Tyr Tyr Ser Asp Tyr Phe Gln Arg Xaa Xaa Gly Cys Arg  
 165 170 175  
 Ala Leu Gly Gln Gly Ser Leu Ala Lys Gln Asp Thr Xaa Leu Xaa Asn  
 180 185 190  
 Cys Thr Cys Thr Leu Lys Ser Leu Leu His Ile Ile Ile Cys Phe Tyr  
 195 200 205  
 Ile Trp Lys Gln Lys Lys Ile Ser Tyr Leu Tyr His Lys Ser Xaa Lys  
 210 215 220  
 Met Asp Leu Tyr Lys Ile Cys His Val Leu Trp Val Thr His Lys Lys  
 225 230 235 240  
 Asn Phe Leu Arg Pro Ser Ser Thr Ser Gln Met Val Gln Gly Lys Met  
 245 250 255  
 Leu Leu Lys Gly Tyr Ile Xaa Phe Trp Arg Met Ser Leu Pro Met Cys  
 260 265 270  
 Ala Ile Phe Ile Phe Val Arg Arg Tyr Tyr Tyr Leu Leu Lys Lys Leu  
 275 280 285  
 Lys Thr Leu Leu Tyr Lys Asn Ser Tyr  
 290 295

<210> 2040  
 <211> 325  
 <212> PRT  
 <213> Homo sapien (3746441-1-1-1386)

<220>

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2040

```

Met Ala Asn Glu Asn Tyr Thr Lys Val Thr Xaa Phe Ile Phe Thr Gly
 1          5          10          15
Leu Asn Tyr Asn Pro Gln Leu Arg Val Phe Leu Phe Leu Phe Leu
 20          25          30
Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
 35          40          45
Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
 65          70          75          80
Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
 85          90          95
Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
 100          105          110
Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
 115          120          125
Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
 130          135          140
Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
 145          150          155          160
Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn
 165          170          175
Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
 180          185          190
Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
 195          200          205
Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
 210          215          220
Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
 225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Leu Tyr Gly Thr Leu
 245          250          255
Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
 260          265          270
Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
 275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His Arg
 290          295          300
Thr Val Thr Gln Arg Lys Phe Cys Lys Ala Xaa Ile Leu Ile Gln Lys
 305          310          315          320
Glu Leu Gly Arg Lys
          325

```

&lt;210&gt; 2041

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3766130-1-61888-64085)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2041

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
 1          5          10          15

```

Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu  
 20 25 30  
 Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu  
 35 40 45  
 Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser  
 50 55 60  
 Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val  
 65 70 75 80  
 Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe  
 85 90 95  
 Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser  
 100 105 110  
 Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val  
 115 120 125  
 Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu  
 130 135 140  
 Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met  
 145 150 155 160  
 Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His  
 165 170 175  
 Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val  
 180 185 190  
 Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu  
 195 200 205  
 Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr  
 210 215 220  
 Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile  
 245 250 255  
 Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys  
 260 265 270  
 Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val  
 290 295 300  
 Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr  
 305 310 315 320  
 Leu Ser Ser Lys Pro Lys Arg Arg  
 325

&lt;210&gt; 2042

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3766130-1-85703-88675)

&lt;400&gt; 2042

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly  
 1 5 10 15  
 Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu  
 20 25 30  
 Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu  
 35 40 45  
 Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys  
 65 70 75 80  
 Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu  
 85 90 95  
 Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys  
 100 105 110

Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu  
 130 135 140  
 Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile  
 145 150 155 160  
 Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met  
 180 185 190  
 Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu  
 195 200 205  
 Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr  
 210 215 220  
 Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala  
 225 230 235 240  
 Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met  
 245 250 255  
 Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile  
 260 265 270  
 Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr  
 290 295 300  
 Cys Gln Ala Ser Arg Ser Asp  
 305 310

&lt;210&gt; 2043

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3831602-1-1-649)

&lt;400&gt; 2043

Phe Val Asp Val Cys Asn Ser Thr Thr Ile Thr Pro Lys Met Leu Ala  
 1 5 10 15  
 Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys Phe Leu  
 20 25 30  
 Gln Met Tyr Phe Phe Ile Ser Leu Ala Thr Thr Glu Cys Ile Leu Phe  
 35 40 45  
 Gly Leu Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu Leu  
 50 55 60  
 Tyr Ser Leu Ile Met Ser Arg Thr Val Tyr Leu Lys Met Ala Ala Gly  
 65 70 75 80  
 Ala Phe Ala Ala Gly Leu Leu Asn Phe Met Val Asn Thr Ser His Val  
 85 90 95  
 Ser Ser Leu Ser Phe Cys Asp Ser Asn Val Ile His His Phe Phe Cys  
 100 105 110  
 Asp Ser Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr Ile Leu Lys  
 115 120 125  
 Glu Ser Ile Ser Ser Ile Leu Ala Gly Val Asn Ile Val Gly Thr Leu  
 130 135 140  
 Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser Ile Phe Ser  
 145 150 155 160  
 Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr Cys Ala Ser  
 165 170 175  
 His Leu Thr Ala Ile Ile Leu Phe Tyr Ala Thr Cys Ile Tyr Thr Tyr  
 180 185 190  
 Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys Val Ala Ser  
 195 200 205  
 Val Phe Tyr Thr Val Val Ile Pro  
 210 215

<210> 2044  
 <211> 217  
 <212> PRT  
 <213> Homo sapien (3831605-1-1-652)

<220>  
 <221> VARIANT  
 <222> (1)...(217)  
 <223> Xaa = Any Amino Acid

<400> 2044  
 Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys Met Ile Glu  
 1 5 10 15  
 Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly Asp Cys Leu Thr  
 20 25 30  
 Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp Asp Met Ile Leu  
 35 40 45  
 Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys His Pro Leu Asn  
 50 55 60  
 Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu Leu Val Leu Val  
 65 70 75 80  
 Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Val  
 85 90 95  
 Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser Asn Phe Phe Cys  
 100 105 110  
 Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp Ser Asp Ile Asn  
 115 120 125  
 Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly Phe Leu Arg Ile  
 130 135 140  
 Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe Pro Ile Leu Arg  
 145 150 155 160  
 Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser Thr Xaa Gly Ser  
 165 170 175  
 Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Val Tyr  
 180 185 190  
 Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp Val Val Ala Ser  
 195 200 205  
 Val Met Tyr Ala Val Val Val Thr Pro  
 210 215

<210> 2045  
 <211> 214  
 <212> PRT  
 <213> Homo sapien (3831606-1-1-644)

<400> 2045  
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val  
 1 5 10 15  
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr  
 20 25 30  
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His  
 50 55 60  
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu  
 65 70 75 80  
 Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met  
 85 90 95  
 Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys  
 100 105 110



Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn  
 115 120 125  
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu  
 130 135 140  
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln  
 145 150 155 160  
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser  
 165 170 175  
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr  
 180 185 190  
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val  
 195 200 205  
 Met His Ala Val Val Thr  
 210

&lt;210&gt; 2046

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3831610-1-1-984)

&lt;400&gt; 2046

Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe Phe  
 1 5 10 15  
 Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile  
 20 25 30  
 Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly Gln  
 35 40 45  
 Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly  
 50 55 60  
 Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Asn Asp Arg  
 65 70 75 80  
 Tyr Met Ala Ile Cys Tyr Leu Leu His Asn Pro Val Ile Val Ser Gly  
 85 90 95  
 Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly  
 100 105 110  
 Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Asn Gly Gly  
 115 120 125  
 Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn  
 130 135 140  
 Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile Leu  
 145 150 155 160  
 Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr  
 165 170 175  
 Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly Arg  
 180 185 190  
 Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Phe Asn Val Val Ile Ile  
 195 200 205  
 Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser  
 210 215 220  
 Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val  
 225 230 235 240  
 Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys  
 245 250 255  
 Arg Ala Leu Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp  
 260 265 270  
 Pro Lys Lys Gly Ser Arg  
 275

&lt;210&gt; 2047

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3831615-1-1-684)

&lt;400&gt; 2047

```

Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu
 1           5           10           15
Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala
          20           25           30
Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu
          35           40           45
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
          50           55           60
His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala
65           70           75           80
Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp
          85           90           95
Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val Asn His Phe Phe
          100          105          110
Cys Asp Ser Pro Pro Val Leu Lys Leu Val Cys Ala Asp Thr Ala Leu
          115          120          125
Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro
          130          135          140
Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu
145          150          155          160
Lys Ile Pro Ser Ala Lys Gly Lys His Lys Ala Phe Ser Thr Cys Ser
          165          170          175
Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr
          180          185          190
Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu
          195          200          205
Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Phe His Leu
          210          215          220
Leu Ser Trp
225

```

&lt;210&gt; 2048

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3831618-1-1-653)

&lt;400&gt; 2048

```

Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu
 1           5           10           15
Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu Cys Ala
          20           25           30
Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys Ala Leu
          35           40           45
Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
          50           55           60
Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr
65           70           75           80
Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe
          85           90           95
Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Phe
          100          105          110
Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala
          115          120          125
Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro
          130          135          140
Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val
145          150          155          160
Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly

```

165 170 175  
 Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr  
 180 185 190  
 Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val  
 195 200 205  
 Phe Tyr Ala Ile Val Thr Pro Met Leu  
 210 215

&lt;210&gt; 2049

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3834584-1-78858-80128)

&lt;400&gt; 2049

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile  
 1 5 10 15  
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn  
 20 25 30  
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu  
 35 40 45  
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu  
 50 55 60  
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu  
 65 70 75 80  
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu  
 85 90 95  
 His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Thr  
 100 105 110  
 Gly Ser Trp Val Val Ala Asn Ser Ser Ala Leu Leu His Thr Leu Leu  
 115 120 125  
 Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe  
 130 135 140  
 Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu  
 145 150 155 160  
 Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro  
 165 170 175  
 Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu  
 180 185 190  
 Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly  
 195 200 205  
 Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro  
 210 215 220  
 Tyr Phe Arg Thr Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala  
 225 230 235 240  
 Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr  
 245 250 255  
 Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala  
 260 265 270  
 Val Lys Phe Phe Ser Val Gln  
 275

&lt;210&gt; 2050

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3924656-1-75882-77814)

&lt;400&gt; 2050

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly  
 1 5 10 15  
 Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu  
 20 25 30

Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr  
 35 40 45  
 Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg  
 50 55 60  
 Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly  
 85 90 95  
 Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val  
 100 105 110  
 Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln  
 115 120 125  
 Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu  
 130 135 140  
 Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu  
 145 150 155 160  
 Ala Leu Ile Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn  
 165 170 175  
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr  
 180 185 190  
 Ser Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile  
 195 200 205  
 Ile Trp Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met  
 210 215 220  
 Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys  
 225 230 235 240  
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr  
 245 250 255  
 Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser  
 260 265 270  
 Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr  
 275 280 285  
 Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys  
 290 295 300  
 Leu Val Ile Cys Arg Glu  
 305 310

&lt;210&gt; 2051

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3962498-1-83664-84695)

&lt;400&gt; 2051

Met Ser Gly Ser Pro Thr Gln Leu Thr Ala Gly Pro Arg Thr Ala Ser  
 1 5 10 15  
 Gly Cys Val Ile Met Ile Cys Phe Ala Leu Thr Val Leu Ser Tyr Ile  
 20 25 30  
 Arg Ile Leu Ala Thr Val Val Gln Ile Arg Ser Ala Ala Ser Arg Arg  
 35 40 45  
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Gly Met Val Leu Leu Phe  
 50 55 60  
 Tyr Gly Thr Gly Ser Ser Thr Tyr Met Arg Pro Thr Thr Arg Tyr Ser  
 65 70 75 80  
 Pro Leu Glu Gly Arg Leu Ala Ala Val Phe Tyr Ser Ile Leu Ile Pro  
 85 90 95  
 Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Met Lys Arg  
 100 105 110  
 Ala Leu Trp Lys Leu Tyr Leu Gln Val Pro Tyr  
 115 120

&lt;210&gt; 2052

<211> 343  
 <212> PRT  
 <213> Homo sapien (3970959-1-83329-85626)

<220>  
 <221> VARIANT  
 <222> (1)...(343)  
 <223> Xaa = Any Amino Acid

<400> 2052

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1          5          10          15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
      20          25          30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
 35          40          45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
 50          55          60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
 65          70          75          80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
      85          90          95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
      100          105          110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His
      115          120          125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
      130          135          140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
      145          150          155          160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165          170          175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180          185          190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195          200          205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210          215          220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
      225          230          235          240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245          250          255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260          265          270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275          280          285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
      290          295          300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
      305          310          315          320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325          330          335
Tyr Leu Ser Tyr Thr His His
      340

```

<210> 2053  
 <211> 312  
 <212> PRT  
 <213> Homo sapien (3982606-1-1-939)

<400> 2053

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
20     25     30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
35     40     45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50     55     60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65     70     75     80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
85     90     95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
100    105    110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
115    120    125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
130    135    140
Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
145    150    155    160
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
165    170    175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
180    185    190
Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
195    200    205
Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
210    215    220
Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
225    230    235    240
Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
245    250    255
Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
260    265    270
Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
275    280    285
Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
290    295    300
Leu Gly Lys Gly Arg Glu Val Gly
305    310

```

&lt;210&gt; 2054

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (3983513-1-17888-18909)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(104)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2054

```

Val Pro Val Arg Cys Pro Gly Arg Val Arg Thr Leu Val Pro Glu Ile
1      5      10      15
Ile Ser Val Asp Phe Pro Xaa Xaa Thr Leu Ile Xaa Gln Glu Val Tyr
20     25     30
Gly Leu Leu Ser Thr Phe Pro Leu Phe Ala Gln Gly Val Cys Gly Pro
35     40     45
Lys Ile Ile Ser Lys Ala Phe Cys Phe Ser Leu Leu Lys Gly Gly Cys
50     55     60
Ser His Ser Leu Gln Leu Ala Lys Gly Gly Gly Val Leu Arg Lys Ala

```

```

<400> 2056
Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe
 1           5           10           15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
      20           25           30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
      35           40           45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
 50           55           60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met

```

```

65          70          75          80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
      85          90          95
Met Met Gln Thr Phe Leu Ph Ser Thr Phe Ala Val Thr Glu Cys Leu
      100        105        110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115        120        125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130        135        140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145        150        155        160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165        170        175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180        185        190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195        200        205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210        215        220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Cys Thr Cys
      225        230        235        240
Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr Gly Thr Ala Ile Ile
      245        250        255
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
      260        265        270
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275        280        285
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
      290        295        300
Gly Val Glu Arg Ala Leu
305          310

```

&lt;210&gt; 2057

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4156187-1-27673-28734)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(127)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2057

```

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
1          5          10          15
Gln Leu Cys Ala Glu Met Glu Ile Phe Leu Ser Cys Ile Phe Ser Arg
      20          25          30
Phe Tyr Ala Phe Ser Leu Leu Arg Asn Gly Met Asn Met Gly Leu Thr
      35          40          45
Tyr Leu Asp Asp Arg Asp Asp Arg Leu His Thr Leu Ile Tyr Ile Phe
      50          55          60
Leu Ser His Leu Ala Ile Asn Asp Met Tyr Tyr Ala Ser Asn Asn Val
      65          70          75          80
Pro Lys Arg Gln Val Asn Gln Met Asn Gln Lys Lys Lys Tyr Phe Val
      85          90          95
Leu Trp Ile Lys Gln Ile Phe Leu Tyr Leu Ala Phe Ala His Thr Glu
      100        105        110
Cys Leu Ile Xaa Ala Met Met Ser Cys Asn Arg Tyr Val Ala Ile
      115        120        125

```

&lt;210&gt; 2058



<211> 312  
 <212> PRT  
 <213> Homo sapien (4156187-1-8673-10070)

<220>  
 <221> VARIANT  
 <222> (1)...(312)  
 <223> Xaa = Any Amino Acid

<400> 2058  
 Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe  
 1 5 10 15  
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu  
 20 25 30  
 Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile  
 35 40 45  
 Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His  
 50 55 60  
 Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met  
 65 70 75 80  
 Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys  
 85 90 95  
 Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met  
 100 105 110  
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro  
 115 120 125  
 Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala  
 130 135 140  
 Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile  
 145 150 155 160  
 Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe  
 165 170 175  
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp  
 180 185 190  
 Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly  
 195 200 205  
 Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile  
 210 215 220  
 Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Cys Val Val Gly Leu Tyr Phe Gly Met Ala Met Val  
 245 250 255  
 Val Tyr Leu Val Pro Asp Asn Ser Gln Arg Gln Lys Gln Gln Lys Ile  
 260 265 270  
 Leu Thr Leu Phe Tyr Ser Leu Phe Asn Pro Leu Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu Tyr Arg Ala Leu  
 290 295 300  
 Gln Lys Lys Arg Thr Met Xaa Met  
 305 310

<210> 2059  
 <211> 315  
 <212> PRT  
 <213> Homo sapien (4160227-1-768-2100)

<220>  
 <221> VARIANT  
 <222> (1)...(315)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 2059

```

Met Pro Leu Thr Asn Glu Ser His Pro Glu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ala Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Thr Ser Leu Leu
      20           25           30
Ile Met Tyr Pro Ile Ala Val Met Gly Asn Ile Thr Ile Ile Leu Met
      35           40           45
Ser Arg Leu Asp Ser Arg Leu His Ser Pro Met Tyr Phe Phe Leu Thr
      50           55           60
Asn Leu Ser Phe Leu Asp Met Cys Tyr Thr Thr Ser Ile Val Pro Gln
      65           70           75           80
Met Leu Phe Asn Leu Gly Ser Ser Lys Lys Thr Ile Ser Tyr Met Gly
      85           90           95
Cys Ala Val Gln Leu Tyr Phe Phe His Ile Met Gly Gly Thr Glu Cys
      100          105          110
Leu Leu Leu Ala Ile Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Arg
      115          120          125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Arg Val Cys Ile His Xaa
      130          135          140
Phe Pro Pro Cys Trp Leu Ile Gly Ile Ile Tyr Ala Val Ser Glu Ala
      145          150          155          160
Thr Ala Thr Leu Gln Leu Pro Leu Cys Gly Ser Asn Lys Leu Asp His
      165          170          175
Leu Val Cys Glu Ile Pro Val Leu Ile Lys Ile Ala Cys Gly Glu Lys
      180          185          190
Gly Ser Asn Glu Leu Thr Leu Ser Val Val Cys Ile Phe Met Leu Ala
      195          200          205
Val Pro Leu Cys Leu Ile Leu Ala Ser Tyr Ala Ser Ile Gly Ser Ala
      210          215          220
Val Phe Lys Ile Lys Ser Ser Lys Gly Arg Lys Lys Ala Phe Gly Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Pro Ala Ile
      245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Ile Ser Arg Asp Gln Pro Lys
      260          265          270
Phe Met Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Phe
      275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asn Val Lys Gly Ala Leu Arg Asn Leu
      290          295          300
Val Arg Ser Ile Phe Ser Phe Lys Xaa Xaa Trp
      305          310          315

```

&lt;210&gt; 2060

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4190944-1-137143-138613)

&lt;400&gt; 2060

```

Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1           5           10           15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
      20           25           30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
      35           40           45
Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
      65           70           75           80
Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
      85           90           95
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp

```

```

      100      105      110
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
      115      120      125
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
      130      135      140
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
      145      150      155      160
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
      165      170      175
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
      180      185      190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195      200      205
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
      210      215      220
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
      225      230      235      240
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
      245      250      255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
      290      295      300
Leu Gln Asp Arg Ile Tyr Arg
      305      310

```

&lt;210&gt; 2061

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4190944-1-141327-142434)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(145)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2061

```

Met Thr Thr Pro Phe Asn Ser Ser Leu Ile Met Phe Ser Leu Leu Asp
  1      5      10      15
Ser Ser Met Pro Glu Ile Leu Cys Pro Leu Pro Tyr Phe Phe Leu Gly
      20      25      30
Ser His Ala Thr His Ser Ser Xaa Leu Ser Ser Leu Thr Leu Ile Asn
      35      40      45
Arg Xaa Asn Met Phe Ser Glu Leu Asn Ser Pro Tyr Phe Ser Ile Glu
      50      55      60
Leu Asn Leu Lys Tyr Leu Tyr Ile Cys Asn Lys Leu Thr Leu Glu Lys
      65      70      75      80
Pro Asn Thr Phe Phe Xaa Thr Phe Cys Val Leu Ser Thr Asn Glu Arg
      85      90      95
Pro Met Val Leu Phe Leu Tyr Cys Ile Gln Pro Ala Phe Trp Ile Pro
      100      105      110
Ile Trp Xaa Asn Lys Glu Leu Ala Arg Arg Phe Leu Val Tyr Ser Gln
      115      120      125
Gly Leu Cys Ser Ser Ile Xaa Asp Asn Val Thr Arg Cys Pro Glu Ala
      130      135      140
Cys
      145

```

&lt;210&gt; 2062

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4190944-1-15386-17112)

&lt;400&gt; 2062

```

Met Met Ser Phe Ala Pro Asn Ala Ser His Ser Pro Val Phe Leu Leu
 1          5          10          15
Leu Gly Phe Ser Arg Ala Asn Ile Ser Tyr Thr Leu Leu Phe Phe Leu
          20          25          30
Phe Leu Ala Ile Tyr Leu Thr Thr Ile Leu Gly Asn Val Thr Leu Val
          35          40          45
Leu Leu Ile Ser Trp Asp Ser Arg Leu His Ser Pro Met Tyr Tyr Leu
          50          55          60
Leu Arg Gly Leu Ser Val Ile Asp Met Gly Leu Ser Thr Val Thr Leu
          65          70          75          80
Pro Gln Leu Leu Ala His Leu Val Ser His Tyr Pro Thr Ile Pro Ala
          85          90          95
Ala Arg Cys Leu Ala Gln Phe Phe Phe Tyr Ala Phe Gly Val Thr
          100          105          110
Asp Thr Leu Val Ile Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asp Pro Leu His Tyr Ala Leu Val Met Asn His Gln Arg Cys Ala
          130          135          140
Cys Leu Leu Ala Leu Ser Trp Val Val Ser Ile Leu His Thr Met Leu
          145          150          155          160
Arg Val Gly Leu Val Leu Pro Leu Cys Trp Thr Gly Asp Ala Gly Gly
          165          170          175
Asn Val Asn Leu Pro His Phe Phe Cys Asp His Arg Pro Leu Leu Arg
          180          185          190
Ala Ser Cys Ser Asp Ile His Ser Asn Glu Leu Ala Ile Phe Phe Glu
          195          200          205
Gly Gly Phe Leu Met Leu Gly Pro Cys Ala Leu Ile Val Leu Ser Tyr
          210          215          220
Val Arg Ile Gly Ala Ala Ile Leu Arg Leu Pro Ser Ala Ala Gly Arg
          225          230          235          240
Arg Arg Ala Val Ser Thr Cys Gly Ser His Leu Thr Met Val Gly Phe
          245          250          255
Leu Tyr Gly Thr Ile Ile Cys Val Tyr Phe Gln Pro Pro Phe Gln Asn
          260          265          270
Ser Gln Tyr Gln Asp Met Val Ala Ser Val Met Tyr Thr Ala Ile Thr
          275          280          285
Pro Leu Ala Asn Pro Phe Val Tyr Ser Leu His Asn Lys Asp Val Lys
          290          295          300
Gly Ala Leu Cys Arg Leu Leu Glu Trp Val Lys Val Asp Pro
          305          310          315

```

&lt;210&gt; 2063

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4190944-1-176262-177597)

&lt;400&gt; 2063

```

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
 1          5          10          15
Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
          20          25          30
Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
          35          40          45
Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
          50          55          60
Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala

```

```

65          70          75          80
Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
      85          90          95
Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
      100        105        110
Asp Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      115        120        125
Ala Ile Arg Asn Pro Leu Leu Tyr Thr Thr Ala Met Ser Gln Arg Leu
      130        135        140
Cys Leu Ala Leu Leu Gly Ala Ser Gly Leu Gly Gly Ala Val Ser Ala
      145        150        155        160
Phe Val His Thr Thr Leu Thr Phe Arg Leu Ser Phe Cys Arg Ser Arg
      165        170        175
Lys Ile Asn Ser Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Ile Ser
      180        185        190
Cys Ser Asp Thr Ser Leu Asn Glu Leu Leu Leu Phe Ala Ile Cys Gly
      195        200        205
Phe Ile Gln Thr Ala Thr Val Leu Ala Ile Thr Val Ser Tyr Gly Phe
      210        215        220
Ile Ala Gly Ala Val Ile His Met Arg Ser Val Glu Gly Ser Arg Arg
      225        230        235        240
Ala Ala Ser Thr Gly Gly Ser His Leu Thr Ala Val Ala Met Met Tyr
      245        250        255
Gly Thr Leu Ile Phe Met Tyr Leu Arg Pro Ser Ser Ser Tyr Ala Leu
      260        265        270
Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Ser
      275        280        285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
      290        295        300
Leu Arg Gln Thr Trp Ser Arg Phe His Cys Pro Gly Gln
      305        310        315

```

&lt;210&gt; 2064

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4190944-1-2029-4183)

&lt;400&gt; 2064

```

Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu Leu Gly
1          5          10          15
Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val Phe Ser
      20          25          30
Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile Thr Leu
      35          40          45
Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe Leu Ser
      50          55          60
Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
      65          70          75          80
Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly
      85          90          95
Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met Glu Asn
      100        105        110
Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
      115        120        125
Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met
      130        135        140
Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu His Thr
      145        150        155        160
Phe Leu Ile Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His
      165        170        175
Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr

```

	180		185		190										
Tyr	Leu	Asn	Thr	Leu	Met	Ile	His	Thr	Glu	Gly	Ala	Val	Val	Ile	Ser
	195						200						205		
Gly	Ala	Leu	Ala	Phe	Ile	Thr	Ala	Ser	Tyr	Ala	Cys	Ile	Ile	Leu	Val
	210						215				220				
Val	Leu	Arg	Ile	Pro	Ser	Ala	Lys	Gly	Arg	Trp	Lys	Thr	Phe	Ser	Thr
225					230					235					240
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ala	Ile	Phe	Tyr	Gly	Thr	Leu	Ser
			245						250					255	
Trp	Val	Tyr	Phe	Arg	Pro	Leu	Ser	Ser	Tyr	Ser	Val	Thr	Lys	Gly	Arg
			260					265					270		
Ile	Ile	Thr	Val	Val	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe
		275					280						285		
Ile	Tyr	Ser	Leu	Arg	Asn	Gly	Asp	Val	Lys	Gly	Gly	Phe	Met	Lys	Trp
	290					295					300				
Met	Ser	Arg	Met	Gln	Thr	Phe	Phe	Phe	Arg						
305					310										

&lt;210&gt; 2065

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (438406-1-1-648)

&lt;400&gt; 2065

Val	Leu	Asp	Val	Gly	Cys	Ile	Thr	Val	Thr	Val	Pro	Ala	Met	Leu	Gly
1				5					10					15	
Arg	Leu	Leu	Ser	His	Lys	Ser	Thr	Ile	Ser	Tyr	Asp	Ala	Cys	Leu	Ser
			20					25					30		
Gln	Leu	Phe	Phe	Phe	His	Leu	Leu	Ala	Gly	Met	Asp	Cys	Phe	Leu	Leu
	35					40						45			
Thr	Ala	Met	Ala	Tyr	Asp	Arg	Leu	Leu	Gly	Ile	Cys	Gln	Ala	Leu	Thr
	50					55					60				
Tyr	Arg	Thr	Arg	Met	Ser	Gln	Thr	Val	Gln	Arg	Met	Leu	Val	Ala	Ala
65					70					75				80	
Ser	Trp	Ala	Cys	Ala	Phe	Thr	Asn	Ala	Leu	Thr	His	Thr	Val	Gly	Met
				85					90					95	
Ser	Thr	Leu	Asn	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asn	His	Phe	Tyr	Cys
		100					105						110		
Asp	Leu	Pro	Gln	Leu	Phe	Lys	Leu	Ser	Cys	Ser	Ser	Thr	Gln	Leu	Asn
		115					120					125			
Glu	Leu	Leu	Leu	Phe	Ala	Val	Gly	Phe	Ile	Met	Ala	Gly	Thr	Pro	Met
	130					135					140				
Ala	Leu	Ile	Val	Ile	Ser	Tyr	Ile	His	Val	Ala	Ala	Ala	Val	Leu	Arg
145					150					155					160
Ile	Arg	Ser	Val	Glu	Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser
				165					170					175	
His	Leu	Thr	Val	Val	Ala	Ile	Phe	Tyr	Gly	Ser	Gly	Ile	Phe	Asn	Tyr
		180						185					190		
Met	Arg	Leu	Gly	Ser	Thr	Lys	Leu	Ser	Asp	Lys	Asp	Lys	Ala	Val	Gly
		195					200						205		
Ile	Phe	Asn	Thr	Val	Ile	Asn	Pro								
	210					215									

&lt;210&gt; 2066

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4581418-1-11548-14170)

&lt;400&gt; 2066

Met	Asp	Gln	Ser	Asn	Tyr	Ser	Ser	Leu	His	Gly	Phe	Ile	Leu	Leu	Gly
1				5					10					15	

Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala  
                   20                  25                  30  
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala  
                   35                  40                  45  
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg  
                   50                  55                  60  
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln  
                   65                  70                  75                  80  
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly  
                   85                  90                  95  
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys  
                   100                  105                  110  
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys  
                   115                  120                  125  
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met  
                   130                  135                  140  
 Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys  
                   145                  150                  155                  160  
 Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His  
                   165                  170                  175  
 Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr  
                   180                  185                  190  
 Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu  
                   195                  200                  205  
 Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala  
                   210                  215                  220  
 Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr  
                   225                  230                  235                  240  
 Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile  
                   245                  250                  255  
 Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys  
                   260                  265                  270  
 Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu  
                   275                  280                  285  
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu  
                   290                  295                  300  
 Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys  
                   305                  310                  315

&lt;210&gt; 2067

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (4581418-1-39007-42459)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(257)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2067

Phe Ile Leu Trp Gly Phe Phe Asp His Pro Xaa Pro Glu Met Phe Leu  
                   1                  5                  10                  15  
 Phe Ile Met Gly Leu Val Gly Leu Ser Leu His Thr Gly Gly Gln His  
                   20                  25                  30  
 Leu Asn Tyr Cys Gly Thr Gln Gly Ile Phe Xaa Gly Ser Thr Lys Cys  
                   35                  40                  45  
 Ile Ile Leu Ala Val Thr Ser Leu Asp Pro Tyr Ile Ala Ile Cys Lys  
                   50                  55                  60  
 His Leu Arg Tyr Pro Ala Ile Met His Gln Gln Leu Cys Val Leu Leu  
                   65                  70                  75                  80  
 Val Ala Met Ala Trp Leu Ser Ser Leu Ala Asn Ser Leu Gln Ser Ser

<400> 2068																
Met	Lys	Lys	Glu	Asn	Gln	Ser	Phe	Asn	Leu	Asp	Phe	Ile	Leu	Leu	Gly	
1				5					10					15		
Val	Thr	Ser	Gln	Gln	Glu	Gln	Asn	Asn	Val	Phe	Phe	Val	Ile	Phe	Leu	
			20					25					30			
Cys	Ile	Tyr	Pro	Ile	Thr	Leu	Thr	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Ile	Cys	Ala	Asp	Ile	Arg	Leu	His	Asn	Pro	Met	Tyr	Phe	Leu	Leu	Ala	
		50				55					60					
Asn	Leu	Ser	Leu	Val	Asp	Ile	Ile	Phe	Ser	Ser	Val	Thr	Ile	Pro	Lys	
65					70					75					80	
Val	Leu	Ala	Asn	His	Leu	Leu	Gly	Ser	Lys	Phe	Ile	Ser	Phe	Gly	Gly	
				85					90					95		
Cys	Leu	Met	Gln	Met	Tyr	Phe	Met	Ile	Ala	Leu	Ala	Lys	Ala	Asp	Ser	
			100					105					110			
Tyr	Thr	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Ala	Val	Ala	Ile	Ser	Cys	
		115					120					125				
Pro	Leu	His	Tyr	Thr	Thr	Ile	Met	Ser	Pro	Arg	Ser	Cys	Ile	Leu	Leu	
	130					135					140					
Ile	Ala	Gly	Ser	Trp	Val	Ile	Gly	Asn	Thr	Ser	Ala	Leu	Pro	His	Thr	
145					150				155					160		
Leu	Leu	Thr	Ala	Ser	Leu	Ser	Phe	Cys	Gly	Asn	Gln	Glu	Val	Ala	Asn	
				165					170					175		
Phe	Tyr	Cys	Asp	Ile	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Val	
			180					185					190			
His	Phe	Asn	Val	Lys	Met	Met	Tyr	Leu	Gly	Val	Gly	Val	Phe	Ser	Leu	
		195					200					205				
Pro	Leu	Leu	Cys	Ile	Ile	Val	Ser	Tyr	Val	Gln	Val	Phe	Ser	Thr	Val	
	210					215					220					
Phe	Gln	Val	Pro	S	r	Thr	Lys	Ser	Leu	Phe	Lys	Ala	Phe	Cys	Thr	Cys
225						230					235					240
Gly	Ser	His	Leu	Thr	Val	Val	Phe	Leu	Tyr	Tyr	Gly	Thr	Thr	Met	Gly	



245 250 255  
 Met Tyr Phe Arg Pro Leu Thr Ser Tyr Ser Pro Lys Asp Ala Val Ile  
 260 265 270  
 Thr Val Met Tyr Val Ala Val Thr Pro Ala Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Trp Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Ser  
 290 295 300  
 Lys Arg Ile Ser Ser  
 305

&lt;210&gt; 2069

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (5262456-1-1-1993)

&lt;400&gt; 2069

Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val  
 20 25 30  
 Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser  
 35 40 45  
 His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn  
 50 55 60  
 Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met  
 65 70 75 80  
 Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys  
 85 90 95  
 Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile  
 100 105 110  
 Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro  
 115 120 125  
 Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala  
 130 135 140  
 Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr  
 145 150 155 160  
 Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe  
 165 170 175  
 Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg  
 180 185 190  
 Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met  
 195 200 205  
 Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val  
 210 215 220  
 Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser  
 245 250 255  
 Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile  
 260 265 270

&lt;210&gt; 2070

&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (5262456-1-22068-24947)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(356)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2070

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
          20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
          35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
          50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
          65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
          100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
          115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
          130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
          145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
          165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
          180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
          195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
          210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
          225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
          245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
          260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
          275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
          290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
          305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
          325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
          340          345          350
Arg Xaa Tyr Pro
          355

```

&lt;210&gt; 2071

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (5679453-1-2929-5456)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(338)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2071

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
 1           5           10           15

```

Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro  
                   20                  25                  30  
 Gln Leu Glu His Ile Ile Ser Val Val Val Phe Ile Ile Tyr Ile Val  
                   35                  40                  45  
 Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr  
                   50                  55                  60  
 Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu  
                   65                  70                  75                  80  
 Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln  
                   85                  90                  95  
 Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe  
                   100                  105                  110  
 Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val  
                   115                  120                  125  
 Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr  
                   130                  135                  140  
 Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala  
                   145                  150                  155                  160  
 Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly  
                   165                  170                  175  
 His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys  
                   180                  185                  190  
 Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe  
                   195                  200                  205  
 Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr  
                   210                  215                  220  
 Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu  
                   225                  230                  235                  240  
 Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu  
                   245                  250                  255  
 Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile  
                   260                  265                  270  
 Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro  
                   275                  280                  285  
 Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser  
                   290                  295                  300  
 Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ala Glu Xaa Met  
                   305                  310                  315                  320  
 Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala  
                   325                  330                  335  
 Phe Ile

&lt;210&gt; 2072

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (5791525-1-119325-122054)

&lt;400&gt; 2072

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly  
   1                  5                  10                  15  
 Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu  
                   20                  25                  30  
 Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu  
                   35                  40                  45  
 Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser  
                   50                  55                  60  
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln  
                   65                  70                  75                  80  
 Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg  
                   85                  90                  95

Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys  
                   100                                  105                  110  
 Leu Leu L u Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn  
                   115                                  120                  125  
 Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu  
                   130                                  135                  140  
 Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile  
                   145                                  150                  155                  160  
 Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe  
                                   165                                  170                  175  
 Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser  
                                   180                                  185                  190  
 Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu  
                   195                                  200                  205  
 Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile  
                   210                                  215                  220  
 Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys  
                                   230                                  235                  240  
 Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser  
                                   245                                  250                  255  
 Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe  
                                   260                                  265                  270  
 Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile  
                   275                                  280                  285  
 Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met  
                   290                                  295                  300  
 Leu Lys Arg Thr  
 305

&lt;210&gt; 2073

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (5791525-1-456-2065)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2073

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly  
   1                                  5                                  10                  15  
 Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu  
                   20                                  25                  30  
 Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala  
                   35                                  40                  45  
 Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala  
                   50                                  55                  60  
 Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Thr Val Pro Lys  
                                   70                                  75                  80  
 Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly  
                                   85                                  90                  95  
 Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn  
                   100                                  105                  110  
 Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His  
                   115                                  120                  125  
 Pro Leu His Tyr Thr Val Val Val Leu Ser Pro Lys Asn Cys Ala Leu  
                   130                                  135                  140  
 Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His  
                   145                                  150                  155                  160  
 Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr

```

      165      170      175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
      180      185      190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
      195      200      205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
      210      215      220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
      225      230      235      240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
      245      250      255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
      260      265      270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
      275      280      285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
      290      295      300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
      305      310

```

<210> 2074  
 <211> 138  
 <212> PRT  
 <213> Homo sapien (5823349-1-32238-32756)

<220>  
 <221> VARIANT  
 <222> (1)...(138)  
 <223> Xaa = Any Amino Acid

```

<400> 2074
Leu Met Leu Leu Asp Leu Leu Ser Asp Ala Glu Val His Ala Val Ser
 1      5      10      15
Ser Ser His Cys Ser Leu His Leu Thr Lys Glu Ile Phe Ser Ile Val
      20      25      30
Ser Asn Gln Ala Leu Ser Pro Glu Ser Thr Leu Gly Leu His Met His
      35      40      45
Leu Cys Ala Phe Leu Thr Leu Phe Pro Leu Pro Arg Thr Pro Leu Pro
      50      55      60
Ser Phe Leu Ile His Arg Asn Leu Ile His Leu Ser Ser His Ala Gln
      65      70      75      80
Gln Leu Ser Phe Pro Xaa Leu Leu Xaa Lys Tyr Ser Leu Phe Asn Leu
      85      90      95
Tyr Val Ile Leu Ser Arg Ile Leu Phe Pro Leu His Pro Leu Val Tyr
      100      105      110
Glu Gln Phe Lys Ser Gly Cys Tyr Gly Xaa Phe Ile Ile Lys Ile Leu
      115      120      125
Asn Phe Cys Leu Leu Xaa Val Met Asn Leu
      130      135

```

<210> 2075  
 <211> 162  
 <212> PRT  
 <213> Homo sapien (5931513-1-1-2929)

```

<400> 2075
Met Asn Val Ser Glu Pro Asn Ser Ser Phe Ala Phe Val Asn Glu Phe
 1      5      10      15
Ile Leu Gln Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe
      20      25      30
Ser Leu Phe Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala

```

35 40 45  
 Ile Ala Phe Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr  
 50 55 60  
 Met Phe Leu Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser  
 65 70 75 80  
 Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile  
 85 90 95  
 Ser Phe Ala Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly  
 100 105 110  
 Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu  
 115 120 125  
 Ala Ile Cys Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu  
 130 135 140  
 Tyr Ala Lys Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe  
 145 150 155 160  
 Leu Ile

&lt;210&gt; 2076

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (6087993-15-1-2211)

&lt;400&gt; 2076

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val  
 1 5 10 15  
 Ser Glu Phe Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His  
 20 25 30  
 Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala  
 35 40 45  
 Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln  
 50 55 60  
 Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu  
 65 70 75 80  
 Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu  
 85 90 95  
 Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn  
 100 105 110  
 Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp  
 115 120 125  
 Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr  
 130 135 140  
 Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala  
 145 150 155 160  
 Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys  
 165 170 175  
 Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser  
 180 185 190  
 Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val  
 195 200 205  
 Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser  
 210 215 220  
 Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala  
 225 230 235 240  
 Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu  
 245 250 255  
 Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg  
 260 265 270  
 Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His  
 275 280 285  
 Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys

290 295 300  
 Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg  
 305 310 315

<210> 2077

<211> 314

<212> PRT

<213> Homo sapien (6087993-21-1-3660)

<400> 2077

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu  
 1 5 10 15  
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu  
 20 25 30  
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile  
 35 40 45  
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu  
 50 55 60  
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr  
 65 70 75 80  
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly  
 85 90 95  
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser  
 100 105 110  
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile  
 130 135 140  
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile  
 145 150 155 160  
 Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile  
 165 170 175  
 Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys  
 180 185 190  
 Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu  
 195 200 205  
 Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile  
 210 215 220  
 Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val  
 245 250 255  
 Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro  
 260 265 270  
 His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro  
 275 280 285  
 Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln  
 290 295 300  
 Arg Val Leu Arg Val Phe Thr Gln Lys Asp  
 305 310

<210> 2078

<211> 327

<212> PRT

<213> Homo sapien (6087993-34-2575-6318)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

&lt;400&gt; 2078

```

Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
 1           5           10           15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe
          20           25           30
Cys Phe Met Phe Phe Leu Ser Leu Thr Gly Asn Gly Val Leu Leu Phe
 35           40           45
Leu Ile Arg Thr Glu Cys Ser Leu Arg Gln Pro Met Phe Leu Phe Leu
 50           55           60
Ala Met Leu Ser Phe Val Asp Leu Val Leu Ser Leu Ser Thr Leu Pro
 65           70           75           80
Lys Met Leu Ala Ile Phe Trp Phe Gly Ala Thr Ala Ile Ser Ser His
          85           90           95
Ser Cys Leu Ser Gln Met Phe Phe Ile His Ala Phe Ser Ala Met Glu
          100          105          110
Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Ser Val Ala Ile Cys
          115          120          125
Asn Pro Leu Arg Tyr Ala Thr Ile Leu Pro Pro Val Val Val Ala Lys
          130          135          140
Ile Gly Gly Leu Val Val Leu Xaa Gly Val Gly Leu Thr Ile Ser Phe
          145          150          155          160
Pro Ser Leu Ala His Arg Leu His Tyr His Gly Ser His Met Ile Ala
          165          170          175
Tyr Thr Phe Cys Glu His Met Ala Val Val Lys Leu Ala Cys Glu Ala
          180          185          190
Thr Thr Val Asp Asn Leu Tyr Ala Phe Val Val Ala Ile Phe Leu Gly
          195          200          205
Gly Gly Asp Val Val Cys Ile Ala Tyr Ser Tyr Gly Leu Ile Val Arg
          210          215          220
Thr Val Met His Phe Pro Ser Pro Glu Glu Arg Ala Lys Ala Gly Ser
          225          230          235          240
Thr Cys Thr Ala His Val Cys Val Ile Leu Phe Phe Tyr Gly Leu Gly
          245          250          255
Phe Leu Ser Val Val Met Gln Arg Phe Gly Ala Pro Thr Ala Ser Thr
          260          265          270
Ala Lys Val Ile Leu Ala Asn Leu Tyr Leu Leu Phe Pro Pro Ala Leu
          275          280          285
Asp Pro Ile Val Tyr Gly Met Glu Thr Lys Gln Ile Xaa Glu Arg Leu
          290          295          300
Leu Met Ile Leu Ser Pro Lys Gln Ile Glu Leu Thr Xaa Val Xaa Leu
          305          310          315          320
Ser Pro Ala Gly Leu Gln Gly
          325

```

&lt;210&gt; 2079

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (6087993-36-10518-12399)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(135)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2079

```

Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1           5           10           15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
          20           25           30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
          35           40           45

```



```

Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
 50          55          60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
65          70          75          80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
          85          90          95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
          100          105          110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
          115          120          125
Arg Arg Leu Xaa Lys Ile Lys
          130          135

```

<210> 2080  
 <211> 141  
 <212> PRT  
 <213> Homo sapien (6094601-37-1-3120)

<220>  
 <221> VARIANT  
 <222> (1)...(141)  
 <223> Xaa = Any Amino Acid

```

<400> 2080
Met Leu Thr Cys Phe Trp Lys His Leu Xaa Tyr Leu Pro Leu Xaa Phe
 1          5          10          15
Val Asp Phe Val Leu Ser Lys Lys Lys Pro Ser Asn Xaa Ser Val Ser
          20          25          30
Ile Asn Val Phe Leu Leu Leu Thr Tyr Xaa Xaa Ser Phe Ala Leu Val
          35          40          45
Tyr Leu Cys Phe Asp Lys Leu Phe Trp Ile Cys Asn Pro Leu Ser Gly
          50          55          60
Leu Met Thr Leu Arg Arg Thr Arg Cys Ala Gly Ile Leu Gly Ala Cys
65          70          75          80
Trp Thr Tyr Ala Phe Thr Ser Thr Ile Arg Xaa Val Phe Phe Phe Phe
          85          90          95
Asn Leu Lys Asp Lys Leu Phe Phe Gln Met Ser Asn Phe Leu Ser Leu
          100          105          110
Xaa Glu Leu Met Xaa Gly Pro Phe Leu Glu Asn Ser His Met Tyr
          115          120          125
Ser Tyr Thr His Lys Leu Cys Leu Leu Phe Xaa Gly Val
          130          135          140

```

<210> 2081  
 <211> 315  
 <212> PRT  
 <213> Homo sapien (6249440-1-23422-29767)

<220>  
 <221> VARIANT  
 <222> (1)...(315)  
 <223> Xaa = Any Amino Acid

```

<400> 2081
Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
          20          25          30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
          35          40          45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```

50		55		60
Phe Phe Leu Ser Thr	Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser			
65	70	75		80
Trp Glu Leu Xaa Val	Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile			
	85	90		95
Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly				
	100	105		110
Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val				
	115	120		125
Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val				
	130	135		140
Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala				
145	150	155		160
Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val				
	165	170		175
Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys				
	180	185		190
Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe				
	195	200		205
Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile				
	210	215		220
Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly				
225	230	235		240
Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met				
	245	250		255
Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val				
	260	265		270
Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr				
	275	280		285
Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys				
	290	295		300
Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn				
305	310	315		

&lt;210&gt; 2082

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (6739493-1-1-1041)

&lt;400&gt; 2082

Met Tyr Ser Phe Met Ala Gly Ser Ile Phe Ile Thr Ile Phe Gly Asn	
1	5
Leu Ala Met Ile Ile Ser Ile Ser Tyr Phe Lys Gln Leu His Thr Pro	
	20
Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp Phe Leu Leu Gly	
	35
Phe Thr Ile Met Pro Tyr Ser Met Ile Arg Ser Val Glu Asn Cys Trp	
	50
Tyr Phe Gly Leu Thr Phe Cys Lys Ile Tyr Tyr Ser Phe Asp Leu Met	
65	70
Leu Ser Ile Thr Ser Ile Phe His Leu Cys Ser Val Ala Ile Asp Arg	
	85
Phe Tyr Ala Ile Cys Tyr Pro Leu Leu Tyr Ser Thr Lys Ile Thr Ile	
	100
Pro Val Ile Lys Arg Leu Leu Leu Leu Cys Trp Ser Val Pro Gly Ala	
	115
Phe Ala Phe Gly Ala Val Phe Ser Glu Ala Tyr Ala Asp Gly Ile Glu	
	130
Gly Tyr Asp Ile Leu Val Ala Cys Ser Ser Ser Cys Pro Val Met Phe	
145	150
Asn Lys Leu Trp Gly Thr Thr Leu Phe Met Ala Gly Phe Phe Thr Pro	

<400> 2083															
Leu 1	Ser	Ser	Met	Cys 5	Leu	Thr	Ile	Val	Met 10	His	Cys	Glu	Phe	Phe 15	Leu
Met	Asp	Leu	Thr	Asp	Asp	Pro	Gln	Leu 25	His	Pro	Thr	Phe	Ser 30	Ala	Leu
Phe	Leu	Pro 35	Ile	Tyr	Val	Val	Met 40	Val	Met	Ala	Asn	Leu 45	Gly	Leu	Leu
Ala	Phe 50	Ile	Val	Val	Ser	Pro 55	Gln	Phe	Leu	Thr	Pro 60	Met	Tyr	Phe	Phe
Leu 65	Ser	Asn	Trp	Ser	Ser 70	Val	Asp	Phe	Cys 75	Tyr	Ser	Ser	Val	Thr 80	Val
Pro	Lys	Ile	Ser	Met 85	Gly	Phe	Phe	Ser 90	Asp	Cys	Gln	Val	Phe 95	Ser	Phe
Ser	Gly	Cys	Met 100	Ala	Gln	Leu	Ser	Cys 105	Phe	Xaa	Ile	Phe	Ala 110	Asp	Thr
Glu	Phe	Phe 115	Leu	Leu	Ala	Ser	Met 120	Val	Tyr	Tyr	Arg	Xaa 125	Glu	Ala	Val
Cys	Asn 130	Pro	Leu	Leu	Tyr	His 135	Ile	Thr	Met	Ser	Pro 140	Lys	Leu	Cys	Leu
Gln 145	Leu	Val	Ala	Thr	Ser 150	Met	Asn	Met	Val	Leu 155	Pro	Ser	Ser	Thr 160	Ile
Phe	His	Leu	Ile	Phe 165	Cys	Lys	Ser	Arg	Ala 170	Ile	Ile	His	Xaa 175	Phe	Cys
Tyr	Phe	Ser	Pro 180	Pro	Pro	Arg	Leu	Xaa 185	Lys	Leu	Ser	Cys	Ser 190	Asp	Met
Gln	Gly	Leu 195	Gln	Leu	Leu	Thr	Phe 200	Ala	Ser	Ser	Ser	Phe 205	Asn	Val	Ser
Val	Ser	Arg 210	Thr	Ile	Phe	Leu	Val 215	Ser	Tyr	Leu	Ile	Met	Arg	Met	Pro
Ser 225	Val	Xaa	Gly	Lys	His 230	Cys	Ala	Ser	His	Leu 235	Thr	Ala	Val	Ser	Leu
Cys	Tyr	Gly	Thr	Thr 245	Val	Phe	Leu	His	Leu 250	His	Leu	Ser	Leu	Lys 255	Cys

Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu  
 260 265 270  
 Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys  
 275 280 285  
 Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu  
 290 295 300

<210> 2084

<211> 274

<212> PRT

<213> Homo sapien (6911343-1-22015-25112)

<220>

<221> VARIANT

<222> (1)...(274)

<223> Xaa = Any Amino Acid

<400> 2084

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp  
 1 5 10 15  
 Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu  
 20 25 30  
 Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile  
 35 40 45  
 Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu  
 50 55 60  
 Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser  
 65 70 75 80  
 Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe  
 85 90 95  
 Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala  
 100 105 110  
 Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr  
 115 120 125  
 Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg  
 130 135 140  
 Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe  
 145 150 155 160  
 Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln  
 165 170 175  
 Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser  
 180 185 190  
 Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys  
 195 200 205  
 Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn  
 210 215 220  
 Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe  
 225 230 235 240  
 Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr  
 245 250 255  
 Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln  
 260 265 270  
 Ile Leu

<210> 2085

<211> 323

<212> PRT

<213> Homo sapien (6911343-1-65670-69060)

<220>

<221> VARIANT  
 <222> (1)...(323)  
 <223> Xaa = Any Amino Acid

<400> 2085

```

Val Glu Asn Ser Pro Met Val Thr Asp Phe Ile Phe Leu Gly Met Thr
1          5          10          15
Asp Asn Ser Gln Leu Glu Val Leu Leu Phe Gly Val Phe Leu Ile Ala
20          25          30
Tyr Ile Ile Thr Val Leu Glu Asn Leu Gly Leu Val Val Leu Ile Arg
35          40          45
Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Gln
50          55          60
Ser Phe Leu Asp Val Cys Phe Ser Ser Ile Thr Ile Pro Gln Asn Leu
65          70          75          80
Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr
85          90          95
Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe
100         105         110
Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu
115         120         125
Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala
130         135         140
Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser
145         150         155         160
Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe
165         170         175
Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile
180         185         190
Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr
195         200         205
Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile
210         215         220
Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys
225         230         235         240
Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr
245         250         255
Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile
260         265         270
Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile
275         280         285
Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu
290         295         300
Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile
305         310         315         320
Leu Xaa Arg

```

<210> 2086  
 <211> 318  
 <212> PRT  
 <213> Homo sapien (7024122-10-14004-16338)

<220>  
 <221> VARIANT  
 <222> (1)...(318)  
 <223> Xaa = Any Amino Acid

<400> 2086

```

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile
1          5          10          15

```

Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe  
                   20                  25                  30  
 Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met  
                   35                  40                  45  
 Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe  
                   50                  55                  60  
 Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile  
                   65                  70                  75                  80  
 Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr  
                   85                  90                  95  
 Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr  
                   100                  105                  110  
 Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile  
                   115                  120                  125  
 Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val  
                   130                  135                  140  
 Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile  
                   145                  150                  155                  160  
 Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu  
                   165                  170                  175  
 Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile  
                   180                  185                  190  
 Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile  
                   195                  200                  205  
 Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser  
                   210                  215                  220  
 Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser  
                   225                  230                  235                  240  
 Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val  
                   245                  250                  255  
 Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile  
                   260                  265                  270  
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr  
                   275                  280                  285  
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys  
                   290                  295                  300  
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile  
                   305                  310                  315

&lt;210&gt; 2087

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7024122-5-2648-5354)

&lt;400&gt; 2087

Met Phe Ser Ser Glu Pro Thr Ile Asp Gly Asn Gln Ser Leu Cys Ala  
                   1                  5                  10                  15  
 Lys Phe Thr Phe Val Ala Phe Ser Ser Ile Glu Glu Leu Gln Leu Val  
                   20                  25                  30  
 Leu Phe Ile Val Phe Leu Ile Ile Tyr Leu Cys Thr Ile Gly Gly Asn  
                   35                  40                  45  
 Ile Ile Ile Ile Ser Leu Ile Trp Ile Thr Pro Ala Leu His Thr Pro  
                   50                  55                  60  
 Met Tyr Phe Phe Leu Val Asn Leu Ser Phe Leu Glu Met Cys Tyr Thr  
                   65                  70                  75                  80  
 Thr Ser Val Val Pro Leu Leu Val His Leu Leu Val Glu Thr Lys Thr  
                   85                  90                  95  
 Ile Ser Val Gly Gly Cys Ala Thr Gln Met Tyr Ile Phe Ala Ile Leu  
                   100                  105                  110  
 Gly Leu Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe  
                   115                  120                  125

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Leu Phe Met Gly Pro Arg  
 130 135 140  
 Val Cys Leu Lys Leu Ala Ala Ser Trp Phe Thr Gly Val Val Val  
 145 150 155 160  
 Glu Ser Ala Gln Ile Thr Leu Ile Phe Thr Leu Pro Phe Cys Gly Thr  
 165 170 175  
 Gly Lys Ile Pro Thr Leu Phe Cys Asp Ile Met Pro Val Leu Lys Leu  
 180 185 190  
 Ala Cys Ile Asp Thr Ser Gln Ile Glu Ile Val Met Phe Ser Leu Ser  
 195 200 205  
 Val Leu Phe Ile Val Ser Pro Cys Phe Leu Ile Leu Cys Ser His Met  
 210 215 220  
 His Ile Pro Val Thr Ile Leu Arg Ile Pro Ser Ala Ala Gly Arg His  
 225 230 235 240  
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Leu Val Val Ser Leu Phe  
 245 250 255  
 Tyr Gly Thr Ala Leu Phe Thr Tyr Leu Gln Pro Lys Thr Ala His Thr  
 260 265 270  
 Pro Glu Thr Asp Lys Ala Thr Ala Leu Met Tyr Thr Met Val Thr Pro  
 275 280 285  
 Ala Leu Asn Pro Val Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu  
 290 295 300  
 Ala Phe Gln Arg Ile Thr Gln Arg Asn Ser Leu Arg Gln Thr  
 305 310 315

&lt;210&gt; 2088

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7024122-6-11866-14009)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2088

Met Gly Asp Lys Gly Thr Gly Asn His Ser Asp Val Thr Asp Phe Ile  
 1 5 10 15  
 Leu Glu Gly Phe Arg Val Arg Pro Glu Phe Tyr Ile Leu Leu Phe Phe  
 20 25 30  
 Leu Phe Leu Leu Ile Tyr Ser Met Val Leu Leu Gly Asn Ile Ser Val  
 35 40 45  
 Met Thr Ile Ile Val Thr Asp Ser Gln Leu Asn Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Gly Asn Leu Ser Phe Ile Asp Val Ser Tyr Ser Thr Val Ile  
 65 70 75 80  
 Ala Pro Lys Ala Met Ala His Phe Leu Ser Glu Lys Lys Thr Val Ser  
 85 90 95  
 Phe Ala Gly Cys Val Ala Gln Leu Phe Leu Phe Ala Leu Phe Ile Val  
 100 105 110  
 Thr Glu Gly Phe Val Leu Ala Ala Met Ala Tyr Asp Arg Phe Ser Ala  
 115 120 125  
 Ile Cys Asn Pro Leu Leu His Ser Val His Met Ser Arg Arg Leu Cys  
 130 135 140  
 Thr Gln Leu Val Ala Gly Ser Tyr Phe Cys Gly Trp Ala Ser Ser Ile  
 145 150 155 160  
 Leu Gln Val Ser Val Thr Phe Ser Val Ser Phe Cys Ala Ser Arg Val  
 165 170 175  
 Ile Ala His Phe Tyr Cys Asp Ser Tyr Gln Ile Glu Lys Ile Ser Cys  
 180 185 190  
 Ser Asn Leu Phe Val Asn Lys Met Val Ser Leu Ser Leu Ser Val Ile

```

      195              200              205
Ile Ile Leu Pro Thr Ile Val Val Ile Ile Val Ser Tyr Leu Tyr Ile
  210              215              220
Val Ser Ser Val Leu Lys Ile Pro Ser Ser Glu Gly Arg Lys Lys Asp
  225              230              235              240
Phe Ser Thr Cys Ser Ser His Arg Gly Val Val Ser Leu Leu Xaa Gly
      245              250              255
Thr Val Ser Phe Val Tyr Leu Thr Pro Pro Ser Asn Pro Glu Leu Arg
      260              265              270
Lys Val Ala Ser Val Phe Tyr Ile Cys Val Thr Pro Met Leu Asn Pro
      275              280              285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys
      290              295              300
Ile Leu Cys Asn Lys Lys Ala Leu Ser Xaa Phe Tyr Phe
  305              310              315

```

&lt;210&gt; 2089

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7107785-12-32121-33524)

&lt;400&gt; 2089

```

Met Ser Pro Asp Gly Asn His Ser Ser Asp Pro Thr Glu Phe Val Leu
  1              5              10              15
Ala Gly Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val
      20              25              30
Phe Leu Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val
      35              40              45
Gly Val Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe
      50              55              60
Leu Gly Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile
      65              70              75              80
Pro Lys Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe
      85              90              95
Ala Ala Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser
      100              105              110
Glu Phe Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile
      115              120              125
Cys His Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe
      130              135              140
Arg Val Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly
      145              150              155              160
Pro Thr Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val
      165              170              175
Val Gln His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys
      180              185              190
Thr Asn Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu
      195              200              205
Val Ile Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile
      210              215              220
Val Leu Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala
      225              230              235              240
Phe Ser Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly
      245              250              255
Ser Ala Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp
      260              265              270
Thr Asn Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu
      275              280              285
Asn Pro Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu
      290              295              300
Lys Asp Met Phe Arg Lys Val Val Ala Gly Val

```



305

310

315

<210> 2090  
 <211> 141  
 <212> PRT  
 <213> Homo sapien (7107785-6-1204-2472)

<220>  
 <221> VARIANT  
 <222> (1)...(141)  
 <223> Xaa = Any Amino Acid

<400> 2090  
 Arg Asn Ile Arg Ile Ser Leu Pro Ile Tyr Phe Leu Ser Val Xaa Glu  
 1 5 10 15  
 Glu Arg Phe Gly Arg Glu Glu Phe Leu Arg Val Trp Thr Tyr Xaa Leu  
 20 25 30  
 Ile Ser Met Arg Asn Cys Phe Leu Arg Gly Cys Leu Met Tyr Xaa Met  
 35 40 45  
 Ile Phe Ser Trp Ser Cys Thr Glu Tyr Val Val His Met Phe Phe Ser  
 50 55 60  
 Leu Leu Asn Ser Gly Ile Ser Thr Glu Cys Gln Ile Ser Tyr Gln Gln  
 65 70 75 80  
 Asn Lys Asp Ile Ala Ile Phe Phe Leu His Asn Leu Xaa Xaa Lys Glu  
 85 90 95  
 Asn Phe Glu Ile Phe Leu Tyr Glu Asp Tyr Cys Ser His Ile Arg Asp  
 100 105 110  
 Leu Thr Lys Ile Ser Leu Gly Glu Ala Gly Xaa Asn Tyr Xaa Gly Lys  
 115 120 125  
 Ser Thr Thr Ile Glu Phe Leu Phe Leu Ala Leu Leu Phe  
 130 135 140

<210> 2091  
 <211> 202  
 <212> PRT  
 <213> Homo sapien (7134787-10-3417-6169)

<220>  
 <221> VARIANT  
 <222> (1)...(202)  
 <223> Xaa = Any Amino Acid

<400> 2091  
 Ile Phe Ala Ile Leu Thr Thr Ile Asp Cys Cys Val Phe Val Trp Glu  
 1 5 10 15  
 Phe Leu Glu Cys Thr Val Phe Val Asn Lys Arg Ala Cys Ala Gln Leu  
 20 25 30  
 Ala Cys Gly Ala Phe Cys Ile Gly Leu Ile Met Thr Val Val Xaa Ile  
 35 40 45  
 Thr Thr Val Ser Gln Arg Tyr Lys Arg Ser Thr Tyr Ala Ile Val Asp  
 50 55 60  
 Cys Phe Leu Phe Asp Thr Leu Leu Val Met Lys Leu Ser Cys Ile Asp  
 65 70 75 80  
 Asn Thr Ile Tyr Glu Ile Ile Gln Tyr Phe Ile His His Thr Cys Val  
 85 90 95  
 Gln Val Ser Met Gly Leu Val Cys Ile Ser Tyr Ile Asp Ile Pro Val  
 100 105 110  
 Thr Ser Ile Val Leu Arg Ile Ser Xaa Ser Glu Val Phe Ala Thr Cys  
 115 120 125  
 Val Pro Gln Pro Pro Pro His His Gly His Cys Leu Tyr Val Cys Ala  
 130 135 140

Cys Thr Ala Tyr Leu Lys His Lys Pro Met Asn Ser Ile Glu Lys Gly  
 145 150 155 160  
 Leu Leu Xaa Glu Thr Tyr Ile Ile Ile His Ser Ala Ser Gly Pro  
 165 170 175  
 Val Val Tyr Thr Leu Arg Tyr Met Glu Ala Lys Asp Thr Met Tyr Arg  
 180 185 190  
 Ala Val Asp Arg Asn Ile Ser Xaa Gln Ile  
 195 200

&lt;210&gt; 2092

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7134787-7-358-5219)

&lt;400&gt; 2092

Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu  
 20 25 30  
 Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile  
 35 40 45  
 Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln  
 65 70 75 80  
 Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly  
 85 90 95  
 Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys  
 100 105 110  
 Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu  
 130 135 140  
 Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val  
 145 150 155 160  
 Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe  
 165 170 175  
 Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr  
 180 185 190  
 Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val  
 195 200 205  
 Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val  
 210 215 220  
 Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys  
 225 230 235 240  
 Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile  
 245 250 255  
 Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu  
 260 265 270  
 Leu Ser Val Thr  
 275

&lt;210&gt; 2093

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7139676-7-1545-4565)

&lt;400&gt; 2093

Met Gln Leu Asn Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Gln Asp Pro Phe Trp Lys Lys Ile Val Phe Val Ile Phe Leu Arg Leu

```

      20      25      30
Tyr Leu Gly Thr Leu Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys
      35      40      45
Ala Ser Gln Ala Leu Lys Asn Pro Met Phe Phe Phe Leu Phe Tyr Leu
      50      55      60
Ser Leu Ser Asp Thr Cys Leu Ser Thr Ser Ile Ala Pro Arg Met Ile
65      70      75      80
Val Asp Ala Leu Leu Lys Lys Thr Thr Ile Ser Phe Ser Glu Cys Met
      85      90      95
Ile Gln Val Phe Ser Ser His Val Phe Gly Cys Leu Glu Ile Phe Ile
      100      105      110
Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Thr Ile Ile Ser Gln Trp Val Cys Gly Val Leu Met Ala
      130      135      140
Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val Gln Ile Phe Leu
145      150      155      160
Ala Leu Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Cys Phe
      165      170      175
Cys Asp Leu Gln Pro Leu Leu Lys Gln Ala Cys Ser Glu Thr Tyr Val
      180      185      190
Val Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ala Val Ser
      195      200      205
Tyr Val Met Leu Ile Phe Ser Tyr Val Ile Phe Leu His Ser Leu Arg
      210      215      220
Asn His Ser Ala Glu Val Ile Lys Lys Ala Leu Ser Thr Cys Val Ser
225      230      235      240
His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Met Tyr
      245      250      255
Thr Cys Pro Ala Thr Val Phe Pro Met Asp Lys Met Ile Ala Val Phe
      260      265      270
Tyr Thr Val Gly Thr Ser Phe Leu Asn Pro Val Ile Tyr Thr Leu Lys
      275      280      285
Asn Thr Glu Val Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Leu
      290      295      300
Ile Thr Asp Asp Lys Arg
305      310

```

&lt;210&gt; 2094

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7139676-9-1-2285)

&lt;400&gt; 2094

```

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
1      5      10      15
Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
      20      25      30
Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
      35      40      45
Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
      50      55      60
Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met
65      70      75      80
Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
      85      90      95
Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
      100      105      110
Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile

```

130	135	140
Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu		
145	150	155
Thr Ile Ph Val Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe		160
	165	170
Cys Asp Val Tyr Pro Leu Leu Lys Leu Ala Cys Ser Asn Ile His Met		175
	180	185
Ile Gly Leu Leu Val Ile Ala Asn Ser Gly Leu Ile Ala Leu Val Thr		190
	195	200
Phe Val Val Leu Leu Leu Ser Tyr Val Phe Ile Leu Tyr Thr Ile Arg		205
	210	215
Ala Tyr Ser Ala Glu Arg Arg Ser Lys Ala Leu Ala Thr Cys Ser Ser		220
225	230	235
His Val Ile Val Val Leu Phe Phe Ala Pro Ala Leu Phe Ile Tyr		240
	245	250
Ile Arg Pro Val Thr Thr Phe Ser Glu Asp Lys Val Phe Ala Leu Phe		255
	260	265
Tyr Thr Ile Ile Ala Pro Met Phe Asn Pro Leu Ile Tyr Thr Leu Arg		270
	275	280
Asn Thr Glu Met Lys Asn Ala Met Arg Lys Val Trp Cys Cys Gln Ile		285
	290	295
Leu Leu Lys Arg Asn Gln Leu		300
305	310	

&lt;210&gt; 2095

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7144617-1-1-995)

&lt;400&gt; 2095

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly	
1	5
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys	10
	15
	20
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala	25
	30
	35
Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu	40
	45
	50
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro	55
65	60
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln	65
	70
	75
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu	80
	85
	90
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys	95
	100
	105
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser	110
	115
	120
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His	125
145	130
	135
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg	140
	145
	150
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp	155
	160
	165
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val	170
	175
	180
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val	185
	190
	195
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly	200
225	205
	210
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser	215
	220
	225
	230
	235
	240

```
<210> 2096
<211> 316
<212> PRT
<213> Homo sapien (7144637-1-1-993)
```

```
<220>
<221> VARIANT
<222> (1)...(316)
<223> Xaa = Any Amino Acid
```

1231

<210> 2097  
 <211> 247  
 <212> PRT  
 <213> Homo sapien (7144976-1-1-1194)

<220>  
 <221> VARIANT  
 <222> (1)...(247)  
 <223> Xaa = Any Amino Acid

<400> 2097  
 Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu  
 20 25 30  
 Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu  
 35 40 45  
 Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe  
 50 55 60  
 Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn  
 65 70 75 80  
 Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln  
 85 90 95  
 Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val  
 100 105 110  
 Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr  
 115 120 125  
 Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser  
 130 135 140  
 Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His  
 145 150 155 160  
 Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp  
 165 170 175  
 Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala  
 180 185 190  
 Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile  
 195 200 205  
 Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His  
 210 215 220  
 Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met  
 225 230 235 240  
 Arg Pro Ile Leu Gly Asn Ser  
 245

<210> 2098  
 <211> 329  
 <212> PRT  
 <213> Homo sapien (7145001-12-25597-26388)

<220>  
 <221> VARIANT  
 <222> (1)...(329)  
 <223> Xaa = Any Amino Acid

<400> 2098  
 Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu  
 20 25 30  
 Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile

```
<210> 2099
<211> 264
<212> PRT
<213> Homo sapien (7145001-12-45102-50811)
```

400> 2099																
Met	Val	Asp	Asn	Leu	Ile	Ile	Val	Val	Thr	Ile	Thr	Thr	Ser	Pro	Ala	
1				5					10					15		
Leu	Asp	Ser	Pro	Val	Tyr	Phe	Phe	Leu	Ser	Phe	Phe	Ser	Phe	Ile	Asp	
			20					25					30			
Gly	Cys	Ser	Ser	Ser	Thr	Met	Ala	Pro	Lys	Met	Ile	Phe	Asp	Leu	Leu	
		35					40					45				
Thr	Glu	Lys	Lys	Thr	Ile	Ser	Phe	Ser	Gly	Cys	Met	Thr	Gln	Leu	Phe	
	50					55					60					
Val	Glu	His	Phe	Phe	Gly	Gly	Val	Glu	Ile	Ile	Leu	Leu	Val	Val	Met	
65					70					75					80	
Ala	Tyr	Asp	Cys	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu	Tyr	Tyr	Leu	Ile	
			85						90					95		
Thr	Met	Asn	Arg	Gln	Val	Cys	Gly	Leu	Leu	Val	Ala	Met	Ala	Trp	Val	
		100						105					110			
Gly	Gly	Phe	Leu	His	Ala	Leu	Ile	Gln	Met	Leu	Leu	Ile	Val	Trp	Leu	
		115					120					125				
Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His	Phe	Ile	Cys	Asp	Leu	Phe	

130                      135                      140  
 Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe  
 145                      150                      155                      160  
 Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu  
                     165                      170                      175  
 Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser  
                     180                      185                      190  
 Thr Cys Ala Phe His Ile Thr Val Val Leu Phe Phe Val Pro Cys  
                     195                      200                      205  
 Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala  
                     210                      215                      220  
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile  
 225                      230                      235                      240  
 Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp  
                     245                      250                      255  
 Ser Gln Ile Ile Trp Gly Asn Asn  
                     260

&lt;210&gt; 2100

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7145001-8-11112-14684)

&lt;400&gt; 2100

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe  
 1                      5                      10                      15  
 Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe  
                     20                      25                      30  
 His Val Leu Thr Val Leu Gly Asn Leu Val Ile Ile Thr Ile Asn  
                     35                      40                      45  
 Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu  
                     50                      55                      60  
 Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile  
 65                      70                      75                      80  
 Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met  
                     85                      90                      95  
 Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu  
                     100                      105                      110  
 Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu  
                     115                      120                      125  
 His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly  
                     130                      135                      140  
 Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu  
 145                      150                      155                      160  
 Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe  
                     165                      170                      175  
 Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met  
                     180                      185                      190  
 Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser  
                     195                      200                      205  
 Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg  
                     210                      215                      220  
 Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser  
 225                      230                      235                      240  
 His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr  
                     245                      250                      255  
 Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe  
                     260                      265                      270  
 Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
                     275                      280                      285  
 Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg



290  
Ser Leu Gly Glu Lys  
305

295

300

<210> 2101  
<211> 296  
<212> PRT  
<213> Homo sapien (7145013-16-7265-9434)

&lt;400&gt; 2101

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met  
1 5 10 15  
Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His  
20 25 30  
Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu  
35 40 45  
Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg  
50 55 60  
Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr  
65 70 75 80  
Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Leu Thr Val Met Ser Tyr  
85 90 95  
Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met  
100 105 110  
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly  
115 120 125  
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe  
130 135 140  
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu  
145 150 155 160  
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe  
165 170 175  
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr  
180 185 190  
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser  
195 200 205  
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val  
210 215 220  
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln  
225 230 235 240  
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu  
245 250 255  
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr  
260 265 270  
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe  
275 280 285  
Glu Lys Arg Met Arg Ala Val Leu  
290 295

<210> 2102  
<211> 162  
<212> PRT  
<213> Homo sapien (7211526-1-1-487)

&lt;400&gt; 2102

Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys  
1 5 10 15  
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His  
20 25 30  
Pro Leu Val His Val Ser Leu Leu Arg Leu Thr Phe Cys Arg Phe  
35 40 45

```

Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50                      55                      60
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Ile Phe Ile Phe Gly
65                      70                      75                      80
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
                      85                      90                      95
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
                      100                      105                      110
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
                      115                      120                      125
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
                      130                      135                      140
Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145                      150                      155                      160
Leu Leu

```

&lt;210&gt; 2103

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211533-1-1-487)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(162)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2103

```

Met Ala Ile Val Asn Pro Leu Leu Tyr Thr Val Ala Met Thr Lys Ile
 1                      5                      10                      15
Val Cys Ile Val Leu Ala Phe Gly Ser Cys Met Gly Gly Leu Ile Ser
                      20                      25                      30
Ser Leu Thr His Thr Ile Gly Leu Val Lys Leu Ser Phe Cys Gly Pro
                      35                      40                      45
Asn Val Ile Ser His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu
                      50                      55                      60
Ser Cys Ser Glu Thr Ser Met Asn Glu Leu Leu Leu Leu Ile Phe Ser
65                      70                      75                      80
Gly Ile Ile Ala Thr Leu Thr Phe Leu Thr Val Val Ile Ser Tyr Ile
                      85                      90                      95
Phe Ile Val Ala Ala Ile Leu Arg Ile Arg Xaa Glu Ala Gly Arg Arg
                      100                      105                      110
Lys Ala Phe Ser Thr Cys Thr Ser His Leu Ile Thr Val Thr Leu Phe
                      115                      120                      125
Tyr Gly Ser Ile Ser Phe Ser Tyr Ile Gln Pro Asn Ser Gln Tyr Ser
                      130                      135                      140
Leu Glu Gln Glu Lys Val Val Ser Val Phe Tyr Thr Leu Val Val Pro
145                      150                      155                      160
Met Leu

```

&lt;210&gt; 2104

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211534-1-1-485)

&lt;400&gt; 2104

```

Val Gly Ile Cys Asn Pro Leu Leu Tyr Thr Val Thr Met Ser Pro Gln
 1                      5                      10                      15
Lys Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ile Phe Gly
                      20                      25                      30

```

Ala Val Ala His Met Gly Asn Ile Met Phe Met Ser Phe Cys Gly Asp  
 35 40 45  
 Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu  
 50 55 60  
 Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Val Phe Ile Ile Val  
 65 70 75 80  
 Thr Val Gly Ile Gly Val Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly  
 85 90 95  
 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser  
 100 105 110  
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe  
 115 120 125  
 Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro  
 130 135 140  
 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Cys Thr Ala Val Val Pro  
 145 150 155 160  
 Met Phe

&lt;210&gt; 2105

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211536-1-1-487)

&lt;400&gt; 2105

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg  
 1 5 10 15  
 Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile  
 20 25 30  
 Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser  
 35 40 45  
 Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile  
 50 55 60  
 Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala  
 65 70 75 80  
 Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu  
 85 90 95  
 Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys  
 100 105 110  
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala  
 115 120 125  
 Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu  
 130 135 140  
 Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro  
 145 150 155 160  
 Leu Leu

&lt;210&gt; 2106

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211538-1-1-487)

&lt;400&gt; 2106

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu  
 1 5 10 15  
 Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser  
 20 25 30  
 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala  
 35 40 45  
 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

```

      50              55              60
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65              70              75              80
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85              90              95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100             105             110
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115             120             125
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130             135             140
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145              150              155              160
Met Leu

```

&lt;210&gt; 2107

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211540-1-1-478)

&lt;400&gt; 2107

```

Val Ala Ile Cys Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln
1              5              10              15
Leu Cys Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His
      20              25              30
Ser Ile Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
      35              40              45
Asn Glu Leu Asp Asn Phe Tyr Cys Asp Val Leu Gln Ile Ile Lys Leu
      50              55              60
Ala Cys Met Asp Thr Tyr Val Val Glu Val Leu Val Ile Ala Asn Ser
65              70              75              80
Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala
      85              90              95
Ile Ile Leu Ile Thr Leu Arg Thr Arg Phe Cys Gln Gly Gln Asn Lys
      100             105             110
Val Leu Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe
      115             120             125
Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
      130             135             140
Asp Lys Ile Phe Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu
145              150              155

```

&lt;210&gt; 2108

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211541-1-1-488)

&lt;400&gt; 2108

```

Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys
1              5              10              15
Val Cys Leu Cys Leu Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn
      20              25              30
Gly Leu Ser Gln Thr Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro
      35              40              45
Asn Asp Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu
      50              55              60
Ala Cys Ser Asp Thr Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala
65              70              75              80
Gly Ser Asn Leu Ile Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr
      85              90              95

```

Phe Ile Phe Thr Ala Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg  
                   100                  105                  110  
 Lys Ala Phe Ser Thr Cys Gly Ser His Val Thr Ala Val Thr Val Phe  
                   115                  120                  125  
 Tyr Gly Thr Leu Phe Cys Met Tyr Leu Arg Pro Pro Ser Glu Thr Ser  
                   130                  135                  140  
 Ile Gln Gln Gly Lys Ile Val Ala Val Phe Tyr Ile Phe Val Ser Pro  
 145                  150                  155                  160  
 Met Leu

&lt;210&gt; 2109

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7211542-1-1-487)

&lt;400&gt; 2109

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys  
   1                  5                  10                  15  
 Leu Cys Thr Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Leu Thr  
                   20                  25                  30  
 Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser  
                   35                  40                  45  
 Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu  
                   50                  55                  60  
 Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala  
 65                  70                  75                  80  
 Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met  
                   85                  90                  95  
 Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys  
                   100                  105                  110  
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser  
                   115                  120                  125  
 Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys  
                   130                  135                  140  
 Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro  
 145                  150                  155                  160  
 Met Leu

&lt;210&gt; 2110

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7230851-8-1-2360)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(243)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2110

Met Gln Ser Glu His Leu Ala Glu Phe Ser Glu Phe Leu Ile Leu Ser  
   1                  5                  10                  15  
 Leu Ser Glu Ile Gln Asn Cys Ser Pro Phe Phe Gly Leu Phe Leu Ser  
                   20                  25                  30  
 Met Asn Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile  
                   35                  40                  45  
 Ser Ser Asp Ser His Leu His Lys Pro Met Tyr Phe Leu Leu Ser Lys  
                   50                  55                  60  
 Leu Ser Met Ala Ala Ile Cys Phe Val Phe Thr Met Ile Gln Lys Met  
 65                  70                  75                  80

```

Met Val Asn Leu Arg Ala Gln Ser Lys Asp Ile Phe Thr Gln Pro Ser
      85                      90                      95
Gly Ser Pro Ile Pro Phe Xaa Met Cys Ser Leu Ile Arg Phe Leu Leu
      100                    105                    110
Ile Gln Gln Lys Ser Val Val Leu Ile Phe Glu Tyr Ser Leu Val Leu
      115                    120                    125
Ile His Pro Ile Xaa Ile Xaa Arg Cys Lys Leu Ile Ile Leu Leu Tyr
      130                    135                    140
Glu Pro Phe Lys Ile Ile Glu Asp Ser Tyr Val Leu Phe Leu Ile Ile
145      150                    155                    160
Thr Ile Leu Ser Ser His Xaa Leu Ile His Asn Cys Xaa Xaa Val Met
      165                    170                    175
Asp Phe Leu Leu Lys Gln Pro Leu Phe Tyr His Leu Met Leu Leu Val
      180                    185                    190
Met Gln Gln Leu Thr Leu Asn Ala Leu Phe Ile Phe Xaa Thr Xaa Xaa
      195                    200                    205
Leu Leu Leu Thr Ser Leu Xaa Asp Leu Lys Ile Ser Leu Cys Thr Val
      210                    215                    220
Val Ser Gln Xaa Ile Thr Thr Ile Ile Leu Lys Asn Lys Ile Lys Val
225      230                    235                    240
Val Ser Met

```

```

<210> 2111
<211> 313
<212> PRT
<213> Homo sapien (7239533-11-790-4930)

```

```

<220>
<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid

```

```

<400> 2111
Met Glu Ser Gln Arg Asn Ile Xaa Lys Phe Ile Leu Met Ser Leu Ser
 1      5      10      15
Ser Ile Gln Asn Ile Gln Ile Phe Val Phe Val Phe Leu Phe Cys Asn
      20      25      30
Val Ala Ile Leu Val Gly Asn Phe Leu Ile Leu Ile Ser Ile Xaa Cys
      35      40      45
Ser Pro Leu Phe Asn Gln Pro Met His Tyr Phe Leu Gly Tyr Met Asn
 50      55      60
Ile Tyr Tyr Thr Ser Cys Val Thr Pro Lys Ile Ile Gly Asp Leu Val
65      70      75      80
Val Gly Arg Ile Asn Ile Ser Tyr Asp Arg Ile Phe Pro Met His Phe
      85      90      95
Phe Gly Ile Ile Glu Ile Phe Ile Leu Thr Val Met Ala Phe Asp His
      100     105     110
Tyr Val Ala Ile Cys Lys Pro Pro Arg Tyr Leu Ile Ile Met Asn Arg
      115     120     125
Thr Lys Tyr Asn Thr Leu Ile Ser Val Ala Trp Leu Leu Gly Leu Ile
      130     135     140
His Ser Leu Phe Gln Phe Ser Met Lys Ile Trp Leu Pro Phe Cys Gly
145     150     155     160
Ser Asn Lys Ile Asp Asp Xaa Tyr Xaa Asp Ile Phe Pro Leu Leu Lys
      165     170     175
Val Ala Cys Thr Asp Thr Cys Ile Thr Gly Val Leu Val Val Ala Asn
      180     185     190
Ser Gly Met Phe Ala Leu Val Thr Phe Val Leu Ser Phe Gly Ser Tyr
      195     200     205
Val Ile Ile Leu Phe Pro Leu Lys Asn His Ser Val Glu Gly Arg Cys

```

210	215	220
Lys Ala Leu Ser Thr Cys Gly Ser His Ile Thr Met Val Ile Phe Phe		
225	230	235
Phe Glu Pro Ser Ile Phe Ala Tyr Leu Arg Pro Ser Thr Phe Pro Glu		240
	245	250
Asp Lys Ile Ser Ala Leu Phe Tyr Thr Ile Ile Ala Pro Met Phe Asn		255
	260	265
His Leu Ile Tyr Asn Leu Arg Asn Thr Glu Met Lys Lys Ala Met Arg		270
	275	280
Lys Val Trp Tyr Gln Ile Ser Phe Ser Glu Glu Lys Gln Leu Ile Cys		285
	290	295
Pro Thr Xaa Cys Thr Lys Glu Leu Tyr		300
305	310	

&lt;210&gt; 2112

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7239533-19-11510-15318)

&lt;400&gt; 2112

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly	
1	5
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu	10
	15
	20
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu	25
	30
	35
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser	40
	45
	50
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys	55
	60
	65
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly	70
	75
	80
	85
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val	90
	95
	100
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn	105
	110
	115
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu	120
	125
	130
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu	135
	140
	145
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His	150
	155
	160
	165
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile	170
	175
	180
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser	185
	190
	195
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr	200
	205
	210
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr	215
	220
	225
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu	230
	235
	240
	245
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys	250
	255
	260
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val	265
	270
	275
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val	280
	285
	290
Met Gly Ser Lys Ile His Ser	295
	300
305	310

<210> 2113  
 <211> 287  
 <212> PRT  
 <213> Homo sapien (7239533-20-19626-20657)

<220>  
 <221> VARIANT  
 <222> (1)...(287)  
 <223> Xaa = Any Amino Acid

<400> 2113  
 Tyr Ile Leu Leu Asp Ile Tyr Ile Cys Leu Asn Asn Thr His Val Xaa  
 1 5 10 15  
 Leu Cys Val Glu Ser Gln Arg Gln Phe Lys Ile Ser Phe Tyr Phe Ser  
 20 25 30  
 Phe Phe Leu Leu Ala Ile Thr Xaa Phe Xaa Xaa Xaa Ile Leu Ile Ile  
 35 40 45  
 Met Lys Thr Xaa Gln Tyr Phe Leu Lys His Lys His Leu Lys Lys Lys  
 50 55 60  
 Phe Ser Xaa Cys Leu Val Tyr Ile Leu Thr Tyr Ile Leu Ser Leu Xaa  
 65 70 75 80  
 Ser Lys Phe Phe Ala Leu Cys Xaa Ile Phe Ala Asp Lys Ala Phe Gln  
 85 90 95  
 Glu Gln Val Ser Gly Asn Xaa Xaa Ser Arg Ser Xaa Glu Ser Pro Val  
 100 105 110  
 His Tyr Thr Leu Thr Met Ser Gln Lys Phe Cys Ser Ile His Pro Ala  
 115 120 125  
 Gly Cys Tyr Asp Gln Gly Ile Xaa Ser Ile Pro Gly His Ser Phe Ser  
 130 135 140  
 His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn  
 145 150 155 160  
 Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala  
 165 170 175  
 Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu  
 180 185 190  
 Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa  
 195 200 205  
 Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His  
 210 215 220  
 Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln  
 225 230 235 240  
 Ala Ile Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met  
 245 250 255  
 Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser  
 260 265 270  
 Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln  
 275 280 285

<210> 2114  
 <211> 256  
 <212> PRT  
 <213> Homo sapien (7239533-8-1261-3491)

<400> 2114  
 Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser  
 1 5 10 15  
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg  
 20 25 30  
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala  
 35 40 45  
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu



50                      55                      60  
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro  
 65                      70                      75                      80  
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu  
                     85                      90                      95  
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly  
                     100                      105                      110  
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser  
                     115                      120                      125  
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile  
                     130                      135                      140  
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr  
 145                      150                      155                      160  
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro  
                     165                      170                      175  
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile  
                     180                      185                      190  
 Phe His Gly Val Ile Leu Leu Leu Tyr Cys Val Pro Asn Ser Lys Ser  
                     195                      200                      205  
 Ser Trp Leu Leu Val Lys Val Ala Thr Val Leu Phe Thr Val Ile Ile  
                     210                      215                      220  
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 225                      230                      235                      240  
 Gly Thr Val Arg Lys Leu Ile Asn Ser Gln Ser Pro Phe His Ser Lys  
                     245                      250                      255

&lt;210&gt; 2115

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7239533-9-1-1650)

&lt;400&gt; 2115

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu  
 1                      5                      10                      15  
 Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val  
                     20                      25                      30  
 Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile  
                     35                      40                      45  
 Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe  
 50                      55                      60  
 Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr  
 65                      70                      75                      80  
 Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr  
                     85                      90                      95  
 Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr  
                     100                      105                      110  
 Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile  
                     115                      120                      125  
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala  
                     130                      135                      140  
 Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val  
 145                      150                      155                      160  
 Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile  
                     165                      170                      175  
 Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser  
                     180                      185                      190  
 Asp Ile Leu Ile Pro His Leu Leu Phe Ser Phe Ala Thr Phe Asn  
                     195                      200                      205  
 Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe  
                     210                      215                      220  
 Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe

225                      230                      235                      240  
 Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr  
                                  245                      250                      255  
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr  
                                  260                      265                      270  
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn  
                                  275                      280                      285  
 Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp  
                                  290                      295                      300  
 Lys Leu Ile His Thr Gln Val Pro Phe His  
 305                      310

&lt;210&gt; 2116

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7239554-20-1-1871)

&lt;400&gt; 2116

Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe  
 1                      5                      10                      15  
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe  
                                  20                      25                      30  
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile  
                                  35                      40                      45  
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn  
                                  50                      55                      60  
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala  
 65                      70                      75                      80  
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys  
                                  85                      90                      95  
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu  
                                  100                      105                      110  
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro  
                                  115                      120                      125  
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala  
                                  130                      135                      140  
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly  
 145                      150                      155                      160  
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe  
                                  165                      170                      175  
 Phe Cys Glu Val Pro Pro Leu Leu Leu Ser Cys Ser Ser Thr Tyr  
                                  180                      185                      190  
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val  
                                  195                      200                      205  
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile  
                                  210                      215                      220  
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys  
 225                      230                      235                      240  
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr  
                                  245                      250                      255  
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu  
                                  260                      265                      270  
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile  
                                  275                      280                      285  
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe  
                                  290                      295                      300  
 Pro Phe Phe Arg  
 305

&lt;210&gt; 2117

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7239554-9-1-1342)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2117

```

Met Gly Glu Ala Arg Asn Arg Thr Val Val Gln Glu Phe Ile Leu Glu
 1           5           10           15
Gly Phe Pro Ala Val Gln His Leu Gly Asn Val Leu Phe Leu Val His
      20           25           30
Leu Leu Ala Tyr Leu Ala Ser Ile Met Ala Asn Met Leu Ile Ile Thr
      35           40           45
Ile Thr Trp Ala Asp His His Leu Gln Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Ser Phe Ser Phe Cys Glu Cys Cys Phe Ile Thr Thr Val Ile Pro
65           70           75           80
Lys Leu Leu Val Ile Leu Leu Ser Gly Arg Ala Lys Ile Pro Leu Ser
      85           90           95
Thr Thr Leu Ser His Ala Val Pro Phe Ser Phe Leu Tyr Ser Trp Val
      100          105          110
Asn Ser Phe Ser Ser Leu Asn Gly Cys Asp Val Pro Leu Asp Xaa Tyr
      115          120          125
Leu Ala Ile Cys Lys Pro Leu His Tyr Ser Thr Ile Met Ser Leu Arg
      130          135          140
Thr Ser Phe His Lys Val Thr Ala Trp Leu Cys Pro Gly
145           150           155

```

&lt;210&gt; 2118

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7239558-10-440-1325)

&lt;400&gt; 2118

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1           5           10           15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
      20           25           30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
      35           40           45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
65           70           75           80
Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
      85           90           95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115          120          125
Pro

```

&lt;210&gt; 2119

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7248974-19-1-3170)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(313)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2119

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Arg Arg Ile Leu Phe Val Asn Phe Phe Phe
          20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Thr Val Ile Ile Val Thr Val
          35           40           45
Cys Val Asp Lys His Leu Gln Ser Pro Met Tyr Phe Phe Leu Gly His
 50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Ala Pro Phe Met
65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
          85           90           95
Cys Ala Ala Gln Leu Leu Tyr Leu Ser Leu Gly Thr Ser Glu Leu Ala
          100          105          110
Leu Met Gly Val Met Ala Val Asp His Tyr Val Ala Val Cys Asn Pro
          115          120          125
Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Cys Val Trp Met Val
          130          135          140
Ile Val Ser Trp Val Phe Gly Phe Leu Phe Gln Ile Trp Pro Val Tyr
145          150          155          160
Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Asn Val Leu Asp His Phe
          165          170          175
Tyr Cys Asp Xaa Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr Leu
          180          185          190
Phe Thr Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile Gly
          195          200          205
Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr Ile
          210          215          220
Leu Lys Ile Pro Leu Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr Cys
225          230          235          240
Ala Ser His Phe Thr Cys Val Val Ile Gly Tyr Ser Ser Cys Leu Phe
          245          250          255
Leu Tyr Thr Lys Pro Lys Gln Thr Gln Ala Ala Lys Tyr Asn Arg Ile
          260          265          270
Ala Ser Leu Leu Val Leu Val Val Thr Pro Phe Leu Asn Pro Phe Ile
          275          280          285
Phe Thr Leu Arg Asn Asp Lys Phe Ile Gln Ala Phe Gly Asp Gly Met
          290          295          300
Lys His Cys Tyr Gln Leu Leu Arg Ile
305          310

```

&lt;210&gt; 2120

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7248974-26-1-596)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(138)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2120

```

Leu Leu Ser Leu Trp Ile Phe Thr Leu Phe Cys Tyr Tyr Val Xaa Tyr
 1           5           10           15
Cys Asp Glu Lys Pro Leu Phe Val Tyr Thr Leu Ile Pro Lys Cys Val
          20           25           30

```

Ser Asp Ile Xaa Gly Met Asn Phe Tyr Lys Cys Asn Cys Trp Val Met  
 35 40 45  
 Gly Met Ser Asn Phe Asn Ser Phe Tyr Gln Val Phe Ile Glu His Arg  
 50 55 60  
 Val Phe Ile Val Xaa Pro Ala Val Gly Gly Cys Phe Phe Ile Val Ser  
 65 70 75 80  
 Asn Ile Val Cys Xaa Xaa Thr Leu Gly Lys Lys Leu Asn Ile Phe Ile  
 85 90 95  
 Lys Ser Asn Ser His Leu Thr Thr Ile Ser Ile Tyr Gln Arg Gly Gly  
 100 105 110  
 Met Val Thr Trp Ile Gly His Ser Asn Ser Ser Ser Tyr Gln Xaa Thr  
 115 120 125  
 Xaa Asp Tyr Ser Leu Leu Tyr Xaa Leu Ile  
 130 135

&lt;210&gt; 2121

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7248974-31-3444-4455)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(161)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2121

Ile Cys Gly Ser His Ser Gly Val Thr Glu Phe Cys Leu Leu Gly Phe  
 1 5 10 15  
 Pro Gly Ser Gln Xaa Val Cys His Leu Leu Pro Ser Ser Phe Val Ser  
 20 25 30  
 Ile Val Ile Arg Asn Tyr Val Ile Ile Ile Val Cys Val Glu Lys Cys  
 35 40 45  
 Leu Leu Phe Leu Leu Tyr Leu Phe Tyr Gly Asp Leu Ser Val Met Glu  
 50 55 60  
 Ile Leu Ile Thr Tyr Thr Ala Val Pro Leu Met Leu Arg Gly Cys Tyr  
 65 70 75 80  
 Phe Pro Xaa Phe Lys Gln Tyr Leu Xaa Xaa His Val Ser Val Gln Leu  
 85 90 95  
 Tyr Met Asn Phe Phe Gly Gly Thr Gln Glu Phe Ala Leu Leu Gly Val  
 100 105 110  
 Met Thr Val Asn His Tyr Val Ala Leu Cys Asn Ser Leu Lys Xaa Asn  
 115 120 125  
 Ile Ile Met Ser Ser Thr His Cys Ile Trp Leu Val Ile Val Leu Leu  
 130 135 140  
 Ile Gly Phe Leu Ser Glu Ile Trp Ser Val Tyr Ala Thr Phe Gln Leu  
 145 150 155 160  
 Pro

&lt;210&gt; 2122

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249005-11-1-1318)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(169)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2122

Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe

```

1           5           10           15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
                20           25           30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
                35           40           45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
                50           55           60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
65           70           75           80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
                85           90           95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
                100          105          110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
                115          120          125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
130          135          140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
145          150          155          160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
                165

```

<210> 2123  
 <211> 110  
 <212> PRT  
 <213> Homo sapien (7249007-9-15200-16107)

<220>  
 <221> VARIANT  
 <222> (1)...(110)  
 <223> Xaa = Any Amino Acid

```

<400> 2123
Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
1           5           10           15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
                20           25           30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
                35           40           45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
50           55           60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65           70           75           80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
                85           90           95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
                100          105          110

```

<210> 2124  
 <211> 241  
 <212> PRT  
 <213> Homo sapien (7249007-9-22951-24848)

<220>  
 <221> VARIANT  
 <222> (1)...(241)  
 <223> Xaa = Any Amino Acid

```

<400> 2124
Leu Arg Gln Leu His Asn Leu Phe Leu Pro Val Gly Phe Phe Leu Ser
1           5           10           15

```

```

Ser Tyr Ser Phe Xaa Val Ile Trp His Asn Leu Asn Ser Val Thr Lys
      20      25      30
Phe Ser Ser Lys Thr Asp Glu Ser Lys Leu Lys Ser Xaa Cys Lys Val
      35      40      45
Lys Ser Leu Phe Phe Thr Tyr Ala Gly Cys Cys Glu Lys Leu Leu Leu
      50      55      60
Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu
      65      70      75      80
His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val
      85      90      95
Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys
      100      105      110
Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu
      115      120      125
Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro
      130      135      140
Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro
      145      150      155      160
His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser
      165      170      175
Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly
      180      185      190
Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val
      195      200      205
Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val
      210      215      220
Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly
      225      230      235      240
Pro

```

&lt;210&gt; 2125

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249162-23-8972-11111)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2125

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
  1      5      10      15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
      20      25      30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
      35      40      45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
      50      55      60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
      65      70      75      80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
      85      90      95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
      100      105      110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
      130      135      140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro

```

145		150		155		160
Asp Val Phe Leu	Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu					
	165		170			175
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala						
	180		185			190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr						
	195		200			205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu						
	210		215			220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu						
	225		230			235
Gly Thr Cys Gly Ser Pro Leu Arg Val Ile Ser Met Phe Tyr Leu Pro						
		245		250		255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Phe						
	260		265			270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met						
	275		280			285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys						
	290		295			300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile						
	305		310			315

&lt;210&gt; 2126

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249220-22-20773-24242)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(322)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2126

Met Ser Val Val Glu Ala Asn Asn Ile Ser Gly Pro Val Ser Glu Phe														
1		5		10										15
Ile Leu Leu Gly Phe Pro Cys Arg Cys Arg Glu Thr Lys Ile Leu Leu														
	20			25										30
Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Met Gly Asn Thr														
	35			40										45
Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met														
	50			55										60
Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Ile Ser														
	65			70										80
Ser Asp Val Pro Asn Met Leu Ala Asn Leu Ile Ser His Ile Lys Ser														
		85		90										95
Ile Ser Tyr Ala Gly Cys Leu Leu Gln Phe Phe Tyr Phe Ser Met Cys														
	100			105										110
Ala Ala Glu Gly Tyr Phe Leu Ser Val Met Ser Phe Asp Arg Phe Leu														
	115			120										125
Thr Ile Cys Arg Pro Leu His Tyr Pro Thr Val Met Thr His His Leu														
	130			135										140
Cys Val Xaa Leu Val Ala Phe Cys Arg Ala Gly Gly Phe Leu Ser Ile														
	145			150										160
Leu Met Pro Ala Val Leu Met Ser Arg Val Pro Phe Cys Gly Pro Asn														
		165		170										175
Ile Thr Asp His Phe Phe Cys Asn Leu Gly Pro Leu Leu Ala Leu Ser														
	180			185										190
Cys Ala Pro Val Pro Lys Thr Thr Leu Thr Cys Ala Thr Val Ser Ser														
	195			200										205
Leu Ile Ile Phe Ile Thr Phe Leu Tyr Ile Leu Gly Ser His Ile Leu														
	210			215										220



Val Leu Arg Ala Val Leu Trp Val Pro Ala Gly Ser Gly Arg Asn Lys  
 225 230 235 240  
 Ala Phe Ser Thr Cys Ala Ser His Phe Leu Val Val Ser Phe Phe Tyr  
 245 250 255  
 Gly Ser Val Met Val Met Tyr Val Ser Pro Gly Ser Arg Ser Arg Pro  
 260 265 270  
 Gly Thr Gln Lys Phe Val Thr Leu Phe Tyr Cys Thr Ala Thr Pro Phe  
 275 280 285  
 Phe Asn Pro Leu Thr Tyr Ser Leu Trp Asn Lys Asp Met Thr Asp Ala  
 290 295 300  
 Leu Lys Lys Val Leu Gly Val Pro Ser Lys Glu Ile Ser Trp Asn Thr  
 305 310 315 320  
 Leu Lys

&lt;210&gt; 2127

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249282-10-14985-16332)

&lt;400&gt; 2127

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly  
 1 5 10 15  
 Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu  
 20 25 30  
 Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile  
 35 40 45  
 Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
 50 55 60  
 His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys  
 65 70 75 80  
 Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys  
 85 90 95  
 Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe  
 100 105 110  
 Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro  
 115 120 125  
 Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val  
 130 135 140  
 Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val  
 145 150 155 160  
 Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe  
 165 170 175  
 Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr  
 180 185 190  
 Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val  
 195 200 205  
 Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile  
 210 215 220  
 Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe  
 245 250 255  
 Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val  
 260 265 270  
 Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met  
 290 295 300  
 Gln Arg Arg Gln Asp Ser Arg  
 305 310

<210> 2128  
 <211> 306  
 <212> PRT  
 <213> Homo sapien (7249282-10-21300-24858)

<220>  
 <221> VARIANT  
 <222> (1)...(306)  
 <223> Xaa = Any Amino Acid

<400> 2128  
 Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly  
 1 5 10 15  
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu  
 20 25 30  
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu  
 35 40 45  
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys  
 65 70 75 80  
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly  
 85 90 95  
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn  
 115 120 125  
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val  
 130 135 140  
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val  
 145 150 155 160  
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp  
 165 170 175  
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu  
 180 185 190  
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu  
 195 200 205  
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn  
 210 215 220  
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His  
 225 230 235 240  
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu  
 245 250 255  
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val  
 260 265 270  
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu  
 275 280 285  
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys  
 290 295 300  
 Leu Phe  
 305

<210> 2129  
 <211> 327  
 <212> PRT  
 <213> Homo sapien (7249282-10-488-2060)

<220>  
 <221> VARIANT  
 <222> (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2129

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile  
 1 5 10 15  
 Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe  
 20 25 30  
 Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val  
 35 40 45  
 Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu  
 50 55 60  
 Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro  
 65 70 75 80  
 Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu  
 85 90 95  
 Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu  
 100 105 110  
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr  
 115 120 125  
 Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro  
 130 135 140  
 Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His  
 145 150 155 160  
 Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg  
 165 170 175  
 His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp  
 180 185 190  
 Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu  
 195 200 205  
 Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu  
 210 215 220  
 Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile  
 245 250 255  
 Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp  
 260 265 270  
 Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg  
 290 295 300  
 Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa  
 305 310 315 320  
 Val Lys Leu Gln Ile Ile Leu  
 325

&lt;210&gt; 2130

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249282-11-14537-16718)

&lt;400&gt; 2130

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr  
 1 5 10 15  
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro  
 20 25 30  
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn  
 35 40 45  
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser

```

65          70          75          80
Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn
85          90          95
Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile
100         105         110
Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg
115         120         125
Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Val Ile Ile Met Ala Glu
130         135         140
Lys Val Leu Trp Val Leu Val Ile Val Pro Tyr Leu Tyr Ser Thr Phe
145         150         155         160
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe Lys Leu Ser Phe Cys Gly
165         170         175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp Cys Ile Pro Leu Met Ser
180         185         190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu Leu Ile Ile Leu Ile Phe
195         200         205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser Ile Val Leu Ile Ser Tyr
210         215         220
Met Phe Ile Leu Val Ala Ile Leu Arg Met Asn Ser Arg Lys Gly Arg
225         230         235         240
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met
245         250         255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His
260         265         270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile
275         280         285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
290         295         300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile
305         310         315

```

&lt;210&gt; 2131

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249282-11-25530-27263)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2131

```

Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu
1          5          10          15
Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu
20         25         30
Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Ile Leu
35         40         45
Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg
50         55         60
Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys
65         70         75         80
Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala
85         90         95
Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu
100        105        110
Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser
115        120        125
Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val
130        135        140

```

Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile  
 145 150 155 160  
 Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe  
 165 170 175  
 Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa  
 180 185 190  
 Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe  
 195 200 205  
 Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val  
 210 215 220  
 Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr  
 225 230 235 240  
 Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe  
 245 250 255  
 Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys  
 260 265 270  
 Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu  
 275 280 285  
 Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser  
 290 295 300  
 Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val  
 305 310 315

&lt;210&gt; 2132

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7249282-5-5312-7865)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2132

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr  
 1 5 10 15  
 Glu Phe Ile Leu Val Gly Val Ser Asp Pro Glu Leu Gln Ile Pro  
 20 25 30  
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn  
 35 40 45  
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser  
 65 70 75 80  
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys  
 85 90 95  
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val  
 100 105 110  
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg  
 115 120 125  
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro  
 130 135 140  
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile  
 145 150 155 160  
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser  
 165 170 175  
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala  
 180 185 190  
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe  
 195 200 205  
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr

210	215	220
Phe Asn Ile Val Ile Thr	Ile Leu Arg Ile Arg	Ser Ser Glu Gly Arg
225	230	235
Gln Lys Ala Phe Ser Thr	Cys Ala Ser His Met	Ile Ala Val Val Val
245	250	255
Phe Tyr Gly Thr Leu Leu	Phe Met Tyr Leu Gln Pro	Arg Ser Asn His
260	265	270
Ser Leu Asp Thr Asp Lys	Met Ala Ser Val Phe Tyr	Thr Leu Val Ile
275	280	285
Pro Val Leu Asn Pro Leu	Ile Tyr Ser Leu Arg	Asn Lys Asn Val Lys
290	295	300
Asp Ala Leu Lys Arg Phe	Leu Asp Asn Pro Cys	Arg Ser Leu
305	310	315

&lt;210&gt; 2133

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7264174-61-26274-29247)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(279)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2133

Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
1 5 10 15
Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys
20 25 30
Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser
35 40 45
Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met
50 55 60
Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu
65 70 75 80
Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp
85 90 95
Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile
100 105 110
Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe
115 120 125
Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val
130 135 140
Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala
145 150 155 160
His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa
165 170 175
Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys
180 185 190
Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu
195 200 205
Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu
210 215 220
Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr
225 230 235 240
Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe
245 250 255
Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu
260 265 270
Ser Ile Ile Leu Thr Leu Val
275

<210> 2134  
 <211> 314  
 <212> PRT  
 <213> Homo sapien (7283250-10-5473-8590)

<400> 2134  
 Met Glu Arg Gly Asn Trp Thr Leu Val Thr Glu Phe Ile Leu Val Gly  
 1 5 10 15  
 Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Val Ile Phe Tyr  
 20 25 30  
 Pro Ala Tyr Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu  
 35 40 45  
 Ile Leu Val Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys  
 65 70 75 80  
 Met Leu Glu Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu  
 85 90 95  
 Cys Ser Ala Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe  
 100 105 110  
 Ile Pro Phe Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu Gln Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu  
 130 135 140  
 Val Ile Leu Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr  
 145 150 155 160  
 Ile Leu Lys Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His  
 165 170 175  
 Phe Phe Cys Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile  
 180 185 190  
 Arg Ala Ile Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu  
 195 200 205  
 Ser Ser Leu Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr  
 225 230 235 240  
 Cys Ala Ser His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile  
 245 250 255  
 Phe Val Tyr Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys  
 260 265 270  
 Ile Leu Phe Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe  
 275 280 285  
 Val Phe Ser Leu Trp Asn Glu Pro Met Lys Asp Ala Leu Lys Asp Ala  
 290 295 300  
 Val Gly Arg Arg Thr Glu Leu Ala Gln Arg  
 305 310

<210> 2135  
 <211> 309  
 <212> PRT  
 <213> Homo sapien (7283250-11-11521-16137)

<400> 2135  
 Met Ala Asn Leu Thr Ile Val Thr Glu Phe Ile Leu Met Gly Phe Ser  
 1 5 10 15  
 Thr Asn Lys Asn Met Cys Ile Leu His Ser Ile Leu Phe Leu Leu Ile  
 20 25 30  
 Tyr Leu Cys Ala Leu Met Gly Asn Val Leu Ile Ile Met Ile Thr Thr  
 35 40 45  
 Leu Asp His His Leu His Thr Pro Val Tyr Phe Phe Leu Lys Asn Leu

50 55 60  
 Ser Phe Leu Asp Leu Cys Leu Ile Ser Val Thr Ala Pro Lys Ser Ile  
 65 70 75 80  
 Ala Asn Ser Leu Ile His Asn Asn Ser Ile Ser Phe Leu Gly Cys Val  
 85 90 95  
 Ser Gln Val Phe Leu Leu Leu Ser Ser Ala Ser Ala Glu Leu Leu Leu  
 100 105 110  
 Leu Thr Val Met Ser Phe Asp Arg Tyr Thr Ala Ile Cys His Pro Leu  
 115 120 125  
 His Tyr Asp Val Ile Met Asp Arg Ser Thr Cys Val Gln Arg Ala Thr  
 130 135 140  
 Val Ser Trp Leu Tyr Gly Gly Leu Ile Ala Val Met His Thr Ala Gly  
 145 150 155 160  
 Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Met Val His Gln Phe Phe  
 165 170 175  
 Cys Asp Ile Pro Gln Leu Leu Ala Ile Ser Cys Ser Glu Asn Leu Ile  
 180 185 190  
 Arg Glu Ile Ala Leu Ile Leu Ile Asn Val Val Leu Asp Phe Cys Cys  
 195 200 205  
 Phe Ile Val Ile Ile Ile Thr Tyr Val His Val Phe Ser Thr Val Lys  
 210 215 220  
 Lys Ile Pro Ser Thr Glu Gly Gln Ser Lys Ala Tyr Ser Ile Cys Leu  
 225 230 235 240  
 Pro His Leu Leu Val Val Leu Phe Leu Ser Thr Gly Phe Ile Ala Tyr  
 245 250 255  
 Leu Lys Pro Ala Ser Glu Ser Pro Ser Ile Leu Asp Ala Val Ile Ser  
 260 265 270  
 Val Phe Tyr Thr Met Leu Pro Pro Thr Phe Asn Pro Ile Ile Tyr Ser  
 275 280 285  
 Leu Arg Asn Lys Ala Ile Lys Val Ala Leu Gly Met Leu Ile Lys Gly  
 290 295 300  
 Lys Leu Thr Lys Lys  
 305

&lt;210&gt; 2136

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7283250-5-1-3004)

&lt;400&gt; 2136

Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu  
 20 25 30  
 Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr  
 35 40 45  
 Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln  
 65 70 75 80  
 Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser  
 100 105 110  
 Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu  
 130 135 140  
 Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr  
 145 150 155 160  
 Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His



```

          165          170          175
Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Val
          180          185          190
Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Gly Leu Leu Ala Leu
          195          200          205
Thr Pro Leu Val Cys Il Leu Val Ser Tyr Gly Leu Ile Phe Ser Thr
          210          215          220
Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala Val Ser Thr
          225          230          235
Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly Thr Ala Ile
          245          250          255
Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu Ser Asp Thr
          260          265          270
Leu Ser Thr Ile Met Tyr Ser Met Val Ala Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Arg Gly Leu Gln Lys Met
          290          295          300
Leu Leu Lys Cys Thr Val Phe Gln Gln
          305          310

```

&lt;210&gt; 2137

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7283250-6-1-1725)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(310)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2137

```

Met Val Asn Phe Thr His Val Ser Glu Phe Val Leu Leu Gly Phe Gln
  1          5          10          15
Gly Gly Pro Gly Met Gln Ala Met Leu Phe Leu Ile Phe Leu Ile Leu
          20          25          30
Tyr Gly Ile Ala Val Val Gly Asn Leu Gly Met Ile Val Ile Ile Trp
          35          40          45
Val Asp Ala His Leu His Thr Pro Met Tyr Ala Phe Leu Gln Ser Leu
          50          55          60
Ser Leu Leu Asp Ile Cys Tyr Ser Ser Thr Ile Ala Pro Arg Ala Leu
          65          70          75          80
Ala Asn Ser Met Gln Glu Asp His Thr Ile Ser Phe Gly Gly Cys Ala
          85          90          95
Ala Gln Phe Phe Phe Leu Ser Leu Phe Gly Ile Thr Glu Ala Phe Leu
          100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu
          115          120          125
Leu Tyr Ser Val Ser Met Ser His Gln Val Cys Val Leu Leu Ile Ser
          130          135          140
Gly Ser Tyr Leu Trp Gly Val Val Asn Ala Ile Ala Gln Thr Thr Met
          145          150          155          160
Thr Phe Arg Leu Pro Phe Cys Gly Ser Asn Glu Ile Asn Asp Phe Phe
          165          170          175
Cys Asp Val Pro Pro Leu Leu Ser Leu Ser Cys Ser Asp Thr Phe Ile
          180          185          190
Asn Gln Leu Val Leu Leu Gly Leu Cys Gly Ser Ile Ile Val Ser Thr
          195          200          205
Phe Leu Ile Val Leu Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
          210          215          220
Arg Ile Pro Thr Met Gln Gly Arg Xaa Lys Ala Phe Ser Thr Cys Ala
          225          230          235          240

```

S r His Leu Thr Gly Val Cys Leu Phe Phe Gly Thr Val Phe Phe Met  
 245 250 255  
 Tyr Ala Gln Pro Ser Ala Ile Phe Phe Met Glu Gln Ser Lys Ile Val  
 260 265 270  
 Ser Ile Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Glu Val Lys Gln Ala Leu Arg Arg Ser Met Gln  
 290 295 300  
 Lys Leu Ser Leu Xaa Ser  
 305 310

&lt;210&gt; 2138

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7321521-20-4435-9278)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2138

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe  
 1 5 10 15  
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln  
 20 25 30  
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met  
 35 40 45  
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His  
 50 55 60  
 Thr Pro Met Tyr Thr Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp  
 65 70 75 80  
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys  
 85 90 95  
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu  
 100 105 110  
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln  
 130 135 140  
 Val Cys Thr Gly Leu Ile Ile Phe Ala Trp Ser Cys Val Phe Val Ile  
 145 150 155 160  
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro  
 165 170 175  
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu  
 180 185 190  
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe  
 195 200 205  
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr  
 210 215 220  
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys  
 225 230 235 240  
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu  
 245 250 255  
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His  
 260 265 270  
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr  
 275 280 285  
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys  
 290 295 300  
 Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile

305

310

315

320

&lt;210&gt; 2139

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7321521-21-4479-8486)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2139

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Val Phe Val Leu Val Leu
      20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Lys
      65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
      115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
      145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
      210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
      225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
      245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
      260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
      275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
      290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Ile Lys Ile Asp Cys
      305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
      325          330

```

&lt;210&gt; 2140

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7321521-22-8611-12801)

&lt;400&gt; 2140

```

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1          5          10          15
Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
          20          25          30
Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
          35          40          45
Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
65          70          75          80
Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
          85          90          95
Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
          100          105          110
Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
          130          135          140
Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
145          150          155          160
Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
          165          170          175
Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
          180          185          190
Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
          195          200          205
Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
          210          215          220
Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
225          230          235          240
Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
          245          250          255
Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
          260          265          270
Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
          275          280          285
Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
          290          295          300
Thr Lys Tyr Ile Leu Cys Lys Glu Lys
305          310

```

&lt;210&gt; 2141

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7321637-16-2663-3767)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(134)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2141

```

His Met Val Asp Ile Leu Asn Arg Gln Thr Leu Leu Tyr Leu Val Leu
 1          5          10          15
Gly Leu Trp Leu Glu His Val Leu Pro Ser Ser Phe Gly Thr Val Met
          20          25          30
Val Pro Leu Cys Gly Pro Arg Met Thr Ala Arg Leu Leu Phe Leu Pro
          35          40          45
Val Pro Leu Ser Ala Glu Asn Glu Leu Arg Arg Ala Leu Leu Ser Thr
          50          55          60

```

Glu Ala His Thr Ile Ser Leu Val Gly Gln Arg Leu Ala Ile Pro Cys  
 65 70 75 80  
 Asn Asn Ile Ser Xaa Phe Ile Tyr Leu Ile Lys Asn Arg Asn Leu Gly  
 85 90 95  
 Gln Gln Pro Ala Tyr Ser Thr Cys Trp Asp His Xaa Leu Leu Val Ser  
 100 105 110  
 Leu Phe Tyr Phe Lys Thr Phe His Ile Xaa Thr His Gly Ser Thr Ser  
 115 120 125  
 Phe Thr Phe Ile Lys Leu  
 130

&lt;210&gt; 2142

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7327747-39-1-1406)

&lt;400&gt; 2142

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu  
 1 5 10 15  
 Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val  
 20 25 30  
 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe  
 35 40 45  
 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro  
 65 70 75 80  
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val  
 85 90 95  
 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu  
 100 105 110  
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser  
 115 120 125  
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln  
 130 135 140  
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln  
 145 150 155 160  
 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn  
 165 170 175  
 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp  
 180 185 190  
 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu  
 195 200 205  
 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly  
 210 215 220  
 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala  
 245 250 255  
 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp  
 260 265 270  
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys  
 290 295 300  
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His  
 305 310 315

&lt;210&gt; 2143

&lt;211&gt; 308

&lt;212&gt; PRT

<213> Homo sapien (7328761-32-2018-4643)

<220>

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 2143

```

Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
 1           5           10           15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
          20           25           30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
 35           40           45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
 50           55           60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
 65           70           75           80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
          85           90           95
Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
          100          105          110
Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
          115          120          125
Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
          130          135          140
Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
          145          150          155          160
Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
          165          170          175
Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
          180          185          190
Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
          195          200          205
Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
          210          215          220
Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
          225          230          235          240
Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
          245          250          255
Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
          260          265          270
Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
          275          280          285
Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
          290          295          300
Trp Lys Asp Ser
305

```

<210> 2144

<211> 101

<212> PRT

<213> Homo sapien (7341899-1-693-1026)

<220>

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 2144

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val

```

```

1           5           10           15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
      20           25           30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr
      35           40           45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
      50           55           60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
      65           70           75           80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
      85           90           95
Cys Cys Leu Ala Glu
      100

```

&lt;210&gt; 2145

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7341899-24-747-1936)

&lt;400&gt; 2145

```

Met Glu Arg Ala Asn Asp Ser Thr Phe Ser Gly Phe Ile Leu Leu Gly
1           5           10           15
Phe Ser Asn Arg Pro Gln Leu Glu Thr Ala Leu Phe Val Val Ile Leu
      20           25           30
Ile Ile Tyr Phe Leu Ser Phe Leu Gly Asn Gly Thr Ile Ile Leu Leu
      35           40           45
Ser Ile Val Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Met Asp Leu Cys Leu Thr Thr Cys Thr Val Pro Gln
      65           70           75           80
Thr Leu Val Asn Phe Lys Gly Lys Asp Lys Thr Ile Thr Tyr Gly Gly
      85           90           95
Cys Val Thr Gln Leu Phe Ile Ala Leu Gly Leu Gly Gly Ser Glu Cys
      100           105           110
Val Leu Leu Ser Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg
      115           120           125
Ser Leu His Tyr Met Val Ser Met His Pro Gln Leu Cys Leu Gln Leu
      130           135           140
Val Val Thr Thr Trp Leu Thr Gly Phe Gly Asn Ser Val Ile Gln Thr
      145           150           155           160
Ala Leu Thr Met Thr Leu Pro Leu Cys Asp Lys Asn Gln Val Asp His
      165           170           175
Phe Phe Cys Glu Val Pro Val Met Leu Lys Leu Ser Cys Thr Asn Thr
      180           185           190
Ser Ile Asn Glu Ala Glu Ile Phe Ala Val Ser Val Phe Phe Leu Val
      195           200           205
Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Gly His Ile Thr His Ala
      210           215           220
Val Leu Lys Ile Lys Ser Ala Gln Gly Arg Gln Lys Ala Phe Gly Thr
      225           230           235           240
Cys Gly Ser His Leu Leu Val Val Ile Ile Phe Phe Gly Thr Leu Ile
      245           250           255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Tyr Ser Gln Asp Val Asn Lys
      260           265           270
Ser Ile Ala Leu Phe Tyr Thr Leu Val Thr Pro Leu Leu Asn Pro Leu
      275           280           285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Thr Lys Lys Thr
      290           295           300
Ser Gly Glu Asp Ile Ala Cys Met Arg Lys Leu Thr Gln Gly Leu Gln
      305           310           315           320
Phe Gln Thr Phe Val His

```

325

<210> 2146  
 <211> 155  
 <212> PRT  
 <213> Homo sapien (7341899-6-1-567)

<220>  
 <221> VARIANT  
 <222> (1)...(155)  
 <223> Xaa = Any Amino Acid

<400> 2146  
 Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His Val Leu Leu Ala  
 1 5 10 15  
 Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu Glu Met Ser Val  
 20 25 30  
 Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu Ile Ser Asn Phe  
 35 40 45  
 Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met Asn Thr Ser Asn  
 50 55 60  
 Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His His His Arg  
 65 70 75 80  
 Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile Ile Val Xaa Met  
 85 90 95  
 Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln Glu Arg Phe Phe  
 100 105 110  
 Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys Leu Leu Val Tyr  
 115 120 125  
 Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg Arg Ile Leu Arg  
 130 135 140  
 Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn  
 145 150 155

<210> 2147  
 <211> 318  
 <212> PRT  
 <213> Homo sapien (7341900-14-7037-9080)

<220>  
 <221> VARIANT  
 <222> (1)...(318)  
 <223> Xaa = Any Amino Acid

<400> 2147  
 Met Ala Glu Ser Gly Thr Thr Val Thr Glu Phe Phe Leu Arg Gly Phe  
 1 5 10 15  
 Arg Leu Lys Ala Glu Leu Gln Ile Gly Leu Phe Phe Val Phe Leu Val  
 20 25 30  
 Ile Phe Leu Ile Thr Met Gly Gly Asn Leu Gly Met Ile Val Leu Met  
 35 40 45  
 Leu Ile Gln Thr Asp Pro Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser His Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Ile Gly Pro  
 65 70 75 80  
 Gln Leu Leu Glu Thr Leu Ala Thr Asp Lys Met Ile Ile Thr Tyr Glu  
 85 90 95  
 Arg Cys Ala Ser Gln Phe Phe Phe Phe Thr Leu Cys Ala Ser Ile Glu  
 100 105 110  
 Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys  
 115 120 125



Asn Pro Leu Leu Tyr Ala Ile Val Met Thr Pro Lys Thr Arg Leu Ala  
 130 135 140  
 Leu Leu Ala Gly Ala Tyr Ser Gly Ala Ile Val Asn Ser Val Ile Cys  
 145 150 155 160  
 Thr Gly Cys Thr Phe Ser Ile Ser Phe Ser Lys Ser Asn His Val Asp  
 165 170 175  
 Phe Phe Phe Cys Asp Leu Pro Pro Leu Lys Leu Ala Cys Ser Glu  
 180 185 190  
 Thr Arg Pro Arg Glu Trp Val Ile Tyr Leu Ser Ala Phe Leu Val Ile  
 195 200 205  
 Thr Thr Ser Ile Ser Val Ile Leu Thr Ser Tyr Leu Phe Ile Ile Gln  
 210 215 220  
 Ser Val Leu Lys Ile Arg Thr Ala Gly Gly Arg Ala Lys Thr Phe Ser  
 225 230 235 240  
 Thr Cys Ala Ser His Met Thr Ala Leu Thr Leu Phe Phe Gly Thr Leu  
 245 250 255  
 Ile Phe Ile Tyr Leu Lys Gly Asn Met Gly Glu Ser Leu Glu Glu Asp  
 260 265 270  
 Lys Ile Val Ser Ile Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Met Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys  
 290 295 300  
 Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu  
 305 310 315

&lt;210&gt; 2148

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7341900-15-17952-19084)

&lt;400&gt; 2148

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met  
 1 5 10 15  
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu  
 20 25 30  
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile  
 35 40 45  
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val  
 65 70 75 80  
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile  
 85 90 95  
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly  
 100 105 110  
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr  
 130 135 140  
 Cys Ile Arg Leu Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro  
 145 150 155 160  
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn  
 165 170 175  
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser  
 180 185 190  
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu  
 195 200 205  
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn  
 210 215 220  
 Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys  
 225 230 235 240

Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile  
 260 265 270  
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met  
 275 280 285  
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala  
 290 295 300  
 Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln  
 305 310 315

&lt;210&gt; 2149

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7341900-16-17098-20843)

&lt;400&gt; 2149

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly  
 1 5 10 15  
 Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu  
 20 25 30  
 Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu  
 35 40 45  
 Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln  
 65 70 75 80  
 Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His  
 85 90 95  
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu  
 130 135 140  
 Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr  
 145 150 155 160  
 Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe  
 165 170 175  
 Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu  
 195 200 205  
 Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr  
 210 215 220  
 Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile  
 245 250 255  
 Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys  
 260 265 270  
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val  
 290 295 300  
 Ala Arg Arg Leu Gln Val Ser Leu Ser Met  
 305 310

&lt;210&gt; 2150

&lt;211&gt; 311

&lt;212&gt; PRT

<213> Homo sapien (7341900-6-1691-2778)

<220>

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 2150

```

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1           5           10           15
Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
      20           25           30
Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
      35           40           45
Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
      50           55           60
Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
      65           70           75           80
Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
      85           90           95
Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
      100          105          110
Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
      115          120          125
Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
      130          135          140
Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
      145          150          155          160
Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
      165          170          175
Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
      180          185          190
Thr Ser Gly Asn Ser Lys Ile Ile Val Ile Leu Thr Ala Phe Met
      195          200          205
Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
      210          215          220
Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
      225          230          235          240
Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
      245          250          255
Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
      260          265          270
Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
      275          280          285
Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
      290          295          300
Ile Gly Asn Phe Trp Val Phe
      305          310

```

<210> 2151

<211> 306

<212> PRT

<213> Homo sapien (7406632-1-90980-93013)

<400> 2151

```

Met Glu Gly Lys Asn Gln Thr Asn Ile Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Phe Ser Ser Trp Gln Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu
      20           25           30
Cys Leu Tyr Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala
      35           40           45

```

Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Leu Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly  
 85 90 95  
 Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn  
 100 105 110  
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu  
 130 135 140  
 Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr  
 145 150 155 160  
 Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His  
 165 170 175  
 Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr  
 180 185 190  
 Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val  
 195 200 205  
 Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala  
 210 215 220  
 Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr  
 245 250 255  
 Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser  
 260 265 270  
 Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr  
 290 295 300  
 Leu Ser  
 305

&lt;210&gt; 2152

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7407927-19-1-4216)

&lt;400&gt; 2152

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser  
 20 25 30  
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr  
 35 40 45  
 Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser  
 50 55 60  
 Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met  
 65 70 75 80  
 Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys  
 85 90 95  
 Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val  
 100 105 110  
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro  
 115 120 125  
 Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val  
 130 135 140  
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu  
 145 150 155 160

<400> 2154  
Met Ile Ser Phe Leu Val Pro Gly Leu Met Glu Glu Glu Asn Gln Arg

```

1           5           10           15
Gly Val Val His Phe His Phe His Phe Phe Ser Thr Asp Leu Val Val
20           25           30
Ala Ser Phe Ile Ile Val Ala Leu Met Leu His Leu Arg Ser Leu Val
35           40           45
Gly His Phe Thr Phe Gly Pro Thr Val Trp Gln Asp Pro Phe Leu His
50           55           60
Ile Pro Met Tyr Leu Phe Leu Phe Ser Leu Ala Leu Thr Met Leu Glu
65           70           75           80
Ile Gly Tyr Ser Thr Asn Ile Ser Pro Pro Thr Leu Ala Thr Val Leu
85           90           95
Tyr Met Gly Lys Met Leu Ile Ser Leu Pro Gly Tyr Gly Thr Gln Met
100          105          110
Leu Phe Val Ile Leu Leu Arg Gly Ser Glu Cys Val Leu Leu Ala Val
115          120          125
Met Ala Tyr Asp Arg Tyr Ile Thr Ile Cys His Pro Phe Asn Tyr Asn
130          135          140
Leu Ile Met Ser Gly Xaa Leu Cys Gly Gln Met Thr Leu Gly Ser Leu
145          150          155          160
Arg Leu Gly Phe Leu Leu Ser Leu Phe Leu Thr Met Leu Ile Xaa His
165          170          175
Pro Pro Phe Cys Gly Leu Asp Glu Thr Tyr His Phe Phe Cys Asp Met
180          185          190
Pro Thr Ala Ser Arg Leu Val Cys Ala Asp Thr Thr Val His Glu Ser
195          200          205
Ala Leu Xaa Leu Pro Cys Gly His His His His Pro Leu Pro Ser Ser
210          215          220
Leu Ile Cys Leu Pro Tyr Gly Cys Leu Ala Ala Thr Ile Leu Arg Met
225          230          235          240
His Ser Ala Lys Arg Lys His Xaa Ala Phe Ser Thr Ser Ser Ser His
245          250          255
Leu Ile Val Val Leu Leu Lys Tyr Trp Cys Cys Ile Leu Ile Cys Leu
260          265          270
Cys Pro Ser Ser Ser Tyr Ser Pro Glu Glu Gly Trp Glu Val Ser Leu
275          280          285
Val His Met Phe Ile Leu Pro Val Trp Asn Pro Leu Ile Tyr Ser Val
290          295          300
Trp Asn Gln Asp Val Thr Asp Ala Val Glu Arg Leu Val Ala Arg Met
305          310          315          320
Ser Leu Xaa Leu Thr Ala Arg Asn Ile Pro Ser Xaa Lys Ile Phe Pro
325          330          335
Xaa Leu

```

&lt;210&gt; 2155

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7467565-10-15924-18962)

&lt;400&gt; 2155

```

Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu
1           5           10           15
Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu
20           25           30
Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu
35           40           45
Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met
50           55           60
Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser
65           70           75           80
Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met

```

```

      85              90              95
Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly
      100              105              110
Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
      115              120              125
Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser
      130              135              140
Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His
145      150      155      160
Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser
      165              170              175
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile
      180              185              190
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser
      195              200              205
Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr
      210              215              220
Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg
225      230      235      240
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
      245              250              255
Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala
      260              265              270
Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro
      275              280              285
Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp
      290              295              300
Ser Phe Thr Lys Met Val Lys Arg Asn Val
305              310

```

&lt;210&gt; 2156

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7533967-9-17699-19044)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2156

```

Gly Val Gly Leu Xaa Lys Leu Xaa Trp Gln Ile Ile Phe Ser Gly Asp
1      5      10      15
Ser Phe Ser Thr Trp Glu Met Phe Ser Leu Ser Ile Leu Gln Leu Pro
      20      25      30
Xaa Met Tyr Thr Val Ala Leu Ser Gly Thr Ser Ile Leu Ile Phe Leu
      35      40      45
Ile Xaa Thr Asp Phe Xaa Val His Thr Ser Leu Tyr Ser Phe Xaa Val
      50      55      60
Leu Ile Asp Ile Ala Ile Ser Val Val Lys Ile Gly Ile Glu Val Phe
65      70      75      80
Ser Gly Lys Ile Asn Phe Ser His Thr Gly Cys Gly Thr Gln Ile Phe
      85      90      95
Phe Phe Leu Thr Ala Gly Ile Phe Lys Tyr Val Leu Leu Thr Tyr Met
      100      105      110
Ala Tyr Asp His Asn Val Ala Ile Cys Asp Leu Arg Xaa Pro Thr Phe
      115      120      125
Met Ser Asp Gln Val Phe Xaa Gln Trp Ala Val Glu Ser Trp Ile Gly
      130      135      140
Gly Lys Leu Ser Ser Leu Ala His Thr Ile Tyr Ile Phe His Leu Phe
145      150      155      160

```

Ser Tyr Lys Ala Lys Glu Ile Ser His Leu Trp Pro Lys Leu Phe Xaa  
 165 170 175  
 Ser Ser Ser Val Gly Ile Pro Tyr Ile Gln Asn Asp Val Phe Phe Thr  
 180 185 190  
 Ile Ile Thr Phe Leu Phe Thr Leu Leu Pro Leu Thr Leu Thr Leu Ser  
 195 200 205  
 Ser Lys Leu Ile Val Phe Thr Ile Leu His Met Asn Ser Ser Asn Gly  
 210 215 220  
 Gly Ala Lys Ser Trp His Thr Tyr Cys Phe His Leu Ser Val Leu Ile  
 225 230 235 240  
 Pro Cys Cys Gly Gln Ala Ile Phe Val Tyr Met Thr Ser Ser Ser Phe  
 245 250 255  
 Xaa Thr Val Asn Lys Tyr Gln Thr Met Ser Val Leu Thr Ala Xaa Leu  
 260 265 270  
 Tyr Pro Leu Leu Lys Pro Leu Ile Asp Ile Leu Lys Asn Ala Glu Val  
 275 280 285  
 Ala Gly Ala Trp Ser Lys Phe Leu Xaa Lys Lys Ala Leu Lys Ser Gln  
 290 295 300  
 His Leu Ile Thr Arg Ser Cys Glu Asn Lys Xaa Thr Thr Glu Gln Ser  
 305 310 315 320

&lt;210&gt; 2157

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7534025-1-1-1622)

&lt;400&gt; 2157

Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu Arg Tyr Ser  
 1 5 10 15  
 Val Leu Met Gly His Gly Val Cys Met Gly Leu Met Ala Ala Ala Cys  
 20 25 30  
 Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr Ser Leu Val Phe His  
 35 40 45  
 Leu Pro Phe His Ser Ser Asn Gln Leu His His Phe Phe Cys Asp Ile  
 50 55 60  
 Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser Gly Phe Ser Gln Leu  
 65 70 75 80  
 Val Ile Phe Met Leu Gly Val Phe Ala Leu Val Ile Pro Leu Leu Leu  
 85 90 95  
 Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala Ile Leu Lys Ile Pro  
 100 105 110  
 Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr Cys Ala Ser His Leu  
 115 120 125  
 Ile Val Val Thr Val His Tyr Ser Cys Ala Ser Phe Ile Tyr Leu Arg  
 130 135 140  
 Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr Leu Ile Ser Val Ser  
 145 150 155 160  
 Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met Ile Tyr Ser Leu Arg  
 165 170 175  
 Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr Ile Gly Gln Thr Phe  
 180 185 190  
 Tyr Pro Leu Ser  
 195

&lt;210&gt; 2158

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7534025-11-6732-9742)

&lt;220&gt;

&lt;221&gt; VARIANT



&lt;222&gt; (1)...(307)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2158

```

Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
 1           5           10           15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Leu Val Tyr Leu Thr Thr Leu
      20           25           30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35           40           45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
      50           55           60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
      65           70           75           80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85           90           95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100          105          110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115          120          125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130          135          140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
      145          150          155          160
Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro
      165          170          175
Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile
      180          185          190
Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe
      195          200          205
Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val
      210          215          220
Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val
      225          230          235          240
Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      245          250          255
Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr
      260          265          270
Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys
      275          280          285
Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser
      290          295          300
Lys Thr Val
305

```

&lt;210&gt; 2159

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7534025-12-11728-15143)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2159

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Gln Ile Leu Phe Leu Val Cys
      20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr

```

```

      35      40      45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
  50      55      60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
  65      70      75      80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
      85      90      95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
      100      105      110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
      130      135      140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
  145      150      155      160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
      165      170      175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
      180      185      190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
      195      200      205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
      210      215      220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
  225      230      235      240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
      245      250      255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
      260      265      270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
      275      280      285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
      290      295      300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
  305      310      315      320
Pro

```

&lt;210&gt; 2160

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7534025-3-4346-5996)

&lt;400&gt; 2160

```

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg
  1      5      10      15
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe
      20      25      30
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu
      35      40      45
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met
      50      55      60
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr
  65      70      75      80
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser
      85      90      95
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe
      100      105      110
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr
      115      120      125
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln

```

```

      130              135              140
Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr
145              150              155              160
Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met
      165              170              175
Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val
      180              185              190
Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala
      195              200              205
Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala
      210              215              220
Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln
      225              230              235              240
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe
      245              250              255
Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala
      260              265              270
Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro
      275              280              285
Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala
      290              295              300
Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn
      305              310              315              320
Gly Ala Phe Ser

```

&lt;210&gt; 2161

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7534103-14-4211-5521)

&lt;400&gt; 2161

```

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
1      5      10      15
Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
      20      25      30
Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
      35      40      45
Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
      50      55      60
Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
      65      70      75      80
Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
      85      90      95
Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
      100      105      110
Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
      130      135      140
Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
      145      150      155      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
      165      170      175
Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
      180      185      190
Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
      195      200      205
Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
      210      215      220
Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser

```

225                      230                      235                      240  
 His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr  
                                  245                      250                      255  
 Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe  
                                  260                      265                      270  
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg  
                                  275                      280                      285  
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val  
                                  290                      295                      300  
 Ile  
 305

<210> 2162  
 <211> 301  
 <212> PRT  
 <213> Homo sapien (7534103-16-19899-21252)

<220>  
 <221> VARIANT  
 <222> (1)...(301)  
 <223> Xaa = Any Amino Acid

<400> 2162  
 Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe  
   1                                 5                                 10                                 15  
 Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val  
                                  20                                 25                                 30  
 Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser  
                                  35                                 40                                 45  
 Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu  
                                  50                                 55                                 60  
 Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr  
                                  65                                 70                                 75                                 80  
 Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala  
                                  85                                 90                                 95  
 Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro  
                                  100                                 105                                 110  
 Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr  
                                  115                                 120                                 125  
 Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe  
                                  130                                 135                                 140  
 Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val  
                                  145                                 150                                 155                                 160  
 Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp  
                                  165                                 170                                 175  
 Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly  
                                  180                                 185                                 190  
 Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile  
                                  195                                 200                                 205  
 Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser  
                                  210                                 215                                 220  
 Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val  
                                  225                                 230                                 235                                 240  
 Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr  
                                  245                                 250                                 255  
 Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu  
                                  260                                 265                                 270  
 Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met  
                                  275                                 280                                 285  
 Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu  
                                  290                                 295                                 300

<210> 2163  
 <211> 134  
 <212> PRT  
 <213> Homo sapien (7534103-16-5480-6475)

<220>  
 <221> VARIANT  
 <222> (1)...(134)  
 <223> Xaa = Any Amino Acid

<400> 2163  
 Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr  
 1 5 10 15  
 Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg  
 20 25 30  
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln  
 35 40 45  
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser  
 50 55 60  
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly  
 65 70 75 80  
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln  
 85 90 95  
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser  
 100 105 110  
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Lys Xaa Ser Gly Glu Arg  
 115 120 125  
 Ser Ser Phe Pro Arg Glu  
 130

<210> 2164  
 <211> 307  
 <212> PRT  
 <213> Homo sapien (7547121-7-14093-14713)

<220>  
 <221> VARIANT  
 <222> (1)...(307)  
 <223> Xaa = Any Amino Acid

<400> 2164  
 Leu Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu  
 1 5 10 15  
 Phe Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg  
 20 25 30  
 Ile Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His  
 35 40 45  
 Gly Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro  
 50 55 60  
 Ser Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr  
 65 70 75 80  
 Asp Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu  
 85 90 95  
 Cys Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser  
 100 105 110  
 Lys Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys  
 115 120 125  
 Lys Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe  
 130 135 140  
 Leu Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys

```

145          150          155          160
Gly Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Pro
          165          170          175
Leu Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly
          180          185          190
Lys Val Asn Phe Ser Phe Thr Leu Leu Pro Phe Gln Phe Phe Ile
          195          200          205
Phe Ser Phe Leu Tyr Phe His Leu Cys Cys Ile Glu Ile Asn Ser
          210          215          220
Ala Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr
225          230          235          240
Val Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser
          245          250          255
Thr Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly
          260          265          270
Val Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met
          275          280          285
Glu Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp
          290          295          300
Cys Trp Lys
305

```

```

<210> 2165
<211> 214
<212> PRT
<213> Homo sapien (7622326-1-2092-6993)

```

```

<220>
<221> VARIANT
<222> (1)...(214)
<223> Xaa = Any Amino Acid

```

```

<400> 2165
Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
1          5          10          15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
          20          25          30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
          35          40          45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
          50          55          60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
65          70          75          80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
          85          90          95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
          100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
          115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
          130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
145          150          155          160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
          165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
          180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
          195          200          205
Gly Lys Ile Ser Cys His
210

```

<210> 2166  
 <211> 321  
 <212> PRT  
 <213> Homo sapien (7622326-2-5218-6423)

<400> 2166  
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu  
 1 5 10 15  
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro  
 20 25 30  
 Phe Cys Phe Ile Tyr Leu Thr Val Ile Leu Gly Asn Leu Thr Ile Leu  
 35 40 45  
 His Val Ile Cys Thr Asp Ala Thr Leu His Gly Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Gly Met Leu Ala Val Thr Asp Leu Gly Leu Cys Leu Ser Thr Leu  
 65 70 75 80  
 Pro Thr Val Leu Gly Ile Phe Trp Phe Asp Thr Arg Glu Ile Gly Ile  
 85 90 95  
 Pro Ala Cys Phe Thr Gln Leu Phe Phe Ile His Thr Leu Ser Ser Met  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ser Met Ser Ile Asp Arg Ser Val Ala Val  
 115 120 125  
 Cys Asn Pro Leu His Asp Ser Thr Val Leu Thr Pro Ala Cys Ile Val  
 130 135 140  
 Lys Met Gly Leu Ser Ser Val Leu Arg Ser Ala Leu Leu Ile Leu Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Lys Arg Phe Gln Tyr Cys His Ser His Val Leu  
 165 170 175  
 Ala His Ala Tyr Cys Leu His Leu Glu Ile Met Lys Leu Ala Cys Ser  
 180 185 190  
 Ser Ile Ile Val Asn His Ile Tyr Gly Leu Phe Val Val Ala Cys Thr  
 195 200 205  
 Val Gly Val Asp Ser Leu Leu Ile Phe Leu Ser Tyr Ala Leu Ile Leu  
 210 215 220  
 Arg Thr Val Leu Ser Ile Ala Ser His Gln Glu Arg Leu Arg Ala Leu  
 225 230 235 240  
 Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Ile Pro  
 245 250 255  
 Met Ile Gly Leu Ser Leu Val His Arg Phe Gly Glu His Leu Pro Arg  
 260 265 270  
 Val Val His Leu Phe Met Ser Tyr Val Tyr Leu Leu Val Pro Pro Leu  
 275 280 285  
 Met Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Arg Gln Arg  
 290 295 300  
 Ile Ile Lys Lys Phe Gln Phe Ile Lys Ser Leu Arg Cys Phe Trp Lys  
 305 310 315 320  
 Asp

<210> 2167  
 <211> 345  
 <212> PRT  
 <213> Homo sapien (7622326-3-3672-5330)

<220>  
 <221> VARIANT  
 <222> (1)...(345)  
 <223> Xaa = Any Amino Acid

<400> 2167

```

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu
 1          5          10          15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
          20          25          30
Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35          40          45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
          50          55          60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
65          70          75          80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
          85          90          95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
          130          135          140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
145          150          155          160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
          165          170          175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
          180          185          190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
          195          200          205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
          210          215          220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
225          230          235          240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
          245          250          255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
          260          265          270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
          275          280          285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
          290          295          300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
305          310          315          320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
          325          330          335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
          340          345

```

&lt;210&gt; 2168

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7622326-4-1-4013)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2168

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
 1          5          10          15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
          20          25          30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met

```



```

      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
  50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
225              230              235              240
Ala Phe Asp Thr Cys Gly Ser His Ile Gly Ala Val Ala Val Phe Tyr
      245              250              255
Ile Pro Trp Val Val Leu Ser Val Val His Arg Phe Phe His Lys Ala
      260              265              270
Ser Pro Tyr Val His Pro Leu Leu Ser Asn Ile Tyr Phe Leu Gly Pro
      275              280              285
Ser Arg Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg
      290              295              300
Arg Ala Ile Leu Lys Leu Phe Gln Thr Lys Ser Lys Glu Met Xaa Trp
305              310              315              320
Gly Leu Phe Phe Leu
      325

```

&lt;210&gt; 2169

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7622326-7-11006-13674)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2169

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1              5              10              15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20              25              30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35              40              45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50              55              60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
65              70              75              80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85              90              95

```

Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser  
 100 105 110  
 Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile  
 115 120 125  
 His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile  
 130 135 140  
 Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu  
 165 170 175  
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser  
 180 185 190  
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr  
 195 200 205  
 Met Leu Asp Leu Val Phe Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg  
 210 215 220  
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Met  
 245 250 255  
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met  
 260 265 270  
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu  
 275 280 285  
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val  
 290 295 300  
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu  
 305 310 315

&lt;210&gt; 2170

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7622326-8-11210-13439)

&lt;400&gt; 2170

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met  
 1 5 10 15  
 Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro  
 20 25 30  
 Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu  
 35 40 45  
 Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His  
 50 55 60  
 Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly  
 65 70 75 80  
 Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly  
 85 90 95  
 Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile  
 100 105 110  
 His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile  
 115 120 125  
 Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu  
 130 135 140  
 Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys  
 145 150 155 160  
 Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr  
 165 170 175  
 Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val  
 180 185 190  
 Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe  
 195 200 205

Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser  
 210 215 220  
 Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp  
 225 230 235 240  
 Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu  
 245 250 255  
 Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu  
 260 265 270  
 Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe  
 275 280 285  
 Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys  
 290 295 300  
 Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly  
 305 310 315 320  
 Gly Ala Gln

&lt;210&gt; 2171

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7631097-4-2553-4836)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2171

Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro  
 1 5 10 15  
 Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp  
 20 25 30  
 Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn  
 35 40 45  
 Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro  
 50 55 60  
 Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr  
 65 70 75 80  
 Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg  
 85 90 95  
 Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser  
 100 105 110  
 Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe  
 115 120 125  
 Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser  
 130 135 140  
 Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val  
 145 150 155 160  
 Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly  
 165 170 175  
 Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg  
 180 185 190  
 Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val  
 195 200 205  
 Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr  
 210 215 220  
 Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg  
 225 230 235 240  
 Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val  
 245 250 255  
 Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg

260 265 270  
 His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val  
 275 280 285  
 Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro  
 290 295 300  
 Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa  
 305 310 315 320  
 Xaa Asn Tyr Lys Ile Leu Xaa Gly  
 325

&lt;210&gt; 2172

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7631097-7-11130-14291)

&lt;400&gt; 2172

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile  
 1 5 10 15  
 Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met  
 20 25 30  
 Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met  
 35 40 45  
 Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys  
 50 55 60  
 Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala  
 65 70 75 80  
 Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro  
 85 90 95  
 Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly  
 100 105 110  
 Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe  
 115 120 125  
 Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser  
 130 135 140  
 Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg  
 145 150 155 160  
 Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val  
 165 170 175  
 Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val  
 180 185 190  
 Leu Glu Leu Ser Ser Arg Arg Ala Ala Leu Lys Ala Phe Asn Thr Cys  
 195 200 205  
 Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly  
 210 215 220  
 Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val  
 225 230 235 240  
 Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu  
 245 250 255  
 Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met  
 260 265 270  
 Phe Ser Gln Gly Gly Lys  
 275

&lt;210&gt; 2173

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7631097-8-20107-27103)

&lt;400&gt; 2173

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15

```

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
  20                      25                      30
Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
  35                      40                      45
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
  50                      55                      60
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
  65                      70                      75                      80
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
  85                      90                      95
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
  100                     105                     110
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
  115                     120                     125
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
  130                     135                     140
Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met
  145                     150                     155                     160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
  165                     170                     175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
  180                     185                     190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
  195                     200                     205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
  210                     215                     220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
  225                     230                     235                     240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
  245                     250                     255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
  260                     265                     270
Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
  275                     280                     285
Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
  290                     295                     300
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
  305                     310                     315

```

&lt;210&gt; 2174

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7637231-2-1-2470)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2174

```

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
  1                      5                      10                      15
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
  20                      25                      30
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
  35                      40                      45
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
  50                      55                      60
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
  65                      70                      75                      80
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu

```

```

      85      90      95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
      100      105      110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
      130      135      140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
      145      150      155      160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
      165      170      175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
      180      185      190
Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu
      195      200      205
Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser
      210      215      220
Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr
      225      230      235      240
Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile
      245      250      255
Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His
      260      265      270
His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro
      275      280      285
Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu
      290      295      300
Ser Tyr Ile Gln Arg Ala Arg
      305      310

```

&lt;210&gt; 2175

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7637231-7-1-1398)

&lt;400&gt; 2175

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
 1      5      10      15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20      25      30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35      40      45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50      55      60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
      65      70      75      80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85      90      95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100      105      110
Pro Arg Lys Asp Val
      115

```

&lt;210&gt; 2176

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7637775-10-2645-3375)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(227)

<223> Xaa = Any Amino Acid

<400> 2176

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
 1          5          10          15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
          20          25          30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
          35          40          45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
          50          55          60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
65          70          75          80
Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe
          85          90          95
Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
          100          105          110
Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly
          115          120          125
Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys
          130          135          140
Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser
145          150          155          160
Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala
          165          170          175
Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile
          180          185          190
Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr
          195          200          205
Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
          210          215          220
Lys Val Lys
225

```

<210> 2177

<211> 316

<212> PRT

<213> Homo sapien (7655430-8-26100-29590)

<220>

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 2177

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
 1          5          10          15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
          20          25          30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
          35          40          45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
          50          55          60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
65          70          75          80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
          85          90          95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
          100          105          110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
          115          120          125

```

Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val  
 130 135 140  
 Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn  
 145 150 155 160  
 Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser  
 165 170 175  
 Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala  
 180 185 190  
 Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu  
 195 200 205  
 Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu  
 210 215 220  
 Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys  
 225 230 235 240  
 Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr  
 245 250 255  
 Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp  
 260 265 270  
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro  
 275 280 285  
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg  
 290 295 300  
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile  
 305 310 315

&lt;210&gt; 2178

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7657777-15-1-798)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(154)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2178

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile  
 1 5 10 15  
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe  
 20 25 30  
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg  
 35 40 45  
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys  
 50 55 60  
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile  
 65 70 75 80  
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu  
 85 90 95  
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe  
 100 105 110  
 Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu  
 115 120 125  
 Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu  
 130 135 140  
 Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr  
 145 150

&lt;210&gt; 2179

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7657777-22-544-1713)



<220>  
 <221> VARIANT  
 <222> (1)...(170)  
 <223> Xaa = Any Amino Acid

<400> 2179  
 His Thr Gln Pro Arg Gly Leu Thr Arg Val Xaa Glu Phe Leu Leu Leu  
 1 5 10 15  
 Gly Leu Ser Gln Asp Pro Gln Leu Gln Pro Val Leu Ser Gly Leu Ser  
 20 25 30  
 Leu Cys Met Cys Leu Gly Thr Gln Leu Gly Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Gly Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Ser Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Gly Ala Asp Ile Ser Phe Thr Ser Thr Thr Gly Pro  
 65 70 75 80  
 Lys Leu Ile Val Asp Ile His Ser Tyr Thr Arg Asp Ile Ser Tyr Ala  
 85 90 95  
 Arg Cys Leu Thr His Thr Pro Leu Phe Ala Ile Phe Gly Gly Val Glu  
 100 105 110  
 Arg Asp Met Leu Leu Arg Val Met Gly Tyr Asp Arg Val Val Asp Ile  
 115 120 125  
 Cys Asp Pro Leu Tyr His Ser His Ala Met Asn Pro Cys Val Cys Gly  
 130 135 140  
 Ser Leu Asp Leu Trp Ser Leu Phe Phe Leu Thr Leu Leu Tyr Thr His  
 145 150 155 160  
 Leu His Asn Ser Ile Ala Leu His Met Thr  
 165 170

<210> 2180  
 <211> 198  
 <212> PRT  
 <213> Homo sapien (7657777-42-1-597)

<220>  
 <221> VARIANT  
 <222> (1)...(198)  
 <223> Xaa = Any Amino Acid

<400> 2180  
 Met Asn Pro Cys Leu Cys Gly Phe Arg Val Val Val Ser Phe Phe Phe  
 1 5 10 15  
 His Ser Leu Leu Gly Ala Gln Val His Asn Leu Ser Ala Ser Gln Met  
 20 25 30  
 Thr Cys Phe Glu Tyr Val Glu Ile His Asn Phe Leu Trp Ala Leu Ser  
 35 40 45  
 Gln Leu Pro His Arg Ala Trp Cys Asp Thr Phe Pro Asn Asn Ile Ile  
 50 55 60  
 Val Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ala Gly Thr  
 65 70 75 80  
 Leu Phe Ser Xaa Tyr Glu Ser Val Ser Ser Ile Glu Arg Val Ser Ser  
 85 90 95  
 Xaa Gly Gly Glu Tyr Lys Ala Phe Pro Thr Cys Gly Ser His Leu Ser  
 100 105 110  
 Val Val Cys Xaa Leu Tyr Gly Thr Gly Val Gly Gly His Leu Ser Ser  
 115 120 125  
 Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr  
 130 135 140  
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Met Arg Asn  
 145 150 155 160

Arg Asp Thr Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa  
                   165                  170                  175  
 Phe Xaa Tyr Leu Leu Ile Cys Pro Ile Pro Phe Val Val Trp Val Lys  
                   180                  185                  190  
 Lys Gly Arg Lys Val Lys  
                   195

<210> 2181  
 <211> 199  
 <212> PRT  
 <213> Homo sapien (7657788-15-11714-13012)

<220>  
 <221> VARIANT  
 <222> (1)...(199)  
 <223> Xaa = Any Amino Acid

<400> 2181  
 Leu Glu Met Xaa Leu Lys Ile Leu Tyr Leu Lys Asn Cys Ser Phe Xaa  
   1                  5                  10                  15  
 Cys Asn Arg Pro Glu His Tyr Asn Xaa Lys Asn Cys Gly Xaa Phe Cys  
                   20                  25                  30  
 Leu Leu Ile Thr Ile Ile Thr Phe Arg Ser Gly Ile Ile Asp Ile Cys  
                   35                  40                  45  
 Leu His His His Lys Thr Ile Phe Ile Phe Lys Lys His Ser Gly Phe  
                   50                  55                  60  
 Glu Gly Xaa Leu Trp Leu Arg Ile Xaa Asn Gln Ser Pro Lys Ser Trp  
   65                  70                  75                  80  
 Ile Ser Ile Ala Cys Asp Cys Cys Val Ala Xaa Asn Met Lys Gln Val  
                   85                  90                  95  
 Ala Ile Ser Cys His Ser Phe Ser Ser Val Lys Xaa Ser Pro Tyr Val  
                   100                  105                  110  
 Ile Trp Lys Tyr Phe Cys Lys Xaa Tyr Lys His Ile Lys Asn Gly Arg  
                   115                  120                  125  
 Asp Xaa Ile Xaa Leu Leu Thr Leu Lys Xaa Ile Lys His Leu Phe Val  
                   130                  135                  140  
 Val Cys Ile Ile Tyr Thr Pro Cys Met Phe His Pro Phe Gln Asn Lys  
   145                  150                  155                  160  
 Tyr Met Val Thr Glu Ser Leu Ile Xaa Ser Tyr Xaa Val Asp Pro Val  
                   165                  170                  175  
 Ser Asn Pro Ala Leu Ile Thr Ala Arg Ser His Xaa Asn His Leu Val  
                   180                  185                  190  
 Ile Ser Gln His Asn Asn Asn  
                   195

<210> 2182  
 <211> 324  
 <212> PRT  
 <213> Homo sapien (7658481-16-11475-15098)

<220>  
 <221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 2182  
 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe  
   1                  5                  10                  15  
 Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile  
                   20                  25                  30  
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu

```

      35              40              45
Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
  50              55              60
Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
  65              70              75              80
Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
      85              90              95
Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
      100              105              110
Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
      115              120              125
Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
      130              135              140
Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
      145              150              155              160
Pro Phe Ile Phe Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val
      165              170              175
Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
      180              185              190
Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu
      195              200              205
Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile
      210              215              220
Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala
      225              230              235              240
Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile
      245              250              255
Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val
      260              265              270
Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro
      275              280              285
Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
      290              295              300
Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile Xaa Met
      305              310              315              320
Leu Ser Arg Ser

```

&lt;210&gt; 2183

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7658481-18-4217-6941)

&lt;400&gt; 2183

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
  1              5              10              15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
      20              25              30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
      35              40              45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
      50              55              60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
      65              70              75              80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
      85              90              95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
      100              105              110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
      115              120              125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly

```

```

      130              135              140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145              150              155              160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
      165              170              175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
      180              185              190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Ile
      195              200              205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
      210              215              220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225              230              235              240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
      245              250              255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
      260              265              270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
      275              280              285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
      290              295              300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305              310              315

```

&lt;210&gt; 2184

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7658481-19-24037-28136)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2184

```

Phe Ser Gln Asn Leu Leu Ile Ser Gly Ser Gly Ser Phe Val Leu Leu
1      5      10      15
Gly Met Pro Gly Leu Glu Ala Leu His Ala Trp Leu Ser Val Leu Val
      20      25      30
Cys Leu Leu Tyr Met Ala Ala Leu Val Gly Asn Ala Leu Leu Val Gly
      35      40      45
Leu Val Val Thr Asp Lys Ala Leu Trp Ala Pro Met Tyr Gln Leu Leu
      50      55      60
Trp Leu Leu Ala Ala Ala Asp Phe Val Leu Ala Thr Ser Thr Val Pro
65      70      75      80
Lys Ala Leu Ala Val Leu Trp Gly Leu Ser Ser Glu Ile Ser Phe Gly
      85      90      95
Gly Cys Leu Ala Gln Leu Phe Val Ala His Ser Val Asn His Cys His
      100      105      110
Ile Ala Glu Ser Ser Val Leu Leu Ser Thr Ala Val Asp Cys Gln Pro
      115      120      125
Leu Arg Tyr Gly Ala Leu Leu Ala Gln Phe Val Val Gly Leu Val Ala
130      135      140
Leu Thr Thr Met Thr Arg Asp Val Cys Val Met Tyr Thr Leu Xaa Phe
145      150      155      160
Leu Phe Lys Lys Leu Pro Tyr Cys Gly Gln Trp Ala Leu Thr His Thr
      165      170      175
Tyr Cys Glu His Met Gly Val Ala Cys Leu Ala Cys Gly Asp Thr Cys
      180      185      190
Pro Ile Ile Arg Tyr Gly Leu Ala Thr Thr Leu Leu Ser Pro Ala Leu
195      200      205

```

Asp Leu Gly Leu Ile Gly Ala Ser Tyr Ala Leu Ile Phe Arg Ala Val  
 210 215 220  
 Cys Arg Leu Pro Ser His Val Ala Cys His Lys Ala Leu Gly Asn Cys  
 225 230 235 240  
 Gly Thr Tyr Ala Ser Ile Ile Gly Leu Phe Tyr Thr Pro Ala Leu Phe  
 245 250 255  
 Ser Phe Leu Ala His Cys Phe Gly Cys His Thr Val Pro Asn His Ile  
 260 265 270  
 His Ile Leu Leu Ala Asn Leu Tyr Ala Val Val Phe Pro Ala Phe Asn  
 275 280 285  
 Pro Val Val Tyr Gly Val Gln Thr Gln Gln Ser Ser Glu Ala Gln Glu  
 290 295 300  
 Leu Ala Ser Thr Phe Leu Gly Arg Ser Ser Glu  
 305 310 315

<210> 2185

<211> 320

<212> PRT

<213> Homo sapien (7658481-19-6742-9039)

<400> 2185

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn  
 1 5 10 15  
 Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His  
 20 25 30  
 Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val  
 35 40 45  
 Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His  
 50 55 60  
 Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile  
 65 70 75 80  
 Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly  
 85 90 95  
 Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu  
 100 105 110  
 His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe  
 115 120 125  
 Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu  
 130 135 140  
 Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser  
 145 150 155 160  
 Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe  
 165 170 175  
 Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val  
 180 185 190  
 Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe  
 195 200 205  
 Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val  
 210 215 220  
 Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Asp  
 225 230 235 240  
 Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile  
 245 250 255  
 Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe  
 260 265 270  
 Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr  
 275 280 285  
 Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr  
 290 295 300  
 Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly  
 305 310 315 320

<210> 2186  
 <211> 315  
 <212> PRT  
 <213> Homo sapien (7658481-2-1-1440)

<220>  
 <221> VARIANT  
 <222> (1)...(315)  
 <223> Xaa = Any Amino Acid

<400> 2186  
 Met Gly Gly Phe Gly Thr Asn Ile Ser Ser Thr Thr Ser Phe Thr Leu  
 1 5 10 15  
 Thr Gly Phe Pro Glu Met Lys Gly Leu Glu His Trp Leu Ala Ala Leu  
 20 25 30  
 Leu Leu Leu Leu Cys Ala Ile Ser Phe Leu Gly Asn Ile Leu Ile Leu  
 35 40 45  
 Phe Ile Ile Lys Glu Glu Gln Ser Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60  
 Leu Ser Leu Phe Ser Val Asn Asp Leu Gly Val Ser Phe Ser Thr Leu  
 65 70 75 80  
 Pro Thr Val Leu Ala Ala Val Cys Phe His Ala Pro Glu Thr Thr Phe  
 85 90 95  
 Asp Ala Cys Leu Ala Gln Thr Phe Phe Ile His Phe Ser Ser Trp Thr  
 100 105 110  
 Glu Phe Gly Ile Leu Leu Ala Met Ser Phe Asp His Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg Tyr Ala Thr Val Leu Thr Asp Val Arg Val Ala  
 130 135 140  
 His Asn Gly Ile Ser Ile Val Ile Arg Ser Phe Cys Met Val Phe Pro  
 145 150 155 160  
 Leu Pro Phe Leu Leu Lys Arg Leu Pro Phe Cys Lys Ala Ser Val Val  
 165 170 175  
 Leu Ser His Ser Tyr Cys Leu His Ala Asp Leu Ile Arg Leu Pro Cys  
 180 185 190  
 Gly Asp Thr Thr Ile Asn Ser Met Tyr Gly Leu Phe Ile Val Ile Ser  
 195 200 205  
 Ala Phe Gly Val Asp Ser Leu Leu Ile Leu Leu Ser Tyr Val Leu Ile  
 210 215 220  
 Leu His Ser Val Leu Ala Ile Ala Ser Arg Gly Glu Arg Leu Lys Thr  
 225 230 235 240  
 Leu Asn Thr Cys Val Ser His Ile Tyr Ala Val Leu Ile Phe Tyr Val  
 245 250 255  
 Pro Met Val Ser Val Ser Met Val His Arg Phe Gly Arg His Ala Pro  
 260 265 270  
 Glu Tyr Val His Lys Phe Met Ser Ser Leu Tyr Leu Pro Met Leu Tyr  
 275 280 285  
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile Arg Arg Arg Leu His  
 290 295 300  
 Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Lys  
 305 310 315

<210> 2187  
 <211> 124  
 <212> PRT  
 <213> Homo sapien (7658497-19-2333-3610)

<220>  
 <221> VARIANT  
 <222> (1)...(124)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2187

```

Leu Ile Leu Ser Ala Gln Ile Cys Arg Ala Leu Xaa Leu Ser Ile Phe
 1           5           10           15
Leu Val Arg Leu His Phe Lys Lys Leu Gly Pro Lys Ser Leu Asp Leu
          20           25           30
Tyr Phe Pro Gly Leu Gly Leu Lys Tyr Lys Ile Asn Ser Thr Asn Asn
          35           40           45
Tyr Arg Thr Ala Leu Glu Phe Xaa Val Phe Arg Gln Ala Val Xaa Leu
          50           55           60
Xaa Phe Thr Phe Phe Leu Phe Lys Tyr Ser Cys Leu Ser Lys Pro Gln
65           70           75           80
Xaa Glu Xaa Gly Ser Ser Asp Xaa Val Pro Cys Gln Tyr Ser Arg Cys
          85           90           95
Ser Glu His Asn Val Ala Leu Leu Ser Pro Gly Phe Ile Val Met Xaa
          100          105          110
Val Leu Val Gln Leu Pro Leu Phe Ser Phe Thr Ser
          115          120

```

&lt;210&gt; 2188

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7670214-14-2036-3224)

&lt;400&gt; 2188

```

Met Leu Leu Gly Asn Leu Ala Ile Ile Ser Phe Ile Cys Leu Asp Ser
 1           5           10           15
Arg Leu His Ser Pro Met Tyr Phe Phe Leu Cys Asn Phe Ser Leu Met
          20           25           30
Glu Met Val Val Thr Ser Thr Val Val His Arg Met Leu Ala Asp Leu
          35           40           45
Leu Ser Thr His Lys Thr Met Ser Leu Ala Lys Cys Leu Thr Gln Ser
          50           55           60
Phe Phe Tyr Phe Ser Leu Gly Ser Ala Asn Phe Leu Ile Leu Met Val
65           70           75           80
Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro
          85           90           95
Thr Ile Thr Asn Gly Pro Val Cys Val Lys Leu Val Val Ala Cys Trp
          100          105          110
Val Val Gly Phe Leu Ser Ile Val Ser Pro Thr Leu Gln Lys Thr Arg
          115          120          125
Leu Trp Phe Cys Gly Pro Asn Ile Ile Gly His Tyr Phe Cys Asp Ser
          130          135          140
Ala Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg His Ile Glu Arg
145           150           155           160
Met Asp Leu Phe Leu Ser Leu Leu Phe Val Leu Thr Thr Met Leu Leu
          165          170          175
Ile Ile Leu Ser Tyr Ile Leu Ile Val Ala Ala Val Leu His Ile Pro
          180          185          190
Ser Ser Ser Gly Cys Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu
          195          200          205
Thr Val Val Val Leu Gly Tyr Gly Ser Ala Ile Phe Ile Tyr Val Arg
          210          215          220
Pro Gly Lys Gly His Ser Thr Tyr Leu Asn Lys Ala Val Ala Met Val
225           230           235           240
Thr Ala Met Val Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Phe Arg
          245          250          255
Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe
          260          265          270
Leu Gly Asp Pro Ala Ala

```

275

<210> 2189  
 <211> 203  
 <212> PRT  
 <213> Homo sapien (7670214-23-12266-12905)

<220>  
 <221> VARIANT  
 <222> (1)...(203)  
 <223> Xaa = Any Amino Acid

<400> 2189  
 Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe  
 1 5 10 15  
 Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp  
 20 25 30  
 Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser  
 35 40 45  
 Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser  
 50 55 60  
 Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr  
 65 70 75 80  
 Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu  
 85 90 95  
 Leu Pro His Phe Leu Leu Val Asn Phe Phe Phe His Leu Met Arg Leu  
 100 105 110  
 Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln  
 115 120 125  
 Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser  
 130 135 140  
 Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp  
 145 150 155 160  
 Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser  
 165 170 175  
 Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys  
 180 185 190  
 Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp  
 195 200

<210> 2190  
 <211> 321  
 <212> PRT  
 <213> Homo sapien (7671636-1-417-2747)

<220>  
 <221> VARIANT  
 <222> (1)...(321)  
 <223> Xaa = Any Amino Acid

<400> 2190  
 Phe Lys Arg Ser Ile Thr Phe Thr Pro Thr Thr Phe Thr Leu Val Gly  
 1 5 10 15  
 Ile Pro Gly Leu Glu Ala Glu His Tyr Trp Ile Ser Ile Pro Phe Cys  
 20 25 30  
 Leu Ile Tyr Thr Ile Ile Phe Pro Gly Asn Gly Ile Ile Leu His Ile  
 35 40 45  
 Ile Arg Ile Asp Ser Ser Leu His Gln Pro Met Tyr Tyr Phe Leu Ala  
 50 55 60  
 Met Pro Ala Phe Val Glu Leu Gly Val Ser Ala Ser Thr Met Pro Thr  
 65 70 75 80



Val Leu Ser Ile Phe Leu Phe Gly Ile Asn Asp Val Ser Phe Gly Gly  
                     85                    90                    95  
 Cys Leu Leu Gln Met Phe Ser Met His Ser Phe Thr Leu Met Glu Ser  
                     100                    105                    110  
 Gly Val Leu Leu Ala Met Ser Val Asp Arg Phe Val Ala Ile Tyr Ser  
                     115                    120                    125  
 Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ile Ala Cys Ile Ser Gly Met  
                     130                    135                    140  
 Gly Ala Ala Ile Ala Leu Arg Ser Val Met Leu Met Leu Pro Leu Leu  
 145                    150                    155                    160  
 Phe Leu Leu Arg Arg Leu Pro Phe Cys Gly His Asn Thr Leu Thr His  
                     165                    170                    175  
 Ser Tyr Cys Leu His Ser Asp Leu Ile Lys Leu Pro Cys Gly Asp Thr  
                     180                    185                    190  
 Arg Pro Asn Ser Ile Leu Ala Leu Phe Val Ile Thr Phe Thr Phe Gly  
                     195                    200                    205  
 Leu Asp Leu Leu Phe Ile Val Val Ser Tyr Val Leu Ile Leu His Thr  
                     210                    215                    220  
 Val Leu Glu Ile Ala Ser Arg Ser Arg Ala Trp Gln Ala Leu Asn Thr  
 225                    230                    235                    240  
 Cys Val Ser His Ile Cys Ala Val Leu Val Tyr Tyr Val Pro Met Ile  
                     245                    250                    255  
 Ser Leu Ser Xaa Val His Arg Phe Gly Arg His Leu Pro Pro Leu Phe  
                     260                    265                    270  
 Gln Thr Val Thr Ala Asn Ala Tyr Leu Phe Phe Pro Pro Val Val Asn  
                     275                    280                    285  
 Pro Ile Val Tyr Ser Ile Lys Ile Lys Glu Ile Arg Asn Ser Val Val  
                     290                    295                    300  
 Leu Thr Leu Ser Arg Lys Arg Gly Glu Phe Xaa Trp Arg Pro Lys Ile  
 305                    310                    315                    320  
 Pro

&lt;210&gt; 2191

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7690091-1-489-1697)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(295)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2191

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr  
   1                    5                    10                    15  
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu  
                     20                    25                    30  
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile  
                     35                    40                    45  
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu  
                     50                    55                    60  
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu  
 65                    70                    75                    80  
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu  
                     85                    90                    95  
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu  
                     100                    105                    110  
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile  
                     115                    120                    125  
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe

130	135	140
Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr		
145	150	155
Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro		160
	165	170
Ile Ser Gly Thr Phe Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu		175
	180	185
Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly		190
	195	200
Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly		205
	210	215
Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala		220
225	230	235
Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr		240
	245	250
Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg		255
	260	265
Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val		270
	275	280
Xaa Val Arg Lys Gly Ser Lys		285
	290	295

&lt;210&gt; 2192

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7705148-11-94-972)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(197)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2192

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu	
1	5
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly	10
	20
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr	25
	30
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr	35
	40
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp	45
	50
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp	55
65	60
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu	65
	70
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr	75
	80
Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His	85
	90
Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu	95
	100
Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val	105
145	110
Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu	115
	120
Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys	125
	130
Leu Leu Pro Xaa Gly	135
	140
	145
	150
	155
	160
	165
	170
	175
	180
	185
	190
	195

&lt;210&gt; 2193

<211> 128  
 <212> PRT  
 <213> Homo sapien (7705148-13-12855-13510)

<220>  
 <221> VARIANT  
 <222> (1)...(128)  
 <223> Xaa = Any Amino Acid

<400> 2193  
 Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe  
 1 5 10 15  
 Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys  
 20 25 30  
 Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe  
 35 40 45  
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe  
 50 55 60  
 Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser  
 65 70 75 80  
 Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro  
 85 90 95  
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu  
 100 105 110  
 Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys  
 115 120 125

<210> 2194  
 <211> 208  
 <212> PRT  
 <213> Homo sapien (7705148-18-30183-31440)

<220>  
 <221> VARIANT  
 <222> (1)...(208)  
 <223> Xaa = Any Amino Acid

<400> 2194  
 Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe  
 20 25 30  
 Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu  
 35 40 45  
 Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys  
 50 55 60  
 Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys  
 65 70 75 80  
 Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly  
 85 90 95  
 Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser  
 100 105 110  
 Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu  
 130 135 140  
 Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr  
 145 150 155 160  
 Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe  
 165 170 175  
 Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr

	180		185		190
Met	His	Asp	Ile	Ile	Leu
			Val	Val	Phe
				Ala	Ser
					Phe
					Val
					Glu
					Ala
					Ile
	195		200		205

&lt;210&gt; 2195

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7705148-8-1-2633)

&lt;400&gt; 2195

Met	Asp	Trp	Glu	Asn	Cys	Ser	Ser	Leu	Thr	Asp	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Ile	Thr	Asn	Asn	Pro	Glu	Met	Lys	Val	Thr	Leu	Phe	Ala	Val	Phe	Leu
		20						25					30		
Ala	Val	Tyr	Ile	Ile	Asn	Phe	Ser	Ala	Asn	Leu	Gly	Met	Ile	Val	Leu
	35						40					45			
Ile	Arg	Met	Asp	Tyr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
His	Leu	Ser	Phe	Cys	Asp	Leu	Cys	Tyr	Ser	Thr	Ala	Thr	Gly	Pro	Lys
65					70				75					80	
Met	Leu	Val	Asp	Leu	Ala	Lys	Asn	Lys	Ser	Ile	Pro	Phe	Tyr	Gly	
			85					90					95		
Cys	Ala	Leu	Gln	Phe	Leu	Val	Phe	Cys	Ile	Phe	Ala	Asp	Ser	Glu	Cys
		100						105					110		
Leu	Leu	Leu	Ser	Val	Met	Ala	Phe	Asp	Arg	Tyr	Lys	Ala	Ile	Ile	Asn
	115						120					125			
Pro	Leu	Leu	Tyr	Thr	Val	Asn	Met	Ser	Ser	Arg	Val	Cys	Tyr	Leu	Leu
	130					135					140				
Leu	Thr	Gly	Val	Tyr	Leu	Val	Gly	Ile	Ala	Asp	Ala	Leu	Ile	His	Met
145					150				155					160	
Thr	Leu	Ala	Phe	Arg	Leu	Cys	Phe	Cys	Gly	Ser	Asn	Glu	Ile	Asn	His
			165					170					175		
Phe	Phe	Cys	Asp	Ile	Pro	Pro	Leu	Leu	Leu	Ser					
			180					185							

&lt;210&gt; 2196

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7705159-18-2705-3893)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2196

Cys	His	Pro	Pro	Leu	Arg	Trp	Gly	Ser	Xaa	Glu	Pro	Ala	Glu	Glu	Glu
1				5					10					15	
Gly	Leu	Ala	Leu	Ser	Ser	Arg	Xaa	Phe	Phe	Phe	Phe	Leu	Ser	Val	Leu
		20						25					30		
Asp	Ala	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Gln
	35					40						45			
Asp	Ala	Glu	Ile	Pro	Asn	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	
	50				55					60					
Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro
65				70					75					80	
Ala	Val	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr
			85					90					95		
Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu	Ser	Val	Ser	Ser	Ser	Arg	Gly	Gln
		100					105					110			
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa

```

      115              120              125
Phe Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser
  130              135              140
Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr
145              150              155              160
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys
      165              170              175
Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu
      180              185              190
Leu Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys
      195              200              205
Val Lys
  210

```

<210> 2197  
 <211> 186  
 <212> PRT  
 <213> Homo sapien (7708872-11-1-1518)

<220>  
 <221> VARIANT  
 <222> (1)...(186)  
 <223> Xaa = Any Amino Acid

```

<400> 2197
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
  1              5              10              15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
      20              25              30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Pro Thr Pro Asn Ile Phe
      35              40              45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
      50              55              60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
65              70              75              80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
      85              90              95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
      100              105              110
Arg Ser His Ser Leu Gln His Ala Ala Val Ala Ser Pro Cys Pro Gly
      115              120              125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
      130              135              140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
145              150              155              160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
      165              170              175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
      180              185

```

<210> 2198  
 <211> 323  
 <212> PRT  
 <213> Homo sapien (7708872-16-23686-24654)

<220>  
 <221> VARIANT  
 <222> (1)...(323)  
 <223> Xaa = Any Amino Acid

<400> 2198

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys  
 1 5 10 15  
 Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser  
 20 25 30  
 Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His  
 35 40 45  
 Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser  
 50 55 60  
 Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe  
 65 70 75 80  
 Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn  
 85 90 95  
 His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu  
 100 105 110  
 Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu  
 115 120 125  
 Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu  
 130 135 140  
 Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val  
 145 150 155 160  
 Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile  
 165 170 175  
 Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr  
 180 185 190  
 Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn  
 195 200 205  
 Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala  
 210 215 220  
 Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ile Leu Arg Ile  
 225 230 235 240  
 Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His  
 245 250 255  
 Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile  
 260 265 270  
 Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met  
 275 280 285  
 Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met  
 290 295 300  
 Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser  
 305 310 315 320  
 His Ser Ser

&lt;210&gt; 2199

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7715624-11-1-3301)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(328)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2199

Leu Ser Ile Cys Phe Phe Leu Cys Ile Phe Ser Ala Asp Ile Xaa Ser  
 1 5 10 15  
 Met Leu Ala Met Glu Gln Asn Asn Gly Thr Glu Val Thr Glu Phe Ile  
 20 25 30  
 Leu Leu Gly Phe Ala Gly Gln His Lys Ser Trp His Ile Leu Ser Ile  
 35 40 45  
 Ala Phe Leu Ala Ile Tyr Val Val Thr Pro Val Gly Asn Ile Gly Met

```

      50              55              60
Ile Leu Leu Ile Lys Ile Asp Ala Ser Leu His Ile Pro Met Xaa Ile
65              70              75              80
Phe Leu Gln His Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Ala Ile
      85              90              95
Thr Pro Lys Met Leu Lys Asn Phe Val Glu Thr Lys Lys Ser Ile Ser
      100              105              110
Cys Ile Gly Cys Met Val Gln Leu Leu Val Tyr Gly Thr Phe Ala Thr
      115              120              125
Ser Asp Cys Tyr Ile Leu Ala Ala Met Ala Val Asp Arg Tyr Val Ala
      130              135              140
Phe Cys Asn Pro Leu His Tyr Pro Gly Val Met Ser Gln Arg Leu Cys
145              150              155              160
Ile Lys Leu Leu Val Ser Ser Tyr Val Met Gly Phe Leu Asn Ala Ser
      165              170              175
Ile Asn Ile Ser Phe Thr Phe Ser Leu Asn Phe Cys Lys Ser Lys Thr
      180              185              190
Ile Asn His Phe Phe Cys Asp Glu Pro Pro Ile Ile Ala Leu Pro Cys
      195              200              205
Ser Asn Ile Asp Leu Asn Ile Met Leu Leu Thr Val Phe Val Gly Leu
      210              215              220
Asn Leu Met Cys Thr Val Met Val Val Ile Ile Ser Cys Ile Tyr Val
225              230              235              240
Leu Val Ala Ile Leu Arg Ile Ser Ser Ala Ala Gly Lys Lys Lys Ser
      245              250              255
Leu Ser Thr Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly
      260              265              270
Val Leu Ser Tyr Met Tyr Leu Cys His Arg Ile Asn Glu Ser Gln Lys
      275              280              285
Gln Glu Lys Val Ala Ser Val Phe Tyr Gly Ile Ile Ile Pro Met Leu
      290              295              300
Asn Pro Leu Ile Tyr Ser Gln Arg Asn Gln Asp Val Ile Glu Ala Ile
305              310              315              320
Lys Leu Thr Glu Lys Lys Tyr Phe
      325

```

&lt;210&gt; 2200

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7768677-1-106933-108798)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(193)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2200

```

Phe Phe Asn Ile Thr Xaa Phe Val Pro Glu Val Met Lys Ser Leu Ser
1              5              10              15
Arg Ser Lys Asp Ile Ser Phe Asn Phe Cys Phe Xaa Phe Phe Phe
      20              25              30
Ser Cys Gly Cys Thr Gly Leu Thr Glu Asp Ile Phe Val Val Phe Lys
      35              40              45
Ser Phe Val Leu Phe Gly Val Leu Ser Xaa Ala His Leu Pro Val Lys
      50              55              60
Lys Lys Lys Lys Arg Phe Cys Ser Leu Leu Tyr Xaa Thr Thr Ile Leu
65              70              75              80
Ile Cys Lys Trp Pro Lys Thr Ser Pro Phe Phe Thr Glu Phe Leu Ser
      85              90              95
Leu Ser Arg Lys Asn Leu Lys Phe Gln Lys Asn Ile Glu Cys Glu Tyr
      100              105              110

```

Met Ile Ser Val Xaa Ala Thr Cys Ile Gly Asn Lys Tyr Leu Asn Cys  
 115 120 125  
 Glu Ile Tyr Leu Arg Ser Leu Thr Phe Pro Asn Ile Ser Ser Ile Val  
 130 135 140  
 Phe Phe Leu Leu Gln Ser Lys Tyr Met Phe Thr Phe Xaa Lys Tyr Arg  
 145 150 155 160  
 Glu Ala Gln Asn Trp Gly Lys Lys Pro Xaa Xaa Ile Pro Pro Ser Arg  
 165 170 175  
 Lys Lys Ala Ile Asn Leu Xaa Arg Ile Ser Ser Xaa Ser Leu Phe Cys  
 180 185 190  
 Val

&lt;210&gt; 2201

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (7770649-26-5915-7266)

&lt;400&gt; 2201

Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly  
 1 5 10 15  
 Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser  
 20 25 30  
 Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr  
 35 40 45  
 Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys  
 65 70 75 80  
 Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met  
 100 105 110  
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Gln Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Met Phe Phe  
 130 135 140  
 Leu Val Ala Ala Trp Val Thr Gly Leu Ile His Ser Val Val Gln Leu  
 145 150 155 160  
 Val Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Ser Asp Ser  
 165 170 175  
 Phe Tyr Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Thr Asp Ser  
 180 185 190  
 Tyr Arg Leu Glu Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu  
 195 200 205  
 Gly Ser Phe Phe Ile Leu Ile Ile Ser Tyr Val Val Ile Ile Leu Thr  
 210 215 220  
 Val Leu Lys His Ser Ser Ala Gly Leu Ser Lys Ala Leu Ser Thr Leu  
 225 230 235 240  
 Ser Ala His Val Ser Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe  
 245 250 255  
 Val Tyr Thr Trp Pro Ser Pro Ser Thr His Leu Asp Lys Phe Leu Ala  
 260 265 270  
 Ile Phe Asp Ala Val Leu Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr  
 275 280 285  
 Phe Arg Asn  
 290

&lt;210&gt; 2202

&lt;211&gt; 92

&lt;212&gt; PRT



<213> Homo sapien (7939486-13-581-990)

<220>

<221> VARIANT

<222> (1)...(92)

<223> Xaa = Any Amino Acid

<400> 2202

```

Cys His Pro Ser His Tyr Phe Ser Ile Leu Ile Arg Phe Leu Cys Leu
 1          5          10          15
Tyr Leu Ser Leu Glu Met Gln Ala Ala Cys Ser Ser Ser Xaa Leu Thr
      20          25          30
His Thr Ile His Phe Met Lys His Lys Pro Val Leu Thr Asn Ser Leu
      35          40          45
Ser Ser Leu Phe Asn Leu Ser Asn Cys Asp Lys Asn His Thr Ala Leu
      50          55          60
Tyr Pro Val Xaa Pro Pro Met Ile Phe Asp Gln Lys Pro Asn Leu Phe
65          70          75          80
Phe Val Val Phe Thr Tyr Gly Gln Leu Gly Ser Thr
      85          90

```

<210> 2203

<211> 168

<212> PRT

<213> Homo sapien (7996320-1-1-801)

<400> 2203

```

Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu
 1          5          10          15
Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu
      20          25          30
Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met
      35          40          45
Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe
      50          55          60
Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile
65          70          75          80
Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu
      85          90          95
Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala
      100          105          110
Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile
      115          120          125
Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His
      130          135          140
Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe
145          150          155          160
Thr Met Ala Leu Ala Ala Pro Leu
      165

```

<210> 2204

<211> 167

<212> PRT

<213> Homo sapien (7996320-11-500-1042)

<220>

<221> VARIANT

<222> (1)...(167)

<223> Xaa = Any Amino Acid

<400> 2204

Gly Leu Gly Gly Gly Gln Ser Cys Ala Asn Lys Lys Trp Gly Thr Gly  
 1 5 10 15  
 Leu Asn Leu Thr Pro Ser Phe His Gly Ser Arg Ser Asn Phe Cys Gly  
 20 25 30  
 Pro Xaa Ile Ser Ile His Ser Tyr Ser Leu Gln Ser Phe Leu Pro Val  
 35 40 45  
 Leu Ile Met Asn Leu Tyr Xaa Thr His Cys Ser Xaa Gln Ser Ser Pro  
 50 55 60  
 Ile Leu His Tyr Pro Val Gln Val Leu Gly Leu Gly Thr Leu Val Leu  
 65 70 75 80  
 Leu Leu Gly Ser Tyr Ser Cys Ile Ile Met Thr Ala Pro Gly Asp Gln  
 85 90 95  
 Leu Cys Xaa Gln Gly Arg Ser Lys Ile Leu Ser Thr Cys Ser Ser His  
 100 105 110  
 Tyr Leu Val Val Thr Ile Phe Tyr Thr Ser Gly Phe Leu Arg Tyr Val  
 115 120 125  
 Ile Leu Tyr Pro Xaa Ile Xaa Met Arg Asp Ile Pro Tyr Pro Lys Trp  
 130 135 140  
 Ser Pro Leu Ala Glu Glu Ser Ile Thr Lys Xaa Gln Asp Ile Gln Lys  
 145 150 155 160  
 Ala Xaa Ala Leu Val Leu Leu  
 165

&lt;210&gt; 2205

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8052042-13-4893-7590)

&lt;400&gt; 2205

Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu  
 1 5 10 15  
 Ser Phe Pro Glu Leu His His Leu Gln Gly Leu Leu Phe Val Ser Leu  
 20 25 30  
 Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly  
 35 40 45  
 Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu  
 50 55 60  
 Ala Gln Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro  
 65 70 75 80  
 Lys Leu Leu Ala Gly Leu Pro Ala Glu Arg Arg Pro Ser Ile Ser Phe  
 85 90 95  
 Ser Gly His Leu Thr Trp Leu Leu Leu Phe Leu Ser Leu Ser Ser  
 100 105 110  
 Glu Cys Val Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val Ile  
 115 120 125  
 Cys His Leu Leu His Tyr Leu Ser Pro Ser Trp Thr Pro Cys Ser Trp  
 130 135 140  
 Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro Ala  
 145 150 155 160  
 Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser Pro  
 165 170 175  
 Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu Ser  
 180 185 190  
 Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln Val  
 195 200 205  
 Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His Ile  
 210 215 220  
 Leu Ala Arg Ser Leu Arg Ile Pro Glu Arg Pro Ser Lys Leu Lys Ala  
 225 230 235 240  
 Phe Pro Thr Tyr Ala Ser His Leu Gly Cys Gly Ser Ser Asn Leu Ile  
 245 250 255

Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys Pro  
 260 265 270  
 Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala Lys  
 275 280 285  
 Leu Leu Gln Ala Leu Pro  
 290

<210> 2206  
 <211> 175  
 <212> PRT  
 <213> Homo sapien (8052042-5-3342-10968)

<220>  
 <221> VARIANT  
 <222> (1)...(175)  
 <223> Xaa = Any Amino Acid

<400> 2206  
 Leu Leu Met Ala Ala Asp Asn His Thr Arg Val Glu Ala Phe Val Leu  
 1 5 10 15  
 Gln Gly Phe Ser Glu Asp Leu Pro Leu Gln Gly Cys Cys Phe Ala Phe  
 20 25 30  
 Phe Leu Leu Tyr Leu Met Ala Leu Val Gly Asn Ile Leu Met Val Met  
 35 40 45  
 Ala Ile Ser Leu Asn Pro Gly Leu His Thr Pro Val Tyr Phe Phe Leu  
 50 55 60  
 Thr Asn Leu Ala Leu Leu Asp Ile Val Cys Thr Ser Met Asp Asn Ser  
 65 70 75 80  
 Arg Val Val Ala Val Leu Tyr Thr Val Val Ser Pro Thr Leu Asn Pro  
 85 90 95  
 Ser Pro Thr Pro Cys Gly Thr Arg Thr Tyr Gln Xaa His Xaa Gly Glu  
 100 105 110  
 Cys Phe Leu Ala Ser Gly Lys Arg Lys Gly Ser Phe Xaa Cys Glu Met  
 115 120 125  
 Phe Gln Val Leu Thr Asn Xaa Phe Gln His Met Thr Leu Arg Ile Ser  
 130 135 140  
 Cys Lys Gln Gln Gly Thr Arg Lys Xaa Leu Met Pro His Ile Tyr Lys  
 145 150 155 160  
 Xaa Cys Ala Pro Ala Arg Gly Cys His His Ser Met Trp Asn Ser  
 165 170 175

<210> 2207  
 <211> 275  
 <212> PRT  
 <213> Homo sapien (8072456-16-39461-40850)

<400> 2207  
 Met Val Gly Asn Leu Leu Ile Trp Val Thr Thr Ile Gly Ser Pro Ser  
 1 5 10 15  
 Leu Gly Ser Leu Met Tyr Phe Phe Leu Ala Tyr Leu Ser Leu Met Asp  
 20 25 30  
 Ala Ile Tyr Ser Thr Ala Met Ser Pro Lys Leu Met Ile Asp Leu Leu  
 35 40 45  
 Cys Asp Lys Ile Ala Ile Ser Leu Ser Ala Cys Met Gly Gln Leu Phe  
 50 55 60  
 Ile Glu His Leu Leu Gly Gly Ala Glu Val Phe Leu Leu Val Val Met  
 65 70 75 80  
 Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro Leu His Tyr Leu Asn  
 85 90 95  
 Ile Met Asn Arg Leu Val Cys Ile Leu Leu Val Val Ala Met Ile  
 100 105 110

Gly Gly Phe Val His Ser Val Val Gln Ile Val Phe Leu Tyr Ser Leu  
           115                          120                          125  
 Pro Ile Cys Gly Pro Asn Val Ile Asp His Ser Val Cys Asp Met Tyr  
           130                          135                          140  
 Pro Leu Leu Glu Leu Leu Cys Leu Asp Thr Tyr Phe Ile Gly Leu Thr  
 145                          150                          155                          160  
 Val Val Ala Asn Gly Gly Ile Ile Cys Met Val Ile Phe Thr Phe Leu  
                           165                          170                          175  
 Leu Ile Ser Cys Gly Val Ile Leu Asn Phe Leu Lys Thr Tyr Ser Gln  
                           180                          185                          190  
 Glu Glu Arg His Lys Ala Leu Pro Thr Cys Ile Ser His Ile Ile Val  
           195                          200                          205  
 Val Ala Leu Val Phe Val Pro Cys Ile Phe Met Tyr Val Arg Pro Val  
           210                          215                          220  
 Ser Asn Phe Pro Phe Asp Lys Leu Met Thr Val Phe Tyr Ser Ile Ile  
 225                          230                          235                          240  
 Thr Leu Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Gln Ser Glu Met  
                           245                          250                          255  
 Lys Asn Ala Met Lys Asn Leu Trp Cys Glu Lys Leu Ser Ile Val Arg  
           260                          265                          270  
 Lys Arg Val  
           275

&lt;210&gt; 2208

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8077072-13-9613-11523)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(316)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2208

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val  
   1                          5                          10                          15  
 Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met  
           20                          25                          30  
 Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile  
           35                          40                          45  
 Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe  
           50                          55                          60  
 Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile  
 65                          70                          75                          80  
 Ile Pro Lys Met Leu Leu Ile Ile Ala Glu Xaa Lys Thr Ile Ser  
           85                          90                          95  
 Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala  
           100                          105                          110  
 Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala  
           115                          120                          125  
 Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys  
           130                          135                          140  
 Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala  
 145                          150                          155                          160  
 Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu  
           165                          170                          175  
 Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys  
           180                          185                          190  
 Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala  
           195                          200                          205  
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val

210	215	220
Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala		
225	230	235
Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly		240
	245	250
Thr Leu Ile Ala Thr Tyr Leu Val Pro Ser Ala Asn Ser Ser Gln Leu		255
	260	265
Leu Cys Lys Gly Ser Ser Leu Leu Tyr Ile Ile Leu Thr Pro Met Phe		270
	275	280
Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Glu Ala Leu		285
	290	295
Lys Lys Cys Leu Arg Lys Lys Ser Gly Val Cys Leu		300
305	310	315

&lt;210&gt; 2209

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8081198-24-6628-8036)

&lt;400&gt; 2209

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr		
1	5	10
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met		15
	20	25
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile		30
	35	40
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu		45
	50	55
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile		60
	65	70
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu		75
	85	90
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu		95
	100	105
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu		110
	115	120
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly		125
	130	135
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe		140
	145	150
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile		155
	165	170
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile		175
	180	185
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile		190
	195	200
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys		205
	210	215
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser		220
	225	230
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr		235
	245	250
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser		255
	260	265
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg		270
	275	280
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu		285
	290	295
Ala Leu Ala Gly Lys		300
305		

<210> 2210  
 <211> 270  
 <212> PRT  
 <213> Homo sapien (8086488-18-2452-4090)

<400> 2210  
 Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu  
 1 5 10 15  
 Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe  
 20 25 30  
 Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile  
 35 40 45  
 Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro  
 65 70 75 80  
 Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu  
 85 90 95  
 Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu  
 100 105 110  
 Cys Cys Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly  
 115 120 125  
 Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys  
 130 135 140  
 Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His  
 145 150 155 160  
 Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln  
 165 170 175  
 His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn  
 180 185 190  
 Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly  
 195 200 205  
 Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala  
 210 215 220  
 Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn  
 225 230 235 240  
 Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala  
 245 250 255  
 Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys  
 260 265 270

<210> 2211  
 <211> 161  
 <212> PRT  
 <213> Homo sapien (8096828-10-670-2127)

<220>  
 <221> VARIANT  
 <222> (1)...(161)  
 <223> Xaa = Any Amino Acid

<400> 2211  
 Gly Trp Lys Ser Ser Thr Phe Asn Ile Ser Cys Thr Lys Phe Phe Leu  
 1 5 10 15  
 Val Gly Phe Pro Gly Leu Arg Glu Trp Trp Pro Leu Leu Val Leu Pro  
 20 25 30  
 Leu Val Phe Leu Phe Val Thr Ile Ile Ser Ala Asn Ala Leu Val Ile  
 35 40 45  
 His Thr Val Val Ala Arg Gln Asn Leu His Gln Pro Thr Cys Met Leu  
 50 55 60  
 Ile Thr Val Leu Leu Ala Val Asn Ile Arg Ala Ala Thr Ala Val Met

```

65          70          75          80
Pro Lys Met Leu Glu Gly Phe Val Tyr Tyr Ala Asn Pro Ile Ser Leu
          85          90          95
His Gly Arg Leu Ala Xaa Val Phe Phe Ile Tyr Phe Thr Leu Leu Leu
          100          105          110
Asp Tyr Asn Phe Leu Trp Pro Trp Pro Trp Thr Gly Tyr Phe Ala Ile
          115          120          125
Cys His Pro Leu Cys Phe Ser Asp Leu Met Thr Ser Gln Leu Leu Gly
          130          135          140
Leu Leu Ala Ile Leu Ala Phe Glu Gln Ser Pro Gly Ser Asp Pro Ala
145          150          155          160
Pro

```

<210> 2212  
 <211> 198  
 <212> PRT  
 <213> Homo sapien (8096828-22-1-1563)

<220>  
 <221> VARIANT  
 <222> (1)...(198)  
 <223> Xaa = Any Amino Acid

```

<400> 2212
Val Ala Ile Cys His Pro Leu Cys Phe Gln Thr Glu Xaa Leu Pro Ser
1          5          10          15
Trp Leu Gly Leu Leu Ala Ile Leu Ala Leu Thr Gln Ser Trp Gly Val
          20          25          30
Thr Val Pro Leu Val Val Leu Thr Ala Lys Ala Asp Phe Cys Arg Thr
          35          40          45
Ala Val Ile Arg His Phe Thr Cys Glu Cys Ile Ala Leu Leu Ser Ile
          50          55          60
Ala Cys Gly Asp Leu Thr Phe Asn Asn Trp Leu Gly Leu Ala Met Cys
65          70          75          80
Leu Val Thr Val Ile Ser Asp Met Ala Leu Leu Gly Thr Ser Tyr Thr
          85          90          95
His Ile Ile Tyr Ala Ala Phe Arg Ile Ser Ser Trp Gly Ala Gln Ala
          100          105          110
Lys Ala Leu His Thr Cys Gly Ser His Leu Leu Val Ile Leu Ser Ile
          115          120          125
Tyr Val Ser Gly Leu Ser Thr Ser Ile Thr Phe Xaa Val Ala Lys Thr
          130          135          140
Val Ser Gln Asn Val Gln Asn Leu Leu Ser Ala Ile Tyr Leu Leu Leu
145          150          155          160
Pro Gly Ala Leu Asn Pro Val Ile Tyr Gly Val Arg Thr Arg Glu Ile
          165          170          175
Gln Gln His Val Glu Lys Met Leu Cys Glu Lys Glu Thr Ala Gln Lys
          180          185          190
Ala Gly Glu Lys Pro Lys
          195

```

<210> 2213  
 <211> 323  
 <212> PRT  
 <213> Homo sapien (8096945-19-338-2509)

<220>  
 <221> VARIANT  
 <222> (1)...(323)  
 <223> Xaa = Any Amino Acid

&lt;400&gt; 2213

Gly Thr Leu Asn Leu Ser Ser Phe Asn Pro Gly Leu Phe Ile Leu Leu  
 1 5 10 15  
 Gly Ile Pro Gly Leu Glu Trp Phe Cys Ile Trp Met Gly Ile Leu Ser  
 20 25 30  
 Phe Thr Ser Tyr Leu Val Ser Leu Ala Gly Asn Val Ile Leu Leu Tyr  
 35 40 45  
 Leu Ile Thr Val Glu His Asn Leu His Lys Pro Met Phe Ser Phe Leu  
 50 55 60  
 Ser Ile Pro Ala Ser Ala Asn Leu Ile Leu Cys Ile Thr Tyr Phe Pro  
 65 70 75 80  
 Lys Thr Phe Gly Ile Phe Xaa Leu Lys Ala Gln Lys Ile Ile Phe Pro  
 85 90 95  
 Gly Cys Phe Thr Arg Phe Phe Phe Phe Gly Leu Leu His Phe Ser Phe  
 100 105 110  
 Phe Leu Asp Leu Ala Ile Leu Leu Gly Leu Ala Phe Asp His Tyr Met  
 115 120 125  
 Thr Ile Gly Phe Leu Leu Arg Tyr Thr Ser Gly Leu Thr Pro Arg Thr  
 130 135 140  
 Leu Gly Lys Ile Val Val Ser Ile Asp Xaa Arg Phe Asn Asn Ile Leu  
 145 150 155 160  
 Pro Ile Asp Phe Leu Gly Lys His Leu Pro Phe Cys Arg Thr His Ile  
 165 170 175  
 Asn Ser Asn Thr Tyr Cys Glu His Ile Gly Val Ala Leu Leu Ser Tyr  
 180 185 190  
 Ala Asp Ile Ser Ile Asn Ile Trp Tyr Asp Phe Thr Ile Leu Val Met  
 195 200 205  
 Thr Ile Ile Ser Asp Leu Ile Leu Thr Asp Ile Ser Tyr Thr Leu Thr  
 210 215 220  
 Leu His Ala Val Phe His Leu Pro Ser Ser Asp Ala Leu Leu Lys Ala  
 225 230 235 240  
 Leu Ser Thr Cys Gly Ser His Val Ser Val Ile Leu Met Leu Tyr Thr  
 245 250 255  
 Pro Thr Met Leu Ser Ala Leu Thr His His Phe Gly Gln Ser Ile Ser  
 260 265 270  
 Cys Thr Phe Tyr Ile Met Phe Val Gly Leu Tyr Arg Ala Ile Pro Pro  
 275 280 285  
 Val Leu Asn Ser Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gly Asn  
 290 295 300  
 Lys Val Ile Leu Leu Phe Phe Leu Lys Gly Met Gln Xaa Tyr Glu Asp  
 305 310 315 320  
 Glu Asn Met

&lt;210&gt; 2214

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8099799-17-8549-9091)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(130)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2214

Phe Xaa Ser Ser Ser Gly Gln Thr Arg His Phe Lys Ala Tyr Glu Xaa  
 1 5 10 15  
 His Leu Val Thr Gln Cys Ser Met Leu Trp Val Xaa Asp Xaa Tyr Phe  
 20 25 30  
 Leu Cys Ala Leu Leu Gln Pro Leu His His Gly Ser Lys Ser Xaa Thr



35 40 45  
 Gln Gly Ser Ser Phe Trp Ala Lys Gly Phe Val Leu Glu Val Ile Leu  
 50 55 60  
 Ser Phe Ser Xaa Xaa Val Ala His Ile Cys Ser Xaa Leu Val Leu Ser  
 65 70 75 80  
 Ala Phe Ser Cys Leu Xaa Asn Phe Met Ser Leu Thr Ala Phe Phe His  
 85 90 95  
 Phe Val Leu Ser Leu Ser Leu Xaa His Lys Leu Val Val Phe Leu Lys  
 100 105 110  
 Leu Tyr His Phe Xaa Lys Pro Gly Ser Pro Met Tyr Val Met Thr Ile  
 115 120 125  
 His Ile  
 130

<210> 2215  
 <211> 188  
 <212> PRT  
 <213> Homo sapien (8102357-9-3785-4449)

<220>  
 <221> VARIANT  
 <222> (1)...(188)  
 <223> Xaa = Any Amino Acid

<400> 2215  
 His Trp Lys Ile Leu Arg Arg Asn Ser Lys Met Ile His Glu Ile Ile  
 1 5 10 15  
 Xaa Thr Leu Cys Gln Ile Leu Tyr Ser Glu Asp Lys Thr Cys Tyr Ile  
 20 25 30  
 Gln Ile Gln Ser Leu Phe Cys Thr Asp Leu Glu Ile Pro Asn Phe Phe  
 35 40 45  
 Cys Glu Leu Asn Xaa Val Val His Leu Ala Cys Ser Asp Thr Phe Leu  
 50 55 60  
 Lys Asp Ile Val Arg Tyr Cys Thr Thr Met Leu Leu Ser Gly Gly Pro  
 65 70 75 80  
 Ile Ala Gly Ile Phe Tyr Ser Phe Ser Lys Ile Ile Ser Ser Ile Cys  
 85 90 95  
 Ala Ile Pro Ser Ala Gln Gly Lys His Lys Ala Phe Pro Thr Cys Val  
 100 105 110  
 Ser His Leu Ser Asn Met Ser Leu Phe Tyr Cys Arg Ser Thr Gly Leu  
 115 120 125  
 Tyr Leu Ser Phe Ala Ala Thr His Asn Ser Cys Ser Asn Ala Thr Ala  
 130 135 140  
 Ser Val Arg His Thr Val Val Lys Pro Leu Leu Asn Val Phe Ile Leu  
 145 150 155 160  
 Lys Ser Ser Asn Lys Asp Ile Lys Xaa Ala Leu Lys Val Phe Phe Arg  
 165 170 175  
 Gly Lys Gln Trp Lys His His Phe Ser Lys Ser Ala  
 180 185

<210> 2216  
 <211> 318  
 <212> PRT  
 <213> Homo sapien (8102369-26-1-1971)

<400> 2216  
 Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu  
 20 25 30  
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu

```

      35      40      45
Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
  50      55      60
Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
  65      70      75      80
Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
      85      90      95
Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
      100      105      110
Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115      120      125
Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
      130      135      140
Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
      145      150      155      160
Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
      165      170      175
His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
      180      185      190
Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
      195      200      205
Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
      210      215      220
Ala Asn Leu Ala Met Gly Leu Thr Gln Ser Arg Arg Lys Val Phe Ser
      225      230      235      240
Thr Cys Ser Ser His Arg Leu Val Val Ser Leu Phe Phe Gly Thr Ala
      245      250      255
Ser Ile Thr Asn Asn Arg Pro Gln Ala Gly Ser Ser Glu Thr Thr Asp
      260      265      270
Arg Val Ile Ser Leu Phe Asn Thr Val Ile Thr Pro Met Leu Asn Pro
      275      280      285
Ile Ile Asn Thr His Gly Asn Lys Asp Val Arg Arg Ala Leu Arg Tyr
      290      295      300
Leu Val Lys Arg Arg Arg Pro Ser Pro Gly Arg Gly Ser Gly
      305      310      315

```

&lt;210&gt; 2217

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8102369-32-1554-1892)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(109)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2217

```

Tyr Met Val Val Thr Leu Val Leu Val Ile Leu Ser Tyr Ala Phe Ile
  1      5      10      15
Ile Lys Thr Ile Leu Lys Leu Pro Ser Ala Gln Gln Arg Thr Lys Ala
      20      25      30
Phe Pro Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser Tyr Gly
      35      40      45
Ser Cys Met Phe Met Tyr Ile Asn Pro Ser Ala Lys Asp Arg Asp Thr
      50      55      60
Phe Asn Lys Gly Val Ala Leu Leu Ile Thr Ser Val Ala Pro Leu Leu
      65      70      75      80
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Gln Gln Val Arg Gln Pro Phe
      85      90      95
Lys Asp Met Val Lys Lys Leu Leu Asn Leu Xaa Arg Ile
      100      105

```

<210> 2218  
 <211> 131  
 <212> PRT  
 <213> Homo sapien (8102369-33-1-1370)

<400> 2218  
 Met Lys Asn Lys Thr Val Leu Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Asp Val Pro Glu Leu Gln Val Ala Val Phe Thr Phe Leu Phe Leu Ala  
 20 25 30  
 Tyr Leu Leu Ser Ile Leu Gly Asn Leu Thr Ile Leu Ile Leu Thr Leu  
 35 40 45  
 Leu Asp Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe  
 50 55 60  
 Ser Phe Leu Glu Ile Ser Phe Thr Asn Ile Phe Ile Pro Arg Val Leu  
 65 70 75 80  
 Ile Ser Ile Thr Thr Gly Asn Lys Ser Ile Ser Phe Ala Gly Cys Phe  
 85 90 95  
 Thr Gln Tyr Phe Phe Ala Met Phe Leu Gly Ala Thr Glu Phe Tyr Leu  
 100 105 110  
 Leu Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Leu Met  
 115 120 125  
 Thr Met His  
 130

<210> 2219  
 <211> 313  
 <212> PRT  
 <213> Homo sapien (8102369-49-1-1012)

<220>  
 <221> VARIANT  
 <222> (1)...(313)  
 <223> Xaa = Any Amino Acid

<400> 2219  
 Met Pro Asn Lys Ile Val Val Thr Glu Phe Phe Leu Thr Arg Pro Asp  
 1 5 10 15  
 Gly Leu Gln Lys Ser Phe Gln Val Ala Val Phe Leu Leu Pro Asp Ala  
 20 25 30  
 Cys His Thr Leu Xaa Leu Ser Leu Gly Thr Xaa Ile Ile Ile Thr Met  
 35 40 45  
 Thr Leu Leu Asp Thr Arg Met Gln Thr Ser Met Tyr Leu Phe Leu Gln  
 50 55 60  
 Asn Leu Ser Cys Leu Glu Ile Trp Phe Gln Thr Val Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Leu Asn Ile Ala Met Gly Thr Lys Thr Val Ser Phe Ala Gly  
 85 90 95  
 Cys Ile Thr Gln Asp Phe Phe His Ile Phe Leu Gly Ala Thr Glu Phe  
 100 105 110  
 Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Tyr Ile Ala Ile Cys Lys  
 115 120 125  
 Pro Leu His Tyr Pro Met Leu Ile Ser Ser Arg Val Cys Thr Gln Leu  
 130 135 140  
 Ile Leu Thr Cys Trp Leu Leu Gly Phe Ser Phe Ile Ile Met Pro Val  
 145 150 155 160  
 Ile Leu Thr Ser Gln Leu Pro Phe Cys Asp Thr His Ile Lys His Phe  
 165 170 175  
 Phe Cys Asp Tyr Thr Pro Leu Met Glu Val Val Cys Ser Gly Pro Lys  
 180 185 190

Val Leu Glu Met Val Asp Phe Thr Leu Ala Leu Val Ala Leu Phe Gly  
 195 200 205  
 Thr Leu Val Leu Ile Thr Leu Ser Tyr Val Gln Ile Ile Gln Thr Ile  
 210 215 220  
 Val Arg Ile Pro Ala Val Gln Glu Arg Lys Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Val Ile Met Val Thr Met Cys Tyr Asp Ser Cys Phe Phe  
 245 250 255  
 Met Tyr Val Lys Pro Ser Pro Gly Lys Trp Val Asp Val Asn Lys Gly  
 260 265 270  
 Val Ser Leu Ile Asn Thr Ile Ile Ala Pro Leu Leu Asn Pro Phe Ile  
 275 280 285  
 Cys Thr Leu Arg Asn Gln Gln Val Lys Gln Val Met Lys Asp Leu Val  
 290 295 300  
 Arg Lys Met Thr Leu Ser Glu Asn Lys  
 305 310

<210> 2220  
 <211> 96  
 <212> PRT  
 <213> Homo sapien (8117362-7-1589-1951)

<220>  
 <221> VARIANT  
 <222> (1)...(96)  
 <223> Xaa = Any Amino Acid

<400> 2220  
 Pro Leu Xaa Leu Met Val Val Ile Phe Ser Gln Val Tyr Thr Leu Ala  
 1 5 10 15  
 Ala Ile Pro Lys Met Ser Ser Thr Ala Gly Arg Thr Gln Gly Phe Phe  
 20 25 30  
 Met Xaa Ala Ser His Leu Thr Ala Val Val Ile Phe Tyr Gly Thr Pro  
 35 40 45  
 Ser Tyr Met Tyr Leu His His Gly Asn Asn Gly Ser Pro Lys Gln Gly  
 50 55 60  
 Lys Val Ser Ser Val Phe Tyr Gly Ile Val Ile Asp Leu Ser Leu Arg  
 65 70 75 80  
 Val Gln Asp Ala Arg Glu Ala Leu Lys Glu Lys Gly Lys Lys Gln Phe  
 85 90 95

<210> 2221  
 <211> 195  
 <212> PRT  
 <213> Homo sapien (8117365-9-1-1453)

<220>  
 <221> VARIANT  
 <222> (1)...(195)  
 <223> Xaa = Any Amino Acid

<400> 2221  
 Arg Met Phe Xaa Thr Xaa Phe Phe Ser Ser Leu Thr Leu Arg Leu Gln  
 1 5 10 15  
 Leu Ser His Leu Phe Pro Cys Leu Gly Tyr Val Phe Ser Leu Leu Gly  
 20 25 30  
 Xaa His Asp Lys Arg Tyr Met Ile Gln Leu Asn Pro Ser Leu Ala Val  
 35 40 45  
 Leu Lys Cys Val Ile Phe Trp Cys Val Cys Val Leu Val Cys Met Ser  
 50 55 60  
 Tyr Glu Glu Gly Glu Arg Leu Ser Thr Ser Phe Leu Ala Pro Cys Val

```

65          70          75          80
Ser Xaa Leu Trp Val Phe Ile Thr Cys Arg Val Gly Glu Val Phe Gly
      85          90          95
Phe Xaa Gly Phe Xaa Ala Ser Gln Xaa Ser His Lys Ile Asn Tyr Cys
      100         105         110
Val Asn Ile Val Leu Leu Gly Gly Cys Ile Leu Gln His Thr Xaa Asp
      115         120         125
Thr Ser Gln Leu Lys Glu Met Ser Ser Glu Met Leu Ala Arg Arg Lys
      130         135         140
Arg Arg Ile Thr Leu Arg Ser Leu Met Gly His Pro Ser Ile Phe Leu
145         150         155         160
Leu Arg Arg Ser Lys Ala Gly Ser Ile Ser Xaa Thr Asp Lys Ser Arg
      165         170         175
Leu Ser His Arg His Ser Arg Val Arg Leu Tyr Ile Ile Thr Gly Thr
      180         185         190
Asn Met Val
      195

```

&lt;210&gt; 2222

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8117535-2-10765-15227)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2222

```

Cys Val Asp Ser Ser Leu Lys Xaa Glu Ile Thr Gln Xaa Cys Leu Ser
1          5          10          15
Leu Leu Leu Xaa Met Ala Glu Gly Trp Arg Leu Tyr Phe Ile Ile Leu
      20         25         30
Ile Ile Ser Tyr Lys Phe Cys Thr Leu Leu Gly Asn Val Ile Phe Arg
      35         40         45
Thr Leu Val Cys Ser Leu Gly Phe His Thr Ser Cys Met Tyr Phe Phe
      50         55         60
Pro Xaa Lys Ile Ser Leu Xaa Leu Ala Xaa Val Cys His Ser Ile Ile
65         70         75         80
Ala Leu Pro Ser Thr Gln Lys Xaa Ala Ile Asn Val Gln Gly Ala Ala
      85         90         95
Val His Val Phe Ser Phe Pro Cys Leu Tyr Cys Pro Glu Ile Phe Leu
      100        105        110
His Ser Leu Thr Gln Cys His Pro Phe Ile Ala Ile Gly Tyr Pro Leu
      115        120        125
Gln Gly Met His Thr Ile Thr His Lys Leu Tyr Ile Leu Leu Thr Thr
      130        135        140
Gly Pro Trp Arg Gly Cys Xaa Leu His Val Asn Leu Leu Thr Ala Leu
145        150        155        160
Leu Gly Ser Tyr Pro Asn Pro Val Pro Thr Lys Leu Trp Leu Ser Phe
      165        170        175
Pro Ser Ile Pro Glu Val Lys Leu Xaa Pro Met Gln Ala Tyr Thr Lys
      180        185        190
Pro Tyr Ala Gly Leu Ser Leu Cys Leu Ser Leu Ser Leu Ser Leu Ser
      195        200        205
Phe Ser Leu Phe Ser Ile Ile Ser Ile Ser Tyr Ile Cys Asn Glu Ile
      210        215        220
Asp Ile Pro Lys Ile Ile Ser Ala Asp Ser Val His Gly Ala Phe Ser
225        230        235        240
Thr Cys Leu Ala His Leu Phe Ala Phe Ser Thr Cys Ile Ala Gln Pro
      245        250        255

```

Ala Val Cys Asn Ser Leu Trp Pro Trp Thr Glu Ala Gln Thr Glu Ser  
                   260                                  265                                  270  
 Ser Arg Asp Ser Val Ile Gln Arg Pro Asn Leu Cys Val Thr Ile Ser  
                   275                                  280                                  285  
 Leu Asn Ser Leu Ile Ser Ser Leu Arg Asn Glu Ser Val Lys Gln Ala  
                   290                                  295                                  300  
 Ser His Lys Ile Phe Lys Glu Gln Thr Leu Phe Met Lys Ile  
 305                                  310                                  315

<210> 2223

<211> 304

<212> PRT

<213> Homo sapien (8117535-5-1968-4011)

<220>

<221> VARIANT

<222> (1)...(304)

<223> Xaa = Any Amino Acid

<400> 2223

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro  
 1                  5                                  10                                  15  
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile  
                   20                                  25                                  30  
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe  
                   35                                  40                                  45  
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp  
                   50                                  55                                  60  
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser  
 65                  70                                  75                                  80  
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe  
                   85                                  90                                  95  
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met  
                   100                                  105                                  110  
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu  
                   115                                  120                                  125  
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu  
                   130                                  135                                  140  
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu  
 145                  150                                  155                                  160  
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro  
                   165                                  170                                  175  
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val  
                   180                                  185                                  190  
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val  
                   195                                  200                                  205  
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser  
                   210                                  215                                  220  
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val  
 225                  230                                  235                                  240  
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Ile Tyr Leu Lys Ser  
                   245                                  250                                  255  
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val  
                   260                                  265                                  270  
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu  
                   275                                  280                                  285  
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val  
                   290                                  295                                  300

<210> 2224

<211> 268

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8117653-5-5695-6912)

&lt;400&gt; 2224

```

Met Met Ala Leu Ile Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr
1      5      10      15
Phe Phe Leu Asn Val Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val
20      25      30
Val Thr Pro Lys Leu Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile
35      40      45
Ser Phe Glu Gly Cys Val Val Gln Leu Ala Phe Phe Val Val His Val
50      55      60
Thr Ala Glu Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu
65      70      75      80
Ala Ile Cys Gln Pro Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr
85      90      95
Cys Leu Gln Leu Val Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser
100     105     110
Ala Ile Gln Thr Gly Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn
115     120     125
Gln Leu Thr His Tyr Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala
130     135     140
Cys Ala Asn Thr Ala Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala
145     150     155     160
Leu Val Thr Leu Leu Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu
165     170     175
Val Leu Val Ala Ile Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys
180     185     190
Asp Leu Ser Thr Cys Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr
195     200     205
Gly Thr Val Val Phe Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn
210     215     220
Thr Asn Gly Gln Val Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met
225     230     235     240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
245     250     255
Leu Gln Arg Lys Leu Gln Val Asn Ile Phe Pro Gly
260     265

```

&lt;210&gt; 2225

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8117705-18-1061-1646)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(184)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2225

```

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr
1      5      10      15
His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile
20      25      30
Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser
35      40      45
His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu
50      55      60
Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys
65      70      75      80
Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His

```

```

      85          90          95
Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile
      100          105          110
Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His
      115          120          125
Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val
      130          135          140
Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys
145          150          155          160
Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr
      165          170          175
Val Tyr Leu Gln Pro Asp Phe Phe
      180

```

&lt;210&gt; 2226

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8117705-9-1-790)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(148)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2226

```

Thr Tyr Asp Val Pro Arg Ser Gly Leu Cys Ile Val Ser Tyr Asn Thr
1      5      10      15
Cys Lys Ser Thr Met Met Ser Ile Lys Ile Gln Leu Lys Tyr Met Xaa
      20      25      30
Xaa Lys Xaa Leu Leu Ile Tyr Ala Gly Val Tyr Leu Asn Val Thr Met
      35      40      45
Leu Ile Val Thr Phe Lys Tyr Thr His Ile Phe His His Pro Glu Leu
      50      55      60
Ala Leu Cys Tyr Val Ser Phe Ser Ala Val Val Phe His Leu Thr Ala
65      70      75      80
Val Thr Ile Phe Phe Gly Ala Leu Ser Tyr Met Asp Leu Gln Pro Glu
      85      90      95
Ser Thr Val Phe Gln Glu Gln Glu Asn Pro Ala Ser Ile Phe Cys Gly
      100      105      110
Ile Met Thr Leu Val Leu Asn Phe Leu Ile Tyr Cys Leu Xaa Asn Xaa
      115      120      125
Glu Val Lys Glu Ala Leu Gln Leu Thr Arg Lys Lys Tyr Xaa Tyr Met
      130      135      140
Xaa Thr Glu Gly
145

```

&lt;210&gt; 2227

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8118143-13-1464-2322)

&lt;400&gt; 2227

```

Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr Pro Leu Leu Ile Ile
1      5      10      15
Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr Leu Arg Ile Cys Ser
      20      25      30
Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr
      35      40      45
Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe Met Tyr Leu Arg Arg
      50      55      60
Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met Val Ala Val Phe Tyr

```



```
<210> 2228
<211> 157
<212> PRT
<213> Homo sapien (8118143-4-5591-10363)
```

```
<220>  
<221> VARIANT  
<222> (1)...(157)  
<223> Xaa = Any Amino Acid
```

<400> 2228																
Ile	Cys	His	Asn	Arg	Lys	Val	Ile	Pro	Ala	Ser	Met	Xaa	Asn	Met	Cys	
1				5					10					15		
Xaa	Phe	Leu	Leu	Lys	Val	Ala	Xaa	Asp	Asn	Phe	Leu	His	Val	Leu	Phe	
		20						25					30			
Ile	Leu	Ala	Lys	Thr	Ala	Pro	Pro	Leu	Leu	Phe	Leu	Xaa	Glu	Ile	Pro	
		35					40					45				
Ser	Tyr	Phe	Ser	Ser	Pro	Ser	Xaa	Ile	Ile	Val	Leu	Xaa	Cys	Leu	Pro	
	50					55					60					
Xaa	Phe	Leu	Lys	Gln	Leu	Val	Ile	Leu	Phe	Val	Phe	Leu	Leu	Leu	Asn	
65				70						75					80	
Xaa	Ser	Tyr	Leu	Thr	Leu	Ile	Phe	Met	Leu	Leu	Thr	Met	Lys	Ile	Thr	
			85						90					95		
Ser	Ser	Phe	Lys	Ala	Ser	Thr	Val	Ile	Ser	Cys	Leu	Gln	Phe	Pro	Ser	
			100					105					110			
Lys	Ala	Thr	Cys	Met	His	Gly	Val	Phe	Ser	Ala	Val	Cys	Ala	Gln	Met	
		115					120					125				
Xaa	Pro	Tyr	Tyr	Asn	Gly	Xaa	Ile	Ile	Xaa	His	Pro	Glu	Ser	Ile	Thr	
	130					135					140					
Glu	Ser	Lys	Xaa	Leu	Thr	Cys	Val	Asn	Pro	Xaa	Phe	Asn				
145					150					155						

```
<210> 2229
<211> 320
<212> PRT
<213> Homo sapien (8118143-4-617-5265)
```

```
<220>
<221> VARIANT
<222> (1)...(320)
<223> Xaa = Any Amino Acid
```

<400> 2229															
Met	Leu	Val	Pro	Lys	Lys	Met	Val	Arg	Gly	Asn	Ser	Thr	Leu	Val	Thr
1				5					10					15	
Glu	Phe	Ile	Leu	Leu	Gly	Leu	Lys	Asp	Leu	Pro	Glu	Leu	Gln	Pro	Ile
			20					25					30		
Leu	Phe	Val	Leu	Phe	Leu	Leu	Ile	Tyr	Leu	Ile	Thr	Val	Gly	Gly	Asn
		35					40					45			
Leu	Gly	Met	Leu	Val	Leu	Ile	Arg	Ile	Asp	Ser	Arg	Leu	His	Thr	Pro
	50					55					60				
Met	Tyr	Phe	Phe	Leu	Ala	Ser	Leu	Ser	Cys	Leu	Asp	Leu	Tyr	Tyr	Ser
65					70					75					80

Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys  
 85 90 95  
 Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala  
 100 105 110  
 Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg  
 115 120 125  
 Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys  
 130 135 140  
 Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu  
 145 150 155 160  
 Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly  
 165 170 175  
 Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg  
 180 185 190  
 Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val  
 195 200 205  
 Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr  
 210 215 220  
 Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg  
 225 230 235 240  
 Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val  
 245 250 255  
 Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg  
 260 265 270  
 Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser  
 275 280 285  
 Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys  
 290 295 300  
 Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn  
 305 310 315 320

&lt;210&gt; 2230

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8118750-5-4885-6910)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2230

Met Xaa Asn Ser Arg Glu Ala Ser Gln Phe Ile Phe Leu Gly Leu Ser  
 1 5 10 15  
 Asn Val Pro Glu Leu Gln Val Pro Phe Phe Ile Met Phe Val Leu Ile  
 20 25 30  
 Tyr Leu Ile Asn Val Val Gly Asn Leu Gly Met Ile Ile Leu Ile Leu  
 35 40 45  
 Trp Tyr Ser Gln Leu His Asn Pro Met Tyr Phe Phe Phe Ser Asn Leu  
 50 55 60  
 Ser Leu Val Asp Phe Phe Tyr Ser Ser Val Val Thr Pro Lys Val Met  
 65 70 75 80  
 Thr Gly Leu Leu Arg Glu Asp Lys Ile Ile Ser Tyr Thr Val Trp Ala  
 85 90 95  
 Thr Gln Thr Phe Phe Ser Asp Ser Phe Ala Ser Val Val Asn Leu Leu  
 100 105 110  
 Leu Ala Leu Met Ala Ser Gly His Tyr Ala Ala Val Cys Lys Pro Leu  
 115 120 125  
 His Tyr Thr Thr Thr Met Met Thr Ser Val Cys Thr Cys Leu Ala Ile  
 130 135 140  
 Gly Xaa Tyr Val Gly Gly Phe Leu Asn Ala Ser Ile His Thr Gly Glu

145                      150                      155                      160  
 Thr Phe Ser Leu Phe Cys Met Ser Ser Glu Val His His Phe Phe Cys  
                                  165                      170                      175  
 Glu Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Arg His Val Asn  
                                  180                      185                      190  
 Val Val Val Leu Val Tyr Val Thr Ser Phe Asn Ile Leu Phe Ala Leu  
                                  195                      200                      205  
 Leu Val Ile Leu Ile Ser Tyr Leu Leu Met Phe Ile Thr Ile Leu Lys  
                                  210                      215                      220  
 Met His Ser Thr Ala Gly Tyr Gln Lys Ala Leu Ala Ile Cys Ala Ser  
 225                                   230                                   235                                   240  
 His Leu Thr Ala Val Ala Ile Phe Tyr Gly Thr Ile Ile Phe Met His  
                                  245                                   250                                   255  
 Ile Gln Pro Ser Ser Ser His Ser Ile Asp Thr Asp Lys Ile Ala Ala  
                                  260                                   265                                   270  
 Val Phe Tyr Thr Ile Val Phe Pro Met Val Asn His Val Val Xaa Arg  
                                  275                                   280                                   285  
 Leu Lys Asn Lys Val Lys Ser Thr Phe Lys Lys Ile Val Glu Lys Val  
                                  290                                   295                                   300  
 Lys Leu Ser Leu Gly Leu Xaa Val  
 305                                   310

&lt;210&gt; 2231

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8118750-8-1-2827)

&lt;400&gt; 2231

Ile Ile Leu Cys Phe Phe Ile Ile Gly Asn Ser Gln Asp Asn Ser Gln  
 1                                   5                                   10                                   15  
 Met Thr Leu Met Asp Asn Ile Ser Glu Val Thr Glu Phe Val Leu Val  
                                  20                                   25                                   30  
 Gly Leu Thr Asp Val Leu Glu Leu Gln Val Pro Leu Phe Ile Ile Phe  
                                  35                                   40                                   45  
 Thr Val Ile Tyr Leu Thr Thr Leu Val Gly Asn Phe Gly Met Ile Met  
                                  50                                   55                                   60  
 Leu Ile Leu Leu Asp Ser Arg Leu His Ile Pro Met Tyr Phe Phe Leu  
 65                                   70                                   75                                   80  
 Gly Lys Leu Ser Leu Val Asp Ser Val Cys Ala Cys Leu Val Thr Gly  
                                  85                                   90                                   95  
 Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His Val Ala Phe Thr  
                                  100                                   105                                   110  
 Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn His Phe Phe Cys  
                                  115                                   120                                   125  
 Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Ile Tyr Ala His  
                                  130                                   135                                   140  
 Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile Phe Phe Thr Leu  
 145                                   150                                   155                                   160  
 Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile Ala Ile Leu Arg  
                                  165                                   170                                   175  
 Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser Thr Cys Ala Tyr  
                                  180                                   185                                   190  
 His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile Thr Phe Met Tyr  
                                  195                                   200                                   205  
 Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Ile Ser Ser  
                                  210                                   215                                   220  
 Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr Ser  
 225                                   230                                   235                                   240  
 Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val Val Ile Gly Lys  
                                  245                                   250                                   255  
 Ala Lys Ser Ser Leu Gly Leu Ala Tyr Tyr Leu

260

265

<210> 2232  
 <211> 309  
 <212> PRT  
 <213> Homo sapien (8118822-9-5564-7217)

<220>  
 <221> VARIANT  
 <222> (1)...(309)  
 <223> Xaa = Any Amino Acid

<400> 2232  
 Glu Xaa Met Gly Thr Ser Asn Asn Val Thr Glu Phe Val Leu Pro Gly  
 1 5 10 15  
 Leu Ser Gln Asp Pro Asp Val Gln Lys Ala Leu Phe Val Met Phe Leu  
 20 25 30  
 Leu Thr Tyr Asn Val Thr Met Val Gly Asn Leu Leu Ile Val Val Thr  
 35 40 45  
 Ile Ile Ala Ile Ala Ser Leu Asp Ser Pro Val Ser Phe Phe Leu Ala  
 50 55 60  
 Cys Leu Ser Phe Ile Asp Ala Val Tyr Ser Thr Ser Phe Ser Pro Lys  
 65 70 75 80  
 Leu Met Ile Asp Leu Leu Cys Asp Lys Lys Thr Val Ser Phe Leu Ala  
 85 90 95  
 Cys Met Gly Gln Leu Phe Ile Asn Tyr Pro Phe Gly Gly Ile Glu Val  
 100 105 110  
 Phe Leu Leu Val Gly Met Ala Cys Asp His Tyr Val Asp Ile Cys Lys  
 115 120 125  
 Leu Leu His Tyr Leu Thr Ile Met Asn Trp Gln Val Cys Ile Leu Leu  
 130 135 140  
 Phe Met Val Ala Val Thr Gly Gly Phe Leu His Ser Met Phe Gln Ile  
 145 150 155 160  
 Val Val Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His  
 165 170 175  
 Phe Cys Asp Met Tyr Pro Leu Leu Glu Met Val Cys Thr Asp Thr Tyr  
 180 185 190  
 Phe Ile Gly Leu Thr Val Ile Ala Asn Gly Gly Ala Val Cys Met Val  
 195 200 205  
 Ile Phe Ile Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu  
 210 215 220  
 Lys Thr Tyr Ser Gln Glu Gly Gly His Lys Ala Leu Ser Thr Cys Ser  
 225 230 235 240  
 Ser Asn Ile Thr Val Val Ser Leu Phe Phe Asp Pro Cys Ile Phe Ile  
 245 250 255  
 Tyr Val Arg Pro Asp Ser Asn Phe Pro Ile Asp Lys Phe Met Thr Val  
 260 265 270  
 Phe Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu  
 275 280 285  
 Arg Asn Leu Glu Val Arg Ile Ala Val Lys Asn Leu Trp Cys Lys Asn  
 290 295 300  
 Xaa Thr Ile Val Arg  
 305

<210> 2233  
 <211> 257  
 <212> PRT  
 <213> Homo sapien (8118832-14-2647-3682)

<220>  
 <221> VARIANT

&lt;222&gt; (1)...(257)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2233

```

Ser Met Tyr Phe Phe Leu Thr Asn Phe Ala Gly Leu Glu Ile Phe Tyr
 1           5           10           15
Phe Phe Thr Ile Ala Pro Leu Thr Leu Ala Asn Val Leu Pro Met Gly
          20           25           30
Arg Asn Leu Ile Ser Leu Pro Gly Cys Gly Gly Gln Met Phe Phe Phe
      35           40           45
Ile Phe Leu Gly Arg Ala Asp Cys Ile Leu Leu Ala Val Met Ala Phe
 50           55           60
Asp Trp Phe Val Ala Ile Cys Cys Pro Leu Cys Tyr Gly Leu Ile Met
65           70           75           80
Ser Trp Arg Leu Cys Val Gln Leu Thr Leu Gly Ser Leu Leu Leu Gly
      85           90           95
Phe Phe Leu Ala Met Gln Leu Thr Val Leu Ile Phe Gln Leu Pro Leu
          100          105          110
Cys Ser Ser Lys Glu Ile Ser Thr Phe Tyr Cys Asp Val Leu Pro Val
      115          120          125
Met Arg Leu Ala Cys Ala Asp Thr Trp Val His Glu Ala Thr Met Ser
      130          135          140
Met Val Ser Thr Thr Phe Leu Thr Val Pro Phe Leu Leu Ile Thr Leu
      145          150          155          160
Ser Tyr Val Ser Ile Met Ala Ala Ile Leu Lys Ile Cys Ser Ala Glu
          165          170          175
Gly Arg His Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val
          180          185          190
Leu Leu Gln Asp Xaa Cys Thr Arg Leu Ala Phe Leu Cys Pro Ser Ser
      195          200          205
Ser Tyr Tyr Pro Glu Arg Gly Gln Ala Val Ser Val Val Tyr Thr Phe
      210          215          220
Ile Thr Pro Val Leu Asn Pro Leu Ile Tyr Ser Met Arg Asn Thr Glu
      225          230          235          240
Leu Lys Asp Ala Leu Lys Arg Ala Met Thr Arg Val Pro Leu Leu Xaa
          245          250          255

```

Thr

&lt;210&gt; 2234

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8118892-3-16899-18792)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2234

```

Met Glu Gln Arg Lys Asn Val Thr Glu Phe Val Leu Val Gly Leu Thr
 1           5           10           15
Gln Ser Pro Gln Gly Gln Lys Ile Leu Phe Leu Val Phe Leu Leu Ile
          20           25           30
Tyr Val Val Thr Met Val Gly Asn Ile Phe Ile Val Val Thr Val Val
      35           40           45
Val Ser Pro Thr Leu Gly Cys Pro Met Tyr Phe Phe Leu Gly Tyr Leu
      50           55           60
Ser Phe Met Asp Ala Val His Ser Thr Thr Val Thr Pro Asn Met Ile
      65           70           75           80
Ile Asp Leu Leu Tyr Glu Lys Lys Thr Ile Ser Phe Gln Ala Cys Ile

```

```

      85      90      95
Thr Gln Ile Phe Ile Gly His Leu Phe Gly Gly Ala Glu Ile Leu Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Gly Tyr Val Thr Ile Cys Lys Pro Leu
      115      120      125
His Tyr Leu Thr Ile Met Asn Gln Arg Val Cys Ile Leu Leu Leu Leu
      130      135      140
Leu Ala Trp Ala Gly Gly Phe Leu His Ala Val Val Gln Leu Leu Phe
145      150      155      160
Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
      165      170      175
Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr Tyr Val
      180      185      190
Thr Gly Leu Thr Val Val Ala Asn Asp Gly Ala Ile Cys Val Val Ile
      195      200      205
Phe Met Leu Leu Leu Phe Ser Tyr Gly Val Ile Leu His Ser Leu Lys
      210      215      220
Asn Leu Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Gly Ser
225      230      235      240
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245      250      255
Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr Val Phe
      260      265      270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275      280      285
Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg Lys Arg
      290      295      300
Lys Xaa Gly Gly Asp Lys Cys Ile Ile Tyr Phe Gln Xaa Arg Val Ala
305      310      315      320
Pro Ser Arg Lys Ala Ile Cys
      325

```

&lt;210&gt; 2235

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8118970-10-4947-6912)

&lt;400&gt; 2235

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
1      5      10      15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
      20      25      30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
      35      40      45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
      50      55      60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
65      70      75      80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
      85      90      95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
      100      105      110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
      115      120      125

```

&lt;210&gt; 2236

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8118970-16-561-1769)

&lt;400&gt; 2236

```

Met Glu Val Lys Asn Cys Cys Met Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Ile Pro His Thr Glu Gly Leu Glu Met Thr Leu Phe Val Leu Phe Leu
      20          25          30
Pro Phe Tyr Ala Cys Thr Leu Leu Gly Asn Val Ser Ile Leu Val Ala
      35          40          45
Val Met Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50          55          60
Asn Leu Ser Val Phe Asp Met Gly Phe Ser Ser Val Thr Val Pro Lys
65          70          75          80
Met Leu Leu Tyr Leu Met Gly Leu Ser Arg Leu Ile Ser Tyr Lys Asp
      85          90          95
Cys Val Cys Gln Leu Phe Phe Phe His Phe Leu Gly Ser Ile Glu Cys
      100          105          110

```

&lt;210&gt; 2237

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8119016-6-4856-7402)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(287)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2237

```

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu
 1          5          10          15
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu
      20          25          30
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr
      35          40          45
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys
      50          55          60
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe
65          70          75          80
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys
      85          90          95
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys
      100          105          110
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe
      115          120          125
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys
      130          135          140
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln
145          150          155          160
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa
      165          170          175
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr
      180          185          190
Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys
      195          200          205
Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile
210          215          220
Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr
225          230          235          240
Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr
      245          250          255
Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu
      260          265          270
Gly Ser Xaa Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr

```

275

280

285

<210> 2238  
 <211> 210  
 <212> PRT  
 <213> Homo sapien (8119057-10-2407-4064)

<220>  
 <221> VARIANT  
 <222> (1)...(210)  
 <223> Xaa = Any Amino Acid

<400> 2238  
 Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr  
 1 5 10 15  
 Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu  
 20 25 30  
 Gly His Ser Val Leu Gly Leu Ser Ser Leu Leu Asn Ile His Gly Glu  
 35 40 45  
 Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr  
 50 55 60  
 Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg  
 65 70 75 80  
 Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile  
 85 90 95  
 Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys  
 100 105 110  
 Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His  
 115 120 125  
 Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser  
 130 135 140  
 Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr  
 145 150 155 160  
 Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp  
 165 170 175  
 Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu  
 180 185 190  
 Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys  
 195 200 205  
 Ala Phe  
 210

<210> 2239  
 <211> 228  
 <212> PRT  
 <213> Homo sapien (8119057-15-786-3116)

<220>  
 <221> VARIANT  
 <222> (1)...(228)  
 <223> Xaa = Any Amino Acid

<400> 2239  
 Met Leu Ile Pro Ser Ser Thr Arg Lys Met Ala Ala Glu Ser His Ser  
 1 5 10 15  
 Thr Val Thr Glu Phe Ile Leu Arg Lys Lys Pro Ala Arg Ala Pro Ala  
 20 25 30  
 Pro Pro Leu Leu Gly Ile Cys Leu Lys Thr Val Val Gly Ala Leu Ile  
 35 40 45  
 Leu Ile Thr Leu Val Phe Leu Asn Ser Gln Leu His Pro Pro Met Tyr  
 50 55 60



Tyr Val Ile Arg Asn Leu Ser Phe Met Asp His Cys Asn Cys Ser Il  
 65 70 75 80  
 Ser Thr Pro Lys Ile Leu Val Lys Phe Val Leu Glu Lys Thr Ile Ile  
 85 90 95  
 Ser Tyr Glu Asp Gly Met Ser Gln Leu Cys Ser Ala Ser Cys Tyr Ile  
 100 105 110  
 Leu Ser Trp Pro Ser Val Thr Cys Gly Pro Ala Thr Ala Val Ile Thr  
 115 120 125  
 Phe His Gln Val Ser Ser Leu Leu Val Val Val Val Tyr Tyr Met Glu  
 130 135 140  
 Leu Thr Gly Thr Thr Ile Glu Phe Cys Leu Val Leu Lys Xaa Tyr Xaa  
 145 150 155 160  
 Cys Glu Leu Phe Ile Ser His Tyr Phe Cys Ser Cys Thr Ser Ile Tyr  
 165 170 175  
 Asp Ile Asp Arg Thr Ile Phe Phe Phe Thr Xaa Cys Asn Ile Val Val  
 180 185 190  
 Thr Arg Leu Thr Val Val Ser Tyr Ser Phe Leu Ser Ser Ile Leu His  
 195 200 205  
 Ile Ser Phe Thr Arg Ala Ala Leu Gly Phe Ser Arg Arg Ser Asp Ala  
 210 215 220  
 Phe Met Leu Cys  
 225

<210> 2240

<211> 277

<212> PRT

<213> Homo sapien (8119057-2-10436-11711)

<220>

<221> VARIANT

<222> (1)...(277)

<223> Xaa = Any Amino Acid

<400> 2240

His Ser Phe Leu Arg Tyr Ile Phe Ala Lys Leu Thr Gly Glu Pro Glu  
 1 5 10 15  
 Leu Gln Pro Ser Leu Tyr Ser Val Phe Trp Ser Pro Xaa Leu Gly Xaa  
 20 25 30  
 Pro His His Thr Ser Met Tyr Pro Leu His Thr Ser Met Tyr Leu Tyr  
 35 40 45  
 Ile Phe Ser Phe Ser Phe Ile Gly Phe Phe Tyr Ser Ser Val Ile Ser  
 50 55 60  
 Pro Gln Met Thr Ile Ser Phe Val Thr Glu Lys Asn Ile Ile Thr Tyr  
 65 70 75 80  
 Val Thr Ser Asn Thr Gln Pro Phe Pro Leu Cys Phe Phe Val Ile Ser  
 85 90 95  
 Asp Tyr Ser Ile Phe Ile Pro Leu Ala Leu Asp His Tyr Glu Ala Met  
 100 105 110  
 Thr Leu Pro Val Ser Phe Ile Ser Phe Ile Ser Val Asp Gly Ser Xaa  
 115 120 125  
 Val Ile Glu Phe Ala Asp Ala Val Val His Gln Gly Ser Met Asp Gln  
 130 135 140  
 Phe Leu Phe Cys Asp His Ser Cys Met Ser Leu Asn Leu Cys Asn Ile  
 145 150 155 160  
 Gly Pro Leu Gln Ala Ala Xaa Ile Ser Thr Tyr Val Ser Lys Gln Val  
 165 170 175  
 Asp Leu Tyr Ser Xaa Glu Pro Ala Val Tyr His Ala Val Leu Ser Phe  
 180 185 190  
 Ser Tyr Phe Val Phe Ile Leu Phe Asn Ile Phe His Xaa Pro Ser Gly  
 195 200 205  
 Pro Asn Leu Gln Pro Asp Ser Ile Asn Leu Phe Ile Ser Phe Phe Gly

210                      215                      220  
 Leu Gly Thr Phe Met Tyr Leu Arg Ser Pro Glu Ala Met Gly Xaa Cys  
 225                      230                      235                      240  
 Lys Phe Thr Val Ser Phe Thr Lys M t Gly Pro Val Met Asn Gly Leu  
                     245                      250                      255  
 Phe Asn Thr Leu Arg Asn Lys Thr Ile Xaa Leu Ala Ala Met Lys Pro  
                     260                      265                      270  
 Leu Ser Phe Ser Ser  
                     275

<210> 2241  
 <211> 125  
 <212> PRT  
 <213> Homo sapien (8119057-22-209-1834)

<220>  
 <221> VARIANT  
 <222> (1)...(125)  
 <223> Xaa = Any Amino Acid

<400> 2241  
 Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys  
 1                      5                      10                      15  
 Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Ser Leu Phe Phe  
                     20                      25                      30  
 Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu  
                     35                      40                      45  
 Asp Gln Gly Lys Val Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met  
                     50                      55                      60  
 Phe Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala  
 65                      70                      75                      80  
 Leu Arg Arg Thr Phe Cys Arg Lys Leu Val Ser Xaa Lys Xaa Met Arg  
                     85                      90                      95  
 Lys Gly Ile Gln Thr Phe Val Asn Gln Gly Val Ser Phe Leu Phe Phe  
                     100                      105                      110  
 Ser Glu Gly Thr Asn Ala Thr Ala Phe Ser Pro Ile Leu  
                     115                      120                      125

<210> 2242  
 <211> 164  
 <212> PRT  
 <213> Homo sapien (8119071-15-1-1473)

<220>  
 <221> VARIANT  
 <222> (1)...(164)  
 <223> Xaa = Any Amino Acid

<400> 2242  
 Trp Lys Asn His Phe Thr Ser Val Asn Cys Gly Phe Ala Ile Cys Arg  
 1                      5                      10                      15  
 Ala Glu Cys Xaa Pro Xaa Pro Lys Ile Leu Ser Ile Ile Gly Leu Lys  
                     20                      25                      30  
 Xaa Asn Ile Asn Glu Thr Leu Xaa Met Leu Asn Tyr Asn Thr Asn His  
                     35                      40                      45  
 Met Val Ser Val Asp Val Leu Ile Val Pro Asn Ser Leu Ile Thr Leu  
                     50                      55                      60  
 Ser Tyr Phe Phe Ile Val Ala Ala Ile Leu His Ile Arg Ser Ala Glu  
 65                      70                      75                      80  
 Gly Arg His Lys Ala Phe Pro Thr Cys Ser Phe His Leu Val Val Ile  
                     85                      90                      95

Leu Leu Gln His Asn Ala Thr Ser Leu Thr Tyr Leu Cys Pro Ser Ser  
                   100                  105                  110  
 Ile Phe Ser Tyr Glu Arg Gly Lys Val Val Ser Thr Val Tyr Thr Cys  
                   115                  120                  125  
 Ile Thr Pro Val Pro Asn Pro Leu Ile Cys Ser Met Arg Lys Lys Glu  
                   130                  135                  140  
 Leu Lys His Ala Leu Lys Lys Lys Glu Glu Ile Ala Arg Phe Leu Leu  
 145                  150                  155                  160  
 Leu Arg Thr His

<210> 2243  
 <211> 131  
 <212> PRT  
 <213> Homo sapien (8131609-2-31657-32554)

<220>  
 <221> VARIANT  
 <222> (1)...(131)  
 <223> Xaa = Any Amino Acid

<400> 2243  
 Ile Ile Tyr Leu Leu Cys Xaa Asp Pro Ala Ile Cys Glu Ser Val Ile  
   1                  5                  10                  15  
 Phe Phe Pro Met Gly Phe Ser Asp Cys Leu Pro Ile Leu Ser Ile Met  
                   20                  25                  30  
 Ile Thr Tyr Leu Phe Thr Phe Ile Asp Leu Leu Ile Pro Leu Pro His  
                   35                  40                  45  
 Val Xaa Leu Gln Lys Asp Tyr Tyr Val Cys Ala Ser Asn Leu Thr Val  
                   50                  55                  60  
 Val Ser Thr Phe Ser Xaa Asp His Leu Phe Ser Cys Leu His Ser Ser  
 65                  70                  75                  80  
 Asp Ala Ala Leu Leu Trp Thr Gln Thr Lys Leu His Ser Tyr Phe Ala  
                   85                  90                  95  
 Ile Val Ile Pro Thr Leu Tyr Pro Leu Val His Ser Leu Lys Asn Arg  
                   100                  105                  110  
 Gly Gly Gln Ser Ala Leu Arg Lys Val Leu Val Lys Ala Lys Ser Gln  
                   115                  120                  125  
 Leu Ser Leu  
 130

<210> 2244  
 <211> 312  
 <212> PRT  
 <213> Homo sapien (8131609-3-27134-29103)

<220>  
 <221> VARIANT  
 <222> (1)...(312)  
 <223> Xaa = Any Amino Acid

<400> 2244  
 Thr Thr Ser Ile Asp Asp Asn Thr Glu Val Asn Glu Phe Ile Xaa Leu  
   1                  5                  10                  15  
 Gly Leu Thr Lys Ala Pro Glu Leu Gln Val His Leu Phe Val Leu Phe  
                   20                  25                  30  
 Asn Phe Ile Tyr Leu Phe Thr Leu Ser Gly Asn Leu Gly Met Met Leu  
                   35                  40                  45  
 Leu Ile Leu Leu Asp Ser Arg Leu His Thr Ser Met Tyr Phe Phe Leu  
                   50                  55                  60  
 Ser Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Glu Thr Val Thr Pro

```

65      70      75      80
Lys Met Met Ala Gly Leu Leu Ile Ala His Lys Val Ile Ser Tyr Asn
      85      90      95
Val Cys Ala Ala Gln Met Phe Phe Phe Ala Val Phe Ala Thr Val Glu
      100      105      110
Ser Tyr Phe Leu Thr Ser Val Ala Tyr Asp Cys Tyr Arg Val Met Cys
      115      120      125
Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Ser
      130      135      140
Leu Ala Ile Ala Cys Tyr Val Leu Gly Leu Leu Thr Ala Ala Val Asp
145      150      155      160
Ile Gly Asp Ile Cys Met Ser Asn Glu Ile His His Phe Phe Cys Asp
      165      170      175
Ile Leu Ala Val Met Thr Leu Thr Cys Ser Asn Lys His Ile Asn Glu
      180      185      190
Leu Ile Leu Val Leu Leu Gln Ala Ile Phe Phe Thr Leu Leu Val Ile
      195      200      205
Leu Ile Ser Cys Leu Phe Val Phe Val Phe Val Thr Ile Leu Lys Met
      210      215      220
His Leu Phe Lys Ser Tyr Lys Lys Val Leu Ser Thr Tyr Gly Ser His
225      230      235      240
Leu Thr Ala Val Pro Leu Phe Tyr Glu Thr Val Leu Ile Thr Tyr Val
      245      250      255
Gln Pro Ser Ser Ser His Phe Met Asn Thr Glu Lys Ile Val Ser Val
      260      265      270
Phe His Ile Met Val Ile Pro Met Leu Ile Pro Val Val Tyr Ser Leu
      275      280      285
Arg Asn Asn Glu Val Lys Ser Ala Phe Lys Thr Val Val Glu Glu Thr
      290      295      300
Lys Tyr Phe Leu Gly Leu Val Phe
305      310

```

&lt;210&gt; 2245

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8131615-11-1-272)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(189)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2245

```

Ala Thr Lys Glu Leu Cys Phe Leu Gly Val Tyr Ile Pro Lys Gly Asp
1      5      10      15
Ala Cys Trp Lys Xaa Leu Xaa Leu Gly Leu His Leu Leu Leu Gly
      20      25      30
Xaa Gln Val Val Ser Met Val Gly Asn Leu Ala Leu Ile Ala Leu Ile
      35      40      45
Gly Xaa Asn Ser Tyr Leu His His Pro Gln Ala Leu Phe Ser Phe Thr
      50      55      60
Gln Ser Phe Pro Asp Leu Tyr Cys Pro Val Cys Thr Pro Arg Met Leu
65      70      75      80
Met Thr Phe Val Ser Lys Lys Asn Ile Phe Tyr Val Arg Cys Met Thr
      85      90      95
Gln Leu Ser Gln Leu Phe Phe Leu Phe Ile Val Leu Ser Ile Lys Tyr
      100      105      110
His Val Leu Met Phe Ile Ala Cys Gly Cys Leu Val Ala Ile Tyr Asn
      115      120      125
Pro Ser Leu His Glu Val Thr Met Ser Pro Gln Val Arg Glu Met Arg
130      135      140

```

Glu Ser Gly Phe Ala Gly Thr Thr Ala His Thr Gly His Ile Leu Arg  
 145 150 155 160  
 Pro Asn Leu Cys Asn Ile Asp Val Ile Asn His His Leu Thr Asp Ser  
 165 170 175  
 Leu Leu Val Leu Xaa Val Ser Cys Thr Ser Thr Cys Ala  
 180 185

<210> 2246

<211> 207

<212> PRT

<213> Homo sapien (8131622-1-12991-13959)

<220>

<221> VARIANT

<222> (1)...(207)

<223> Xaa = Any Amino Acid

<400> 2246

Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe  
 1 5 10 15  
 Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys  
 20 25 30  
 Asn Met Arg Leu Pro Ser Asp Phe Leu Ser Gln Ala Ile Tyr Tyr  
 35 40 45  
 Xaa Trp Ala Leu Met Cys Val Leu Glu Asn Lys Thr Tyr Ala Ser Val  
 50 55 60  
 Arg Leu Val Xaa Arg Phe Gly Trp Xaa Lys Leu Ala Asn Xaa Met Ser  
 65 70 75 80  
 Val Leu Tyr Leu Glu Ala Asn Leu Gly Asn Met Asp Asn Ala Leu Leu  
 85 90 95  
 Lys Xaa Leu Lys Arg Asn Tyr Phe Val Phe Val Phe Thr Ser Phe Leu  
 100 105 110  
 Phe Gly Cys Ile Ala Phe Lys Xaa Lys Glu Ile Phe Tyr Pro Tyr Thr  
 115 120 125  
 Ser Ile Cys Ile Tyr His Leu Leu Met Met Glu Arg Lys Val Ser Cys  
 130 135 140  
 Leu Thr Leu Ile Cys Leu Ala Xaa Asp Leu Xaa His Phe Xaa Cys Ser  
 145 150 155 160  
 Leu Val Thr Val Leu Ser Leu Glu Cys Xaa Gln Leu Asp Ile Cys Asn  
 165 170 175  
 Val Val Thr Tyr Phe Asn Thr Met Val Xaa Ser Thr Thr Gly Ser Asn  
 180 185 190  
 Ser Xaa Thr Pro Asn His Ser Val Leu Ile Cys Asn Met Leu Lys  
 195 200 205

<210> 2247

<211> 311

<212> PRT

<213> Homo sapien (8131622-11-1950-4442)

<400> 2247

Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu  
 1 5 10 15  
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe  
 20 25 30  
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val  
 35 40 45  
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro  
 65 70 75 80

Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val  
                             85                            90                            95  
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu  
                             100                            105                            110  
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys  
                             115                            120                            125  
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp  
                             130                            135                            140  
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln  
 145                            150                            155                            160  
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg  
                             165                            170                            175  
 His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp  
                             180                            185                            190  
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly  
                             195                            200                            205  
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile  
 210                            215                            220  
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Ser Pro Lys Ala Phe Asn  
 225                            230                            235                            240  
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly  
                             245                            250                            255  
 Ile Phe Val Tyr Leu Arg Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp  
                             260                            265                            270  
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro  
                             275                            280                            285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg  
 290                            295                            300  
 Leu Gln Lys Arg Lys Cys Cys  
 305                            310

&lt;210&gt; 2248

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8131622-13-5638-8129)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(444)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2248

Met Thr Val Glu Arg Ser Ser Met Thr Ile Thr Lys Phe Ile Leu Leu  
 1                            5                            10                            15  
 Gly Phe Ser Glu Tyr Ser Lys Thr Thr Ile Phe Leu Phe Ser Val Phe  
                             20                            25                            30  
 Leu Gly Ile Tyr Leu Leu Thr Met Ser Xaa Asn Val Ser Leu Ile Ala  
                             35                            40                            45  
 Leu Ile Arg Thr Asp Ser His Leu His Ala Pro Val Tyr Phe Phe Leu  
                             50                            55                            60  
 Ser Asn Pro Ser Phe Leu Asp Ile Cys Cys Val Ser Thr Ile Ala Pro  
 65                            70                            75                            80  
 Lys Met Pro Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met  
                             85                            90                            95  
 Gly Cys Thr Met Gln Tyr Phe Ser Ser Leu Asn Val Thr Glu Cys Cys  
                             100                            105                            110  
 Leu Leu Thr Ala Met Ala Tyr Asp Xaa Tyr Ala Ala Ile Cys Asp Pro  
                             115                            120                            125  
 Leu Leu Tyr Thr Ala Ile Met Ser Pro Ala Leu Cys Met Pro Met Val  
                             130                            135                            140  
 Ala Gly Ser Cys Thr Thr Gly Tyr Phe Val Ser Phe Ile Gln Leu Cys

145 150 155 160  
 Ala Leu Leu Leu Leu His Phe Cys Glu Ser Asn Ser Ser His Phe Phe  
 165 170 175  
 Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser His Thr Val Phe  
 180 185 190  
 Phe Phe Ser Ser His Asp His Tyr Ala His Ser Asn Leu Tyr Thr His  
 195 200 205  
 Leu Tyr Leu Gly Tyr His Asp Asn Leu Trp Leu Tyr His Cys Gln His  
 210 215 220  
 Ser Ser Leu Leu Trp Asp Ala Pro Cys Asn Thr Ser Ser Leu Ala Trp  
 225 230 235 240  
 Val Xaa Leu Ser Ala Val Phe Trp Lys Leu Trp Leu Ile Ile Asp Met  
 245 250 255  
 Leu Pro Phe Val Thr Leu Cys Ser Thr Trp Pro Ser Met Ser Pro Thr  
 260 265 270  
 Ser Val Cys Thr Xaa Trp Leu Glu Pro Val Xaa Leu Ser Leu Ala  
 275 280 285  
 His Leu Ser Asn Tyr Val Leu Cys Phe Ser Ser Ile Ser Val Gly Gln  
 290 295 300  
 Ile Val Asn His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser  
 305 310 315 320  
 Cys Tyr Asp Thr Phe Phe Cys Gln Val Met Thr Ser Met Leu Thr Val  
 325 330 335  
 Val Phe Gly Leu Thr Ser Val Leu Val Ile Met Ile Phe Tyr Gly Tyr  
 340 345 350  
 Val Ile Ala Thr Ile Leu Lys Ile Ile Ser Val Glu Gly Arg Ser Lys  
 355 360 365  
 Val Phe Asn Thr Gly Gly Ser His Leu Ile Ala Val Thr Leu Phe Tyr  
 370 375 380  
 Cys Ser Arg Ile Phe Val Tyr Met Cys Ser His Ser Asp Ala Ser Leu  
 385 390 395 400  
 Ser Arg Asn Lys Val Asp Ser Ile Val Tyr Thr Val Val Ile Pro Arg  
 405 410 415  
 Leu Asn Pro Leu Ile Tyr Ser Leu Ser Asp Lys Xaa Ile Lys Asp Ala  
 420 425 430  
 Leu Lys Arg Trp Thr Lys Arg Ile Phe Ser Trp Pro  
 435 440

&lt;210&gt; 2249

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8131671-12-1836-3192)

&lt;400&gt; 2249

Met Gly Val Lys Asn His Ser Thr Val Thr Glu Phe Leu Leu Ser Gly  
 1 5 10 15  
 Leu Thr Glu Gln Ala Glu Leu Gln Leu Pro Leu Phe Cys Leu Phe Leu  
 20 25 30  
 Gly Ile Tyr Thr Val Thr Val Val Gly Asn Leu Ser Met Ile Ser Ile  
 35 40 45  
 Ile Arg Leu Asn Arg Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
 50 55 60  
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Ser Gly Phe Leu Cys Arg Asp Arg Ser Ile Ser Tyr Ser Gly  
 85 90 95  
 Cys Met Ile Gln Leu Phe Phe Phe Cys Val Cys Val Ile Ser Glu Cys  
 100 105 110  
 Tyr Met Leu Ala Ala Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Ser  
 115 120 125  
 Pro Leu Leu Tyr Arg Val Ile Met Ser Pro Arg Val Cys Ser Leu Leu

130 135 140  
 Val Ala Ala Val Phe Ser Val Gly Phe Thr Asp Ala Val Ile His Gly  
 145 150 155 160  
 Gly Cys Ile Leu Arg Leu Ser Phe Cys Gly Ser Asn Ile Ile Lys His  
 165 170 175  
 Tyr Phe Cys Asp Ile Val Pro Leu Ile Lys Leu Ser Cys Ser Ser Thr  
 180 185 190  
 Tyr Ile Asp Glu Leu Leu Ile Phe Val Ile Gly Gly Phe Asn Met Val  
 195 200 205  
 Ala Thr Ser Leu Thr Ile Ile Ser Tyr Ala Phe Ile Leu Thr Ser  
 210 215 220  
 Ile Leu Arg Ile His Ser Lys Lys Gly Arg Cys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Thr Ala Val Leu Met Phe Tyr Gly Ser Leu Met  
 245 250 255  
 Ser Met Tyr Leu Lys Pro Ala Ser Ser Ser Leu Thr Gln Glu Lys  
 260 265 270  
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Leu Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Asn Glu Val Arg Asn Ala Leu Met Lys Leu  
 290 295 300  
 Leu Arg Arg Lys Ile Ser Leu Ser  
 305 310

&lt;210&gt; 2250

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8131682-2-1-1878)

&lt;400&gt; 2250

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly  
 20 25 30  
 Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile  
 35 40 45  
 Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Val Gly Asn  
 50 55 60  
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile  
 65 70 75 80  
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys  
 85 90 95  
 Leu Cys Gln Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr  
 100 105 110  
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro  
 115 120 125  
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val  
 130 135 140  
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys  
 145 150 155 160  
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe  
 165 170 175  
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly  
 180 185 190  
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys  
 195 200 205  
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val  
 210 215 220  
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys  
 225 230 235 240  
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr



245 250 255  
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile  
 260 265 270  
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu  
 290 295 300

Pro  
305

<210> 2251

<211> 306

<212> PRT

<213> Homo sapien (8131682-3-415-2331)

<400> 2251

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe  
 1 5 10 15  
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly  
 20 25 30  
 Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile  
 35 40 45  
 Cys Asn Asp Ser Arg Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn  
 50 55 60  
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val His Thr Pro Lys Ile  
 65 70 75 80  
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys  
 85 90 95  
 Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu  
 100 105 110  
 Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu  
 115 120 125  
 Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu  
 130 135 140  
 Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn  
 145 150 155 160  
 Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe  
 165 170 175  
 Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Val Arg Glu Ser  
 180 185 190  
 Tyr Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro  
 195 200 205  
 Thr Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu  
 210 215 220  
 Arg Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser  
 225 230 235 240  
 Ser His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn  
 245 250 255  
 Tyr Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val  
 260 265 270  
 Ser Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr  
 275 280 285  
 Ser Leu Arg Ser Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys  
 290 295 300  
 Ser Ala  
 305

<210> 2252

<211> 324

<212> PRT

<213> Homo sapien (8152118-1-59952-61847)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2252

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Arg Ser Glu Ser Pro Leu His Thr Thr Met Tyr Phe
          50           55           60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65           70           75           80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Lys Val Ile Ser
          85           90           95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
          115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
          210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
          245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
          260          265          270
Asn Gly Val Val Val Ser Val Lys Xaa Ala Val Val Thr Pro Met Pro
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Arg Arg Leu Pro Asn Lys Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310          315          320
Phe Phe Trp Cys

```

&lt;210&gt; 2253

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8247820-10-10207-11695)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(212)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2253

```

Thr Met Phe Tyr Lys Ile Ser Ala Leu Phe Xaa Cys Xaa Cys Ile Thr
 1          5          10          15
Leu Phe Xaa Xaa Lys Leu Ser Lys Gln Lys Ile Tyr Trp Val Leu Thr
      20          25          30
Ile Phe Gly Phe Leu Glu Ala Phe Ile Ala Met Asn Lys Leu Xaa Lys
      35          40          45
Leu Tyr Ser Ser Leu Ile Cys Leu Tyr Phe Ile Ile Xaa Ile Phe Lys
      50          55          60
Phe Ser Asn Met Phe Ile Phe Tyr Asn Met Asn Ile Ser Val His Tyr
65          70          75          80
Phe Leu Lys Cys Ile Phe Phe Phe Cys Ile Cys Cys Leu Xaa Leu Leu
      85          90          95
Ile Phe Asp Ser Phe Ser Thr His Pro Pro Leu Pro Leu Leu Xaa Glu
      100          105          110
Ala Asp Ile Cys Ala Asn Ser Xaa Pro Cys Tyr Thr Asn Thr Thr Ala
      115          120          125
Ser Xaa Xaa His Phe Tyr Ile Ile Leu Asn Phe Cys Leu Ser Tyr Xaa
      130          135          140
Pro Ser Val Ser Ser Met Leu Tyr Gly Arg Leu Phe Leu Met Tyr Leu
145          150          155          160
Met Pro Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe Tyr
      165          170          175
Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Trp Ser Pro Arg Asn
      180          185          190
Lys Asp Val Thr Ser Ala Leu Arg Lys Val Met Val Asn Arg Lys Gln
      195          200          205
Ala Leu Phe Cys
      210

```

&lt;210&gt; 2254

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8247820-11-34143-40656)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2254

```

Ile Xaa Met Ala Asp Arg Asn Val Thr Val Ile Thr Glu Phe Ile Leu
 1          5          10          15
Leu Gly Leu Thr Asp Asn Pro Glu Met Asn Val Val Leu Ser Val Leu
      20          25          30
Phe Leu Leu Ile Tyr Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile
      35          40          45
Ile Ile Ile Leu Ala Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe
      50          55          60
Leu Ser Gln Leu Ala Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile
65          70          75          80
Pro Lys Met Leu Val Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr
      85          90          95
His Gly Cys Leu Leu Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr
      100          105          110
Glu Cys Phe Leu Leu Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val
      115          120          125
Cys His Pro Leu His Tyr Lys Gly Leu Met Thr Pro Thr Phe Xaa Ile
      130          135          140
Tyr Leu Val Thr Val Ser Tyr Leu Leu Gly Ser Val Asn Ser Leu Thr
145          150          155          160
His Leu Ser Ser Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Val Ile

```

```

          165          170          175
Asn Arg Tyr Phe Cys Asp Ile Pro Leu Leu Phe Gln Leu Ser Cys Ser
          180          185          190
Asn Thr Gln His Ser Lys Ile Leu Phe Thr Val Leu Ser Gly Ala Thr
          195          200          205
Ser Val Thr Thr Phe Leu Ile Val Val Ser Ser Tyr Leu Val Ile Leu
          210          215          220
Leu Ile Val Leu Lys Ile His Ser Thr Arg Gly Arg Asn Lys Ala Ile
          225          230          235          240
Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Tyr Arg Thr
          245          250          255
Val Ile Phe Thr Tyr Leu Gly Ala Asn Pro Gly Tyr Ser Gln Asp Arg
          260          265          270
Pro Lys Ile Leu Pro Val Glu Cys Thr Leu Leu Leu Ser Ile Leu Asn
          275          280          285
Leu Leu Ile Tyr Ser Val Arg Asn Arg Glu Val Lys Glu Ala Ile Lys
          290          295          300
Ile Ile Ile Lys Arg Lys Ile Leu Pro Gln
          305          310

```

&lt;210&gt; 2255

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8247820-7-4578-5918)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(245)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2255

```

Met Ser Xaa Xaa Ile Phe Cys Leu Pro Lys Ile Ile Ile Thr Leu Leu
  1          5          10          15
Gln Xaa Glu Trp Asp Ala Leu Asn Leu Glu Thr Arg Val Phe Leu Glu
          20          25          30
Glu Asp Phe Pro Cys Gly Phe Ser Leu Trp Ile Val Arg Gln Leu Ser
          35          40          45
Phe Phe Leu Glu Ile Asn Xaa Phe Ala His Leu Lys Lys Xaa Cys Arg
          50          55          60
Lys His Thr Ser Thr Phe Ser Leu Ser Asn Leu Ala Phe Xaa Asp Phe
          65          70          75          80
Cys Tyr Ala Ser Val Ile Thr Ser Lys Met Phe Gly Ser Phe Leu Tyr
          85          90          95
Lys Gln Lys Lys Leu Thr Phe Asn Ala Leu Gly Cys Ser Leu Thr Phe
          100          105          110
Met Thr Thr Glu Cys Leu Leu Leu Ala Phe Met Ala Cys Asp Gln Tyr
          115          120          125
Leu Val Ile Cys Asn Pro Pro Leu Tyr Met Val Thr Met Ser Pro Pro
          130          135          140
Gln Gly Val Cys Ile Gln Leu Met Pro Ala Ser Tyr Ser Tyr Ser Phe
          145          150          155          160
Leu Met Thr Leu Ser His Tyr Leu Ser Ala Phe Arg Leu Pro Tyr Cys
          165          170          175
Pro Ser Val Ser Leu Met Phe Asn Gly Ser Leu Phe Leu Tyr Cys Thr
          180          185          190
Xaa Cys Ser Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe
          195          200          205
Tyr Thr Val Val Ile Pro Met Leu Ser Pro Leu Ile Trp Ser Leu Arg
          210          215          220
Asn Lys Asp Val Lys Asp Ala Leu Arg Lys Val Ile Val Asn Arg Asn
          225          230          235          240

```

Gln Ala Leu Phe Cys  
245

<210> 2256  
<211> 302  
<212> PRT  
<213> Homo sapien (8308370-1-1-2758)

<220>  
<221> VARIANT  
<222> (1)...(302)  
<223> Xaa = Any Amino Acid

<400> 2256  
Ile Arg Glu Thr His Ser His Val Pro Tyr Thr Ser Val Phe Leu Pro  
1 5 10 15  
Val Phe Tyr Thr Ala Val Phe Leu Thr Gly Val Leu Gly Asn Leu Val  
20 25 30  
Leu Met Gly Ala Leu His Phe Lys Pro Gly Ser Arg Arg Leu Ile Asp  
35 40 45  
Ile Phe Ile Ile Asn Leu Ala Ser Asp Phe Ile Val Ser Cys His  
50 55 60  
Ile Ala Ser Leu Gly Gly Xaa Arg Thr Ser Leu Gly Leu Trp Arg Thr  
65 70 75 80  
Gly Ser Phe Leu Cys Lys Gly Ser Ser Tyr Met Ile Ser Val Asn Met  
85 90 95  
His Cys Ser Val Leu Leu Leu Thr Cys Met Ser Val Asp Arg Tyr Leu  
100 105 110  
Ala Ile Val Trp Pro Val Val Ser Arg Lys Phe Arg Arg Thr Asp Cys  
115 120 125  
Ala Tyr Val Val Cys Ala Ser Ile Trp Phe Asn Leu Leu Pro Ala Gly  
130 135 140  
Val Ala Tyr Ser Ser Val Gln Gly Ala His Ala Val Asp Asp Lys Pro  
145 150 155 160  
Tyr Cys Ala Glu Lys Lys Ala Thr Pro Ile Lys Leu Ile Trp Ser Leu  
165 170 175  
Val Ala Leu Ile Phe Thr Phe Phe Val Pro Leu Leu Ser Ile Val Thr  
180 185 190  
Cys Tyr Cys Cys Ile Ala Arg Lys Leu Cys Ala His Tyr Gln Gln Ser  
195 200 205  
Gly Lys His Asn Lys Lys Leu Lys Lys Ser Ile Lys Ile Ile Phe Ile  
210 215 220  
Val Val Ala Ala Phe Leu Val Ser Trp Leu Pro Phe Asn Thr Phe Lys  
225 230 235 240  
Phe Leu Ala Ile Val Ser Gly Leu Arg Gln Glu His Tyr Leu Pro Ser  
245 250 255  
Ala Ile Leu Gln Leu Gly Met Glu Val Ser Gly Pro Leu Ala Phe Ala  
260 265 270  
Asn Ser Cys Val Asn Pro Phe Ile Tyr Tyr Ile Phe Asp Ser Tyr Ile  
275 280 285  
Arg Arg Ala Ile Val His Cys Leu Cys Pro Cys Leu Lys Asn  
290 295 300

<210> 2257  
<211> 336  
<212> PRT  
<213> Homo sapien (8318124-7-422-2124)

<220>  
<221> VARIANT  
<222> (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2257

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu  
 1 5 10 15  
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe  
 20 25 30  
 Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu  
 35 40 45  
 Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro  
 65 70 75 80  
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu  
 100 105 110  
 Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 His Pro Leu Tyr Arg Ser Ala Thr Leu Asn Pro Cys Phe Cys Gly Phe  
 130 135 140  
 Leu Asp Leu Leu Ser Phe Phe Phe Ser Leu Arg Leu Leu Asp Ser  
 145 150 155 160  
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val  
 165 170 175  
 Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala  
 180 185 190  
 Cys Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala  
 195 200 205  
 Val Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys  
 210 215 220  
 Met Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys  
 225 230 235 240  
 Ala Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr  
 245 250 255  
 Gly Thr Gly Phe Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro  
 260 265 270  
 Arg Lys Gly Ala Val Ala Ser Val Met Tyr Ser Val Val Thr Pro Met  
 275 280 285  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val  
 290 295 300  
 Leu Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile  
 305 310 315 320  
 Cys Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys  
 325 330 335

&lt;210&gt; 2258

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8348136-100-2086-3409)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2258

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu  
 1 5 10 15  
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu  
 20 25 30

Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile  
 35 40 45  
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr  
 65 70 75 80  
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser  
 85 90 95  
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys  
 100 105 110  
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys  
 130 135 140  
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu  
 145 150 155 160  
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser  
 165 170 175  
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp  
 180 185 190  
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe  
 195 200 205  
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser  
 210 215 220  
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile  
 245 250 255  
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val  
 260 265 270  
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu  
 290 295 300  
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser  
 305 310 315

&lt;210&gt; 2259

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8389427-13-4913-5701)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(186)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2259

Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu  
 1 5 10 15  
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser  
 20 25 30  
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn  
 35 40 45  
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val  
 50 55 60  
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr  
 65 70 75 80  
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp  
 85 90 95  
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly

```

      100      105      110
Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His
      115      120      125
Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr
      130      135      140
Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg
145      150      155      160
Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr
      165      170      175
Tyr Val Asn His Leu Leu Pro Phe Leu Leu
      180      185

```

&lt;210&gt; 2260

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8389428-12-1-2464)

&lt;400&gt; 2260

```

Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro
 1      5      10      15
Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr
      20      25      30
Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp
      35      40      45
Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu
      50      55      60
Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu
      65      70      75      80
Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu
      85      90      95
Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile
      100      105      110
Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu
      115      120      125
His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu
      130      135      140
Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu
      145      150      155      160
Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr
      165      170      175
Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile
      180      185      190
Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser
      195      200      205
Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu
      210      215      220
Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala
      225      230      235      240
Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met
      245      250      255
Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val
      260      265      270
Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr
      275      280      285
Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr
      290      295      300

```

&lt;210&gt; 2261

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8439748-1-6412-8052)



&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(275)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2261

```

Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
 1           5           10           15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20           25           30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35           40           45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
      50           55           60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
      65           70           75           80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85           90           95
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100          105          110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115          120          125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130          135          140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
      145          150          155          160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165          170          175
Cys Lys Leu Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180          185          190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195          200          205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210          215          220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
      225          230          235          240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245          250          255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260          265          270
Gln Tyr Ser
      275

```

&lt;210&gt; 2262

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8439748-5-3942-6516)

&lt;400&gt; 2262

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
      20           25           30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
      35           40           45
Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
      50           55           60
Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
      65           70           75           80
Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val

```

```
<210> 2263
<211> 320
<212> PRT
<213> Homo sapien (8439993-14-9565-12410)
```

1348

195	200	205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val		
210	215	220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys		
225	230	235
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe		
245	250	255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His		
260	265	270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser		
275	280	285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg		
290	295	300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe		
305	310	315
		320

&lt;210&gt; 2264

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8439993-17-12459-15729)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2264

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu		
1	5	10
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro		
20	25	30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile		
35	40	45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe		
50	55	60
Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val		
65	70	75
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe		
85	90	95
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met		
100	105	110
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile		
115	120	125
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr		
130	135	140
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro		
145	150	155
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile		
165	170	175
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly		
180	185	190
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile		
195	200	205
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile		
210	215	220
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe		
225	230	235
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro		
245	250	255
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro		
260	265	270

His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro  
 275 280 285  
 Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu  
 290 295 300  
 Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp  
 305 310 315 320  
 Ile Asn Leu Xaa Tyr Arg Ser Leu Asn  
 325

&lt;210&gt; 2265

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8439993-2-191-1624)

&lt;400&gt; 2265

Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr  
 1 5 10 15  
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His  
 20 25 30  
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val  
 35 40 45  
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His  
 50 55 60  
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu  
 65 70 75 80  
 Leu Thr Cys Thr Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe  
 85 90 95  
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe  
 100 105 110  
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala  
 115 120 125  
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr  
 130 135 140  
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg  
 145 150 155 160  
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro  
 165 170 175  
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser  
 180 185 190  
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly  
 195 200 205  
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser  
 210 215 220  
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser  
 225 230 235 240  
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala  
 245 250 255  
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg  
 260 265 270  
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn  
 275 280 285  
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val  
 290 295 300  
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp  
 305 310 315 320  
 Lys Gly Ala Gly

&lt;210&gt; 2266

&lt;211&gt; 312

&lt;212&gt; PRT

<213> Homo sapien (8516051-13-18887-21998)

<400> 2266

```

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1          5          10          15
Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
 20          25          30
Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35          40          45
Val Cys Leu Asp Ser Arg Leu His Thr Pro-Met Tyr His Phe Val Ser
 50          55          60
Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65          70          75          80
Met Leu Ala Asn Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85          90          95
Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100         105         110
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115         120         125
Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130         135         140
Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145         150         155         160
Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165         170         175
Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180         185         190
Ser Ile Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195         200         205
Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210         215         220
Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225         230         235         240
Cys Ala Ser His Phe Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245         250         255
Ser Met Tyr Val Gln Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260         265         270
Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275         280         285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln
 290         295         300
Leu Lys Arg Ile Gly Ile Leu Ala
 305         310

```

<210> 2267

<211> 289

<212> PRT

<213> Homo sapien (8516051-8-7333-8874)

<220>

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 2267

```

Leu Leu Phe Phe Ile Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1          5          10          15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
 20          25          30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
 35          40          45

```

Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu  
 50 55 60  
 Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe  
 65 70 75 80  
 Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met  
 85 90 95  
 Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr  
 100 105 110  
 Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly  
 115 120 125  
 Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe  
 130 135 140  
 Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile  
 145 150 155 160  
 Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val  
 165 170 175  
 Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val  
 180 185 190  
 Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser  
 195 200 205  
 Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala  
 210 215 220  
 Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe  
 225 230 235 240  
 Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe  
 245 250 255  
 Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu  
 260 265 270  
 Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr  
 275 280 285  
 His

&lt;210&gt; 2268

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8516144-1-909-1747)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(166)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2268

Met Tyr Thr Thr Leu Leu Met Ala Arg Leu Cys Leu Cys Ala Asp Asn  
 1 5 10 15  
 Val Ile Pro His Ser Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala  
 20 25 30  
 Leu Ser Asp Thr Arg Val Asn Glu Xaa Val Ile Phe Ile Met Gly Gly  
 35 40 45  
 Leu Ile Leu Val Ile Pro Ser Ile Leu Ile Leu Gly Ser Tyr Ala Arg  
 50 55 60  
 Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Cys Ile Cys Lys  
 65 70 75 80  
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr  
 85 90 95  
 Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr  
 100 105 110  
 Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met  
 115 120 125  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala

130                      135                      140  
 Leu Ser Arg Val Ile His Gln Lys Lys Thr Phe Phe Ser Leu Xaa Xaa  
 145                      150                      155                      160  
 Xaa His Leu Glu Leu Leu  
                          165

<210> 2269  
 <211> 540  
 <212> PRT  
 <213> Homo sapien (8516144-24-10674-13726)

<220>  
 <221> VARIANT  
 <222> (1)...(540)  
 <223> Xaa = Any Amino Acid

<400> 2269  
 Met Asp Leu Gly Asn Ser Gly Asn Asp Ser Val Val Thr Lys Phe Val  
 1                      5                      10                      15  
 Leu Leu Gly Leu Thr Glu Thr Ala Ala Leu Gln Pro Ile Leu Phe Val  
                          20                      25                      30  
 Ile Phe Leu Leu Ala Tyr Val Thr Thr Ile Gly Gly Thr Leu Ser Ile  
                          35                      40                      45  
 Leu Ala Ala Ile Leu Met Glu Thr Lys Leu His Ser Pro Met Tyr Phe  
                          50                      55                      60  
 Phe Leu Gly Asn Leu Ser Leu Pro Asp Val Gly Cys Val Ser Val Thr  
 65                      70                      75                      80  
 Val Pro Ala Met Leu Ser His Phe Ile Ser Asn Asp Arg Ser Ile Pro  
                          85                      90                      95  
 Tyr Lys Ala Cys Leu Ser Glu Leu Phe Phe Phe His Leu Leu Ala Gly  
                          100                      105                      110  
 Ala Asp Cys Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Leu Ala  
                          115                      120                      125  
 Ile Cys Gln Ser Leu Thr Tyr Ser Ser Arg Met Ser Trp Gly Ile Gln  
                          130                      135                      140  
 Gln Ala Leu Val Gly Met Ser Trp Val Phe Ser Phe Thr Asn Ala Leu  
 145                      150                      155                      160  
 Thr Gln Thr Val Ala Leu Ser Pro Leu Asn Phe Cys Gly Pro Asn Val  
                          165                      170                      175  
 Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Pro Phe Gln Leu Ser Cys  
                          180                      185                      190  
 Ser Ser Val His Leu Asn Gly Gln Leu Leu Phe Val Ala Ala Ala Phe  
                          195                      200                      205  
 Met Gly Val Ala Pro Leu Val Leu Ile Thr Val Ser Tyr Ala His Val  
                          210                      215                      220  
 Ala Ala Ala Val Leu Arg Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala  
 225                      230                      235                      240  
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly  
                          245                      250                      255  
 Thr Gly Val Phe Ser Tyr Thr Arg Leu Gly Ser Val Glu Ser Ser Asp  
                          260                      265                      270  
 Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Val Ile Ser Pro Met Leu  
                          275                      280                      285  
 Asn Pro Leu Ile Tyr Trp Thr Ser Leu Leu Asp Val Gly Cys Ile Ser  
                          290                      295                      300  
 His Cys Ser Ser Asp Ala Gly Val Ser Pro Gly Pro Pro Val Gln Ser  
 305                      310                      315                      320  
 Pro Tyr Ala Ala Cys Ser Ser Gln Leu Phe Phe Pro His Leu Leu Ala  
                          325                      330                      335  
 Gly Val Asp Cys His Leu Leu Ile Ala Met Ala Tyr Asp Arg Tyr Leu  
                          340                      345                      350

Ala Ile Cys Gln Leu Leu Thr Asn Ser Thr Arg Met Ser Cys Glu Val  
           355                          360                          365  
 Gln Gly Ala Leu Val Gly Ile Cys Cys Thr Val Ser Phe Ile Asn Ala  
           370                          375                          380  
 Leu Thr His Thr Val Ala Val Ser Ala Leu Asp Phe Cys Gly Pro Asn  
 385                          390                          395                          400  
 Val Val Asn His Phe Tyr Cys Asp Leu Pro Pro Leu Phe Gln Leu Ser  
                           405                          410                          415  
 Cys Ser Ser Ile His Leu Asn Gly Gln Leu Leu Leu Val Gly Ala Thr  
                           420                          425                          430  
 Phe Ile Gly Val Ile Pro Met Ile Phe Ile Ser Val Ser Tyr Ala His  
                           435                          440                          445  
 Val Thr Ala Ala Ile Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys  
                           450                          455                          460  
 Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Xaa Ile Phe Tyr  
 465                          470                          475                          480  
 Gly Thr Gly Phe Phe Ser Tyr Met Cys Leu Gly Ser Val Ser Ala Ser  
                           485                          490                          495  
 Asp Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Ile Leu Ser Pro Met  
                           500                          505                          510  
 Leu Asn Pro Val Ile Tyr Ser Leu Gln Asn Pro Asp Val Gln Gly Thr  
                           515                          520                          525  
 Leu Lys Arg Val Leu Thr Gly Lys Arg Pro Pro Ala  
                           530                          535                          540

<210> 2270  
 <211> 106  
 <212> PRT  
 <213> Homo sapien (8518017-12-460-1010)

<220>  
 <221> VARIANT  
 <222> (1)...(106)  
 <223> Xaa = Any Amino Acid

<400> 2270  
 Gln Leu Leu Ile Leu Ala Cys Ser Glu Ser Ser Leu Asn Ser Leu Tyr  
   1                          5                          10                          15  
 Ser Phe Ile His Ser Phe Phe Cys Ser Phe Leu Pro Asn Ser Gly Tyr  
           20                          25                          30  
 Leu Val Ser Gln Thr Asp Leu Val Pro Asp Leu Arg Glu Phe Arg Ile  
           35                          40                          45  
 Xaa Ser Arg Arg His Ile Arg Asn Trp Asn Val Met Gly Ala Met Ile  
           50                          55                          60  
 Leu Asn Val Cys Glu Ala Thr Gly Asn Gly Val Ala Leu Pro Ile Ser  
 65                          70                          75                          80  
 Lys Ala Ala Thr Pro Glu Ala Met Thr Gly Val Xaa Ser Glu His Asp  
                           85                          90                          95  
 Ile Ala Leu Leu Phe Trp Leu Leu Arg Leu  
                           100                          105

<210> 2271  
 <211> 223  
 <212> PRT  
 <213> Homo sapien (8546599-5-2194-2867)

<220>  
 <221> VARIANT  
 <222> (1)...(223)  
 <223> Xaa = Any Amino Acid



&lt;400&gt; 2271

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
 1           5           10           15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
          20           25           30
Leu Val Leu Phe Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
          35           40           45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
          50           55           60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
65           70           75           80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
          85           90           95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Arg Gly Lys Tyr Lys Ala
          115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
          165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
          180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
          195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
          210          215          220

```

&lt;210&gt; 2272

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8546616-1-110163-110999)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(120)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2272

```

Val Cys Ile Asn Ile Ser Xaa His His Xaa His Met Tyr Phe Xaa Leu
 1           5           10           15
Ser Tyr Gly Ser Phe Xaa Glu Leu Leu Val His Ser Ala Glu Leu Pro
          20           25           30
Ser Arg Ile Trp Arg Leu Lys Ser Ser Xaa Ser Cys Lys Ile Leu Ser
          35           40           45
Gly Tyr Ser Asn Glu Val Trp Phe His Cys Ile Phe Leu Cys Leu Leu
          50           55           60
Ser Lys Arg Leu Lys Xaa Ala His Ser Asp Lys Cys Gly Gln Val Ser
65           70           75           80
Leu Pro Leu His Pro Ser Leu Cys Leu Leu Leu Ser Leu Gly Asn Trp
          85           90           95
Cys Gly Lys Ser Leu Cys Pro Gly Met Ala Thr Leu Leu Val Ser Arg
          100          105          110
Leu Ile Gln Ser Ser Leu Cys Ser
          115          120

```

&lt;210&gt; 2273

&lt;211&gt; 260

&lt;212&gt; PRT

<213> Homo sapien (8547576-2-9950-11981)

<220>

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 2273

```

Val Leu Cys Val Ile Phe Cys Lys Xaa Asn His His Ile Ser Leu Leu
 1           5           10           15
Ser Phe Phe Glu Tyr Leu Met Thr Xaa Xaa Lys Lys Tyr Gly Ser Ile
      20           25           30
Cys Ser Thr Met Leu Val Ser Ile Arg Ile Lys Tyr Leu Glu Val Phe
      35           40           45
Ala Glu Asn Leu Phe Gly Ala Ala Glu Ile Ile Pro Leu Met Trp Met
 50           55           60
Val His Gly Cys Tyr Val Thr Val Cys Asn Tyr Met Thr Ile Val Asn
 65           70           75           80
Gln Tyr Arg Cys Ser His Leu Thr Gly Met Ala Trp Thr Glu Ser Phe
      85           90           95
Ile His Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr
      100          105          110
Asp Pro Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Phe Leu
      115          120          125
Lys Leu Leu Cys Met Gly Thr Thr Asn Thr Ile Gly Phe Phe Val Ala
      130          135          140
Ala Asn Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val
      145          150          155          160
Ser Xaa Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu
      165          170          175
Arg Cys Xaa Ser Leu Ser Thr Cys Ile Ser His Thr Thr Met Val Ile
      180          185          190
Leu Phe Phe Glu Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu
      195          200          205
Leu Pro Ile Asn Lys Ala Met Ala Val Phe His Thr Val Ile Asn Pro
      210          215          220
Met Leu Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser
      225          230          235          240
Ala Leu Arg Lys Val Trp Val Lys Arg Xaa Pro Glu Glu Arg Asn Asn
      245          250          255
Leu Asn Ile Arg
      260

```

<210> 2274

<211> 328

<212> PRT

<213> Homo sapien (8567470-5-1-1337)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> -2274

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
 1           5           10           15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
      20           25           30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
      35           40           45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys

```

50	55	60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys		
65	70	75
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly		80
	85	90
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu		95
	100	105
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys		110
	115	120
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe		125
	130	135
Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu		140
145	150	155
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile		160
	165	170
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys		175
	180	185
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe		190
	195	200
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val		205
	210	215
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe		220
225	230	235
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr		240
	245	250
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys		255
	260	265
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn		270
	275	280
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp		285
	290	295
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His		300
305	310	315
Leu Phe His Ser Phe Cys Arg Met		320
	325	

<210> 2275  
 <211> 310  
 <212> PRT  
 <213> Homo sapien (8567878-9-2833-5012)

<220>  
 <221> VARIANT  
 <222> (1)...(310)  
 <223> Xaa = Any Amino Acid

<400> 2275
Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
1 5 10 15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
20 25 30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
35 40 45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
50 55 60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ile Thr Pro Asn
65 70 75 80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
85 90 95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
100 105 110

Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met  
 130 135 140  
 Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala  
 145 150 155 160  
 Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn  
 165 170 175  
 Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn  
 180 185 190  
 His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe  
 195 200 205  
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val  
 210 215 220  
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala  
 225 230 235 240  
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Phe Tyr Gly  
 245 250 255  
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp  
 260 265 270  
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met  
 290 295 300  
 Glu Asn Leu Cys Leu Thr  
 305 310

&lt;210&gt; 2276

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8567902-2-5416-6914)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(358)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2276

Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro  
 1 5 10 15  
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala  
 20 25 30  
 Thr Asn Ala Thr Pro Pro Met Leu Val Asn Phe Val Phe Ser Lys Arg  
 35 40 45  
 Lys Thr Val Ser Phe Ile Gly Cys Phe Ile Gln Phe His Leu Phe Ile  
 50 55 60  
 Ala Leu Val Ile Thr Asp Tyr His Met Leu Thr Val Met Val Tyr Asp  
 65 70 75 80  
 His Tyr Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Ser  
 85 90 95  
 Arg Cys Val Cys Leu Cys Leu Thr Ala Ala Pro Tyr Ile Tyr Gly Ser  
 100 105 110  
 Ala Asn Gly Leu Val Gln Val Ile Leu Met Leu Cys Leu Phe Phe Cys  
 115 120 125  
 Glu Pro His Glu Ile Asn His Phe Phe Phe Phe Gly Glu Asn Ala Leu  
 130 135 140  
 Tyr Ala His Leu Ile Pro Leu Xaa Ile Phe Glu Trp Thr Val Gly Glu  
 145 150 155 160  
 Glu Gly Arg Asn Asn Ile Asn Gly Glu Asn Thr Thr Gln Lys Val Tyr  
 165 170 175  
 Thr Met Gly Glu Arg Asn Leu Leu Ile Gln Val Ser Ile Phe Leu Leu

```

      180      185      190
Trp His Ile Arg Ser Xaa Leu Phe Ser Gln Tyr Glu Ala Ser Pro Arg
      195      200      205
Ala Asp Ser Asp Val Lys Leu Glu Ile Asn His Phe Tyr Tyr Ala Glu
      210      215      220
Pro Pro Leu Leu Val Leu Ala Cys Leu Asp Thr Tyr Val Lys Glu Thr
      225      230      235      240
Ala Met Phe Met Val Ala Gly Ser Asn Leu Ile Cys Pro Leu Thr Ile
      245      250      255
Ile Phe Ile Ser Tyr Thr Phe Ile Phe Thr Asp Ile Leu His Ile Cys
      260      265      270
Thr Ala Glu Gly Arg Tyr Asn Ala Phe Ser Thr Cys Gly Ser Leu Val
      275      280      285
Thr Ala Val Thr Val Phe Gln Gly Thr Leu Phe His Met Cys Leu Arg
      290      295      300
Pro Pro Ser Glu Ala Ser Val Glu Gln Gly Lys Ile Val Ala Ala Phe
      305      310      315      320
Tyr Ile Phe Val Ser Pro Thr Leu Asn Pro Leu Ile Tyr Arg Leu Arg
      325      330      335
Asn Lys Asn Val Lys Arg Thr Ile Arg Glu Val Ile Gln Lys Lys Leu
      340      345      350
Phe Ala Lys Xaa Gly Arg
      355

```

&lt;210&gt; 2277

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8567902-4-4497-6890)

&lt;400&gt; 2277

```

Met Ser Asn Thr Asn Gly Ser Ala Ile Thr Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Thr Asp Cys Pro Glu Leu Gln Ser Leu Leu Phe Val Leu Phe Leu
      20      25      30
Val Val Tyr Leu Val Thr Leu Leu Gly Asn Leu Gly Met Ile Met Leu
      35      40      45
Met Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Asn Ala Thr Pro Gln
      65      70      75      80
Met Ser Thr Asn Ile Val Ser Glu Lys Thr Ile Ser Phe Ala Gly Cys
      85      90      95
Phe Thr Gln Cys Tyr Ile Phe Ile Ala Leu Leu Leu Thr Glu Phe Tyr
      100      105      110
Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr Asp Pro
      115      120      125
Leu Arg Tyr Ser Val Lys Thr Ser Arg Arg Val Cys Ile Cys Leu Ala
      130      135      140
Thr Phe Pro Tyr Val Tyr Gly Phe Ser Asp Gly Leu Phe Gln Ala Ile
      145      150      155      160
Leu Thr Phe Arg Leu Thr Phe Cys Arg Ser Ser Val Ile Asn His Phe
      165      170      175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ser Cys Ser Asp Thr Tyr
      180      185      190
Val Lys Glu His Ala Met Phe Ile Ser Ala Gly Phe Asn Leu Ser Ser
      195      200      205
Ser Leu Thr Ile Val Leu Val Ser Tyr Ala Phe Ile Leu Ala Ala Ile
      210      215      220
Leu Arg Ile Lys Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys
      225      230      235      240
Gly Ser His Met Met Ala Val Thr Leu Phe Tyr Gly Thr Leu Phe Cys

```

245 250 255  
 Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile  
 260 265 270  
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu  
 290 295 300  
 Arg  
 305

<210> 2278

<211> 319

<212> PRT

<213> Homo sapien (8567954-21-10804-13693)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2278

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly  
 1 5 10 15  
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala  
 20 25 30  
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala  
 35 40 45  
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala  
 50 55 60  
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys  
 65 70 75 80  
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg  
 85 90 95  
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys  
 100 105 110  
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser  
 115 120 125  
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val  
 130 135 140  
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu Leu His Val  
 145 150 155 160  
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln  
 165 170 175  
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met  
 180 185 190  
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile  
 195 200 205  
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr  
 245 250 255  
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala  
 260 265 270  
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val  
 275 280 285  
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu  
 290 295 300  
 Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr  
 305 310 315

<210> 2279  
 <211> 307  
 <212> PRT  
 <213> Homo sapien (8567954-21-4824-8043)

<400> 2279  
 Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys  
 1 5 10 15  
 Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr  
 20 25 30  
 Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr  
 35 40 45  
 Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala  
 50 55 60  
 Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly  
 65 70 75 80  
 Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser  
 85 90 95  
 Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe  
 100 105 110  
 Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
 115 120 125  
 Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met  
 130 135 140  
 Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile  
 145 150 155 160  
 Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys  
 165 170 175  
 Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn  
 180 185 190  
 Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe  
 195 200 205  
 Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg  
 210 215 220  
 Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser  
 225 230 235 240  
 His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr  
 245 250 255  
 Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala  
 260 265 270  
 Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser  
 275 280 285  
 Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe  
 290 295 300  
 Leu Lys His  
 305

<210> 2280  
 <211> 104  
 <212> PRT  
 <213> Homo sapien (8568141-22-12851-13662)

<220>  
 <221> VARIANT  
 <222> (1)...(104)  
 <223> Xaa = Any Amino Acid

<400> 2280  
 Leu Pro Pro Asn Ile Leu Cys Val Ile Ile Ser Tyr Ser Arg His Phe  
 1 5 10 15

Ser Lys Leu Leu Lys Ile Pro Asn Ile Arg Thr Gln Ile Gln Lys Phe  
                   20                  25                  30  
 Ser His Ile Ser Xaa Asn Leu Lys Lys Val Ser Val Leu Arg Leu Thr  
                   35                  40                  45  
 Trp Thr Arg Tyr Pro Ser Xaa Met Leu Pro Xaa Tyr Pro Ala Pro Thr  
                   50                  55                  60  
 Leu Thr Lys His Ile Pro Cys Gly Leu Val Thr Cys Leu Leu Gln Pro  
 65                  70                  75                  80  
 Arg Met Ser Cys Trp Arg Ala Arg Asn Ala Pro Ser Thr Cys Leu Ala  
                   85                  90                  95  
 Leu Thr Ala Lys His Ile Ser Ala  
                   100

&lt;210&gt; 2281

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8568143-10-1394-2684)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2281

Met Gly Pro Lys Asn Leu Thr Arg Val Leu Glu Phe Phe Leu Leu His  
   1                  5                  10                  15  
 Phe Leu Asp Asp Leu Glu Leu Gln Pro Phe Leu Ser Gly Cys Pro Xaa  
                   20                  25                  30  
 Thr Met His Leu Val Thr Val Leu Ala Asn Leu Leu Thr Ser Phe Xaa  
                   35                  40                  45  
 Leu Ser Ala Leu Pro His Leu His Asn Pro Met Asn Phe Asn Leu Ser  
                   50                  55                  60  
 Leu Ala Asp Ile Gly Phe Thr Pro Ala Thr Ile Ser Lys Ile Thr Val  
 65                  70                  75                  80  
 Asp Leu Gln Thr His Ser Arg Ile Ile Leu Tyr Met Ser Cys Leu Lys  
                   85                  90                  95  
 Xaa Met Ser Phe Lys Ile Ile Phe Gly Cys Leu His Asn Leu Leu Ile  
                   100                  105                  110  
 Thr Val Met Ala Tyr Asp Pro Phe Val Ala Thr Cys His Leu Leu Tyr  
                   115                  120                  125  
 Tyr Thr Val Ile Arg Asn Pro His Leu Cys Gly Leu Leu Leu Val  
                   130                  135                  140  
 Ser Leu Phe Ser Leu Ser Phe Phe Phe Leu Ile Ser Leu Leu Glu Thr  
 145                  150                  155                  160  
 Gln Leu Tyr Ser Leu Met Val Ser Gln Val Leu Cys Met Gln Asp Val  
                   165                  170                  175  
 Asp Ile Pro His Phe Phe Cys Asp Pro Ser Gln Phe Leu His Leu Ser  
                   180                  185                  190  
 Cys Ser Asp Thr Ala Thr Asn Asn Thr Leu Met His Phe Ile Gly Ala  
                   195                  200                  205  
 Ile Phe Cys Gly Pro Phe Ser Gly Ile Leu Tyr Cys Tyr Thr Gln Ile  
                   210                  215                  220  
 Met Phe Ser Ile Leu Ile Thr Leu Xaa Asn Val Gly Ser Ile Lys Gln  
 225                  230                  235                  240  
 Thr Phe Ser Thr His Arg Ser His Leu Ser Val Val Cys Leu Phe Tyr  
                   245                  250                  255  
 Gly Thr Gly Leu Gly Val Tyr Leu Ser Leu Ala Gly Ser Pro Ser Pro  
                   260                  265                  270  
 Arg Thr Gly Val Val Ala Ser Met Val Tyr Thr Thr Val Thr Leu Met  
                   275                  280                  285  
 Leu Asn Pro Val Ile His Ser Leu Arg Asn Arg Asp Ile Lys Asn Thr



290                      295                      300  
 Trp Trp Trp Leu Leu Ser Ile Thr Ala Trp Tyr Gln Tyr Leu Cys Tyr  
 305                      310                      315                      320  
 Pro Leu Trp Ser Val Val Arg Lys Asn Ser Lys Leu Lys  
                     325                      330

<210> 2282  
 <211> 157  
 <212> PRT  
 <213> Homo sapien (8568247-23-1134-2556)

<220>  
 <221> VARIANT  
 <222> (1)...(157)  
 <223> Xaa = Any Amino Acid

<400> 2282  
 Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met  
 1                      5                      10                      15  
 Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe  
                     20                      25                      30  
 Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg  
                     35                      40                      45  
 Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro  
                     50                      55                      60  
 Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu  
 65                      70                      75                      80  
 Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg  
                     85                      90                      95  
 Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His  
                     100                      105                      110  
 Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln  
                     115                      120                      125  
 Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu  
                     130                      135                      140  
 Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu  
 145                      150                      155

<210> 2283  
 <211> 91  
 <212> PRT  
 <213> Homo sapien (8568259-4-1499-2114)

<220>  
 <221> VARIANT  
 <222> (1)...(91)  
 <223> Xaa = Any Amino Acid

<400> 2283  
 Gln Glu Ile Ser Ala Ala Arg Glu Arg Lys Ala Thr Lys Ile Leu Gly  
 1                      5                      10                      15  
 Ile Ile Leu Gly Ala Phe Ile Ile Cys Trp Leu Pro Phe Phe Val Val  
                     20                      25                      30  
 Ser Leu Val Leu Pro Ile Cys Arg Asp Ser Cys Trp Ile His Pro Ala  
                     35                      40                      45  
 Leu Phe Asp Phe Phe Thr Trp Leu Gly Tyr Leu Asn Ser Leu Ile Asn  
                     50                      55                      60  
 Pro Ile Ile Tyr Thr Val Phe Asn Glu Glu Phe Arg Gln Ala Phe Gln  
 65                      70                      75                      80  
 Lys Ile Val Pro Phe Arg Lys Ala Ser Xaa Ser  
                     85                      90

<210> 2284  
 <211> 320  
 <212> PRT  
 <213> Homo sapien (8569904-8-5520-7957)

<400> 2284  
 Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln  
 1 5 10 15  
 Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu Leu  
 20 25 30  
 Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val  
 35 40 45  
 Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys  
 50 55 60  
 Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg  
 65 70 75 80  
 Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile  
 85 90 95  
 Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly  
 100 105 110  
 Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu  
 130 135 140  
 Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser  
 145 150 155 160  
 Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg  
 165 170 175  
 Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala  
 180 185 190  
 Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu  
 195 200 205  
 Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala  
 210 215 220  
 Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys  
 225 230 235 240  
 Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr  
 245 250 255  
 Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro  
 260 265 270  
 Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu  
 275 280 285  
 Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala  
 290 295 300  
 Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly  
 305 310 315 320

<210> 2285  
 <211> 130  
 <212> PRT  
 <213> Homo sapien (8569934-12-21632-22280)

<220>  
 <221> VARIANT  
 <222> (1)...(130)  
 <223> Xaa = Any Amino Acid

<400> 2285  
 Lys Val Cys Leu Phe Gln Ala Leu Met Cys Trp Leu Ser Leu Xaa Gln  
 1 5 10 15

Gln Pro Phe Thr Gln Ser Ala Ser Thr Leu Leu Leu Pro Leu Cys Ile  
                   20                  25                  30  
 Pro Arg Gln Ala Pro Gln Cys Pro Gly Asp Leu Arg Thr Ala Leu Arg  
           35                  40                  45  
 Ala Val Met Cys Thr Arg Gly Cys Val Phe Xaa Ala Trp Glu Trp Val  
           50                  55                  60  
 Ala Ser Tyr Ile His Leu Ile Pro Leu Cys Ile Pro Val Arg Ser Ala  
   65                  70                  75                  80  
 Tyr Asn Leu Gly Arg Val Leu Asn Gly Val Lys Trp Cys Ser Xaa Gly  
                   85                  90                  95  
 Gln Gln Val Glu Phe Cys Ser Cys Lys Ala Lys Leu Met Leu Leu Ala  
                   100                  105                  110  
 Ser Val Asp Val Val Leu Val Ser Thr Gln Pro Xaa Asn Pro Arg Pro  
           115                  120                  125  
 His Glu  
       130

&lt;210&gt; 2286

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8569993-13-6018-8083)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(318)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2286

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe  
   1                  5                  10                  15  
 Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser  
           20                  25                  30  
 Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser  
           35                  40                  45  
 Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr  
   50                  55                  60  
 Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr  
  65                  70                  75                  80  
 Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile  
                   85                  90                  95  
 Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser  
           100                  105                  110  
 Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile  
           115                  120                  125  
 Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val  
           130                  135                  140  
 Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val  
  145                  150                  155                  160  
 Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn  
                   165                  170                  175  
 Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr  
           180                  185                  190  
 Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile  
           195                  200                  205  
 Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu  
           210                  215                  220  
 Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg  
  225                  230                  235                  240  
 Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr  
                   245                  250                  255  
 Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala

```

      260      265      270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
      275      280      285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
      290      295      300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
305      310      315

```

<210> 2287  
 <211> 235  
 <212> PRT  
 <213> Homo sapien (8570235-22-3034-4808)

<220>  
 <221> VARIANT  
 <222> (1)...(235)  
 <223> Xaa = Any Amino Acid

```

<400> 2287
Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1      5      10      15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro
      20      25      30
Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val Tyr Val Leu
      35      40      45
Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg Val Tyr Ser
      50      55      60
His Leu His Thr Pro Lys Tyr Tyr Phe Leu Thr Asn Leu Ser Phe Ile
      65      70      75      80
Asp Leu Trp Phe Phe Thr Val Met Val Pro Lys Met Pro Arg Thr Leu
      85      90      95
Leu Ser Leu Cys Gly Lys Ala Val Ser Phe His Ser Cys Met Thr Gln
      100      105      110
Leu Tyr Phe Phe Tyr Phe Leu Gly Ser Thr Glu Cys Leu Leu Tyr Thr
      115      120      125
Val Met Ser Tyr Asp Arg Tyr Arg Gly Asn Thr Gln His Phe Pro Gly
      130      135      140
Ser Glu Asn Leu Pro Thr Lys Xaa Ala Lys Cys Xaa Trp Pro Gly Gly
      145      150      155      160
His Thr Gly Xaa Pro Leu Ile Ile Leu Ala Asp Leu Ser Gly Xaa Leu
      165      170      175
Arg Val Asp Ser Ser Xaa Trp Ala Ile Gln Asn Xaa Xaa Tyr Asn Leu
      180      185      190
Val Ile Gln Val Lys Phe Ile Thr Cys Ile Gly Leu Ser Ile Lys His
      195      200      205
Tyr Ser Lys Gln Leu Ala Gln Leu Xaa Phe Phe His Arg Leu Ser Lys
      210      215      220
Thr Phe Leu Asn Ser Gln Leu Asp Phe Tyr Leu
      225      230      235

```

<210> 2288  
 <211> 325  
 <212> PRT  
 <213> Homo sapien (8570522-1-103735-108559)

<220>  
 <221> VARIANT  
 <222> (1)...(325)  
 <223> Xaa = Any Amino Acid

<400> 2288

```

Met Lys Ile Asn Gln Thr Ile Leu Lys Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Ser Val Tyr Pro His Val Gln Thr Phe Leu Phe Val Val Phe Phe Cys
          20          25          30
Leu Tyr Leu Leu Thr Leu Ala Gly Asn Leu Thr Ile Met Gly Leu Thr
          35          40          45
Xaa Val Asp Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Ser Ala
 50          55          60
Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Thr Ile Val Pro Lys Met
 65          70          75          80
Leu Glu Asp Leu Leu Ala Lys Asp Arg Ser Ile Ser Val Thr Gly Cys
          85          90          95
Ser Leu Gln Met Cys Phe Phe Leu Gly Leu Gly Gly Thr Asn Cys Ile
          100          105          110
Ile Leu Thr Leu Met Gly Tyr Asp Arg Phe Leu Ala Ile Cys Asn Pro
          115          120          125
Leu Arg Tyr Pro Leu Leu Met Thr Asn Ile Val Cys Gly Gln Leu Val
          130          135          140
Ala Ser Ala Cys Thr Ala Gly Phe Phe Ile Ser Leu Thr Glu Thr Ala
 145          150          155          160
Leu Ile Phe Arg Asp Ser Phe Cys Arg Pro Asn Leu Val Lys His Phe
          165          170          175
Phe Cys His Met Leu Ala Val Ile Arg Leu Ser Cys Ile Asp Ser Asn
          180          185          190
His Thr Glu Phe Ile Ile Thr Leu Ile Ser Val Ser Gly Leu Leu Gly
          195          200          205
Thr Leu Leu Leu Ile Ile Leu Thr Asp Val Phe Ile Ile Ser Thr Val
          210          215          220
Leu Arg Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Thr Thr Cys
 225          230          235          240
Ala Ser His Leu Thr Val Val Ile Ile His Phe Gly Phe Ala Ser Ile
          245          250          255
Val Tyr Leu Lys Pro Glu Ala Ser Gly Asp Asp Thr Leu Ile Ala Val
          260          265          270
Pro Tyr Thr Val Ile Thr Pro Phe Leu Ser Pro Ile Ile Phe Ser Leu
          275          280          285
Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr
          290          295          300
Val Ala Leu Lys Lys Xaa Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu
 305          310          315          320
Gly Leu Asn Val Pro
          325

```

&lt;210&gt; 2289

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8570523-1-20584-21124)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(151)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2289

```

Cys Val Ser Xaa Gln Arg Ser Pro His Phe Leu Cys Ser Gly Asp Ser
 1          5          10          15
Val Phe Cys Leu Val His Ser Val Gly Cys Cys Thr Leu Leu Ser
          20          25          30
Gln Ser Leu Arg Leu Leu Ser Val Phe Leu Leu Ser Ser Cys Ala Ala
          35          40          45
Ser Trp Lys Lys Val His Ser Met Asn Leu Tyr Thr Pro Phe Cys Leu

```

```

      50              55              60
Ser Lys Trp Xaa Asn His Val Asn Asn Ala Phe Asn Leu Pro Ser Trp
65              70              75              80
Lys Lys Ser Lys Ser Val Val Thr Met Phe Xaa Gly Pro Ala Met Ile
      85              90              95
Thr Tyr Leu Arg Ser Asp Ser Xaa Tyr Asn Pro Thr Val Gly Lys Gln
      100              105              110
Leu Val Leu Phe Tyr Ser Ile Val Ser Ala Phe Ile Lys Pro Ile Ile
      115              120              125
Ser Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Ser Trp Lys Val Leu
      130              135              140
Arg Val Lys Gly Thr Ala Gln
145              150

```

<210> 2290  
 <211> 96  
 <212> PRT  
 <213> Homo sapien (8570526-1-82280-82723)

<220>  
 <221> VARIANT  
 <222> (1)...(96)  
 <223> Xaa = Any Amino Acid

```

<400> 2290
Ile Val Val Asp Tyr Leu Ile Ile Lys Ser Ser Ile Phe Pro Pro Ala
1              5              10              15
Asn Ser Asn Leu Phe Lys Leu Ile Arg Lys Ser Ile Pro Ile Leu Ala
      20              25              30
Cys Xaa Arg Val Met Met Asp Leu Gly Xaa Thr Gln Asn Val Ser Thr
      35              40              45
Ser Lys Xaa Gly Cys Val Asp Lys Glu Tyr Asn Cys Phe Ile Pro Phe
      50              55              60
Leu Ile Ala Trp His Leu Xaa His Arg Glu Xaa Arg Ile Ile Xaa Asp
65              70              75              80
Arg Ile Ser Ile Leu Val Xaa Lys Ala Leu Trp Met Lys Asn Lys Gly
      85              90              95

```

<210> 2291  
 <211> 162  
 <212> PRT  
 <213> Homo sapien (8575931-7-5387-5879)

<220>  
 <221> VARIANT  
 <222> (1)...(162)  
 <223> Xaa = Any Amino Acid

```

<400> 2291
Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu
1              5              10              15
Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr
      20              25              30
Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val
      35              40              45
Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met
      50              55              60
Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met
65              70              75              80
Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg
      85              90              95

```

Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr  
 100 105 110  
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu  
 115 120 125  
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser  
 130 135 140  
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr  
 145 150 155 160  
 Val Gln

&lt;210&gt; 2292

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8648586-17-1126-4850)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(264)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2292

Ala Cys Val Thr Phe Leu Val Glu Val Thr Val Met Pro Phe Ser Thr  
 1 5 10 15  
 Val Arg Phe Val Lys Ser Cys Trp Tyr Phe Gly Asp Ser Ser Cys Lys  
 20 25 30  
 Phe Asn Thr Trp Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His  
 35 40 45  
 Xaa Gly Cys Ile Ser Val Asp Arg Tyr Met Leu Val Ser Asp Leu Leu  
 50 55 60  
 Thr Tyr Pro Thr Lys Phe Thr Val Ser Val Leu Gly Ile Cys Met Val  
 65 70 75 80  
 Leu Cys Trp Phe Leu Phe Cys Pro Tyr Ser Phe Ser Ile Phe Asn Thr  
 85 90 95  
 Gly Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys  
 100 105 110  
 Val Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys  
 115 120 125  
 Phe Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser  
 130 135 140  
 Lys Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr  
 145 150 155 160  
 Ala Ser Gln Ala Gln Ser Ser Ser Glu Ser Tyr Lys Glu Arg Val Ala  
 165 170 175  
 Lys Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala  
 180 185 190  
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala  
 195 200 205  
 Tyr Met Asn Phe Ile Thr Pro Tyr Val Tyr Glu Ile Leu Val Trp  
 210 215 220  
 Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe  
 225 230 235 240  
 Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val  
 245 250 255  
 Leu Arg Thr Asp Ser Ser Thr Thr  
 260

&lt;210&gt; 2293

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8648858-36-1-1206)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(126)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2293

```

Leu Cys Met Leu Cys Trp Gln Trp Pro Ala Val Met Thr Asp Arg Thr
1          5          10          15
Ile Ala Thr Cys Lys Ser Arg His Phe Leu Phe Leu Ile Leu Val Leu
20          25          30
Thr Cys Ser Leu Ile Pro Ala Xaa Ala Trp Phe Thr Tyr Phe Phe Phe
35          40          45
Asn Ser Lys Ser Cys Val Val Leu Phe Gln His Ile His Phe Cys Leu
50          55          60
Leu Xaa Ile Pro Ser Asn Phe Tyr Cys Leu Xaa Thr Thr Ala Tyr Leu
65          70          75          80
Lys Xaa Leu Leu Asn Met Xaa Leu Lys His Xaa Ile Lys Xaa Thr Tyr
85          90          95
Ile Val Phe Leu Ala Val Arg Ile Leu Xaa Ala Phe Leu Ile Leu Ile
100         105         110
Cys Ile Met Asn Leu Gln Leu Arg Gln Cys Ala Thr His Phe
115         120         125

```

&lt;210&gt; 2294

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (8649180-1-4193-6564)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(183)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2294

```

Val Ile Met His Lys Lys Glu Cys Xaa Lys Lys Thr His Asn Ile Val
1          5          10          15
Phe Leu Leu Met Val Trp Glu Phe Phe Tyr Lys Phe Leu Val Phe Phe
20          25          30
Phe Phe Ser Leu His Xaa Cys Val Ser Ser Ile Ile Met Ser Val Tyr
35          40          45
Tyr Xaa Lys Ile Asn Ile Phe Ile Xaa Ile Glu Thr Lys Leu Leu Phe
50          55          60
His Ile Ser Arg Xaa Asp Arg Met Ile Arg Cys Ser Phe Gln Lys Asn
65          70          75          80
Tyr Leu Leu Asn His Asn Gly Leu Met Cys Arg Ser Lys Cys Gln Leu
85          90          95
Val Tyr Gln Thr Val Ser Asn Ser Leu Asn Tyr Phe Tyr Ile Thr Pro
100         105         110
Ile Xaa Leu Phe Gln Ile Val Val Tyr Lys Lys Tyr Lys Phe Leu His
115         120         125
Cys Ile Val Leu Asp Val Pro Ala Tyr Ile Asn Ile Leu Gly Cys Ile
130         135         140
Val Ser Phe Leu His Val Ile Cys Asn Val Xaa Leu Tyr Val Ile Asn
145         150         155         160
Lys Thr Xaa Asn Xaa Tyr Lys Ser Arg Phe Ser Thr Cys Leu Ser His
165         170         175
Ser Asp Ile Thr Asp Leu Phe
180

```

&lt;210&gt; 2295



&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapien (902315-1-1-472)

&lt;400&gt; 2295

```

Ile Cys His Pro Leu Gln Tyr Thr Ile Leu Met Asn Pro Glu Leu Cys
 1           5           10           15
Val Phe Met Thr Val Ala Ser Trp Thr Leu Gly Ser Leu Asp Gly Ile
      20           25           30
Ile Val Leu Ala Ala Val Leu Ser Phe Ser Tyr Cys Ser Ser Leu Glu
      35           40           45
Ile His His Phe Phe Cys Asp Val Ala Ala Leu Leu Pro Leu Ser Cys
      50           55           60
Thr Glu Thr Ser Ala Phe Glu Arg Leu Leu Val Ile Cys Cys Val Val
      65           70           75           80
Met Leu Ile Phe Pro Val Ser Val Ile Ile Leu Ser Tyr Ser His Val
      85           90           95
Leu Arg Ala Val Ile His Met Gly Ser Gly Glu Ser Arg Arg Lys Ala
      100          105          110
Phe Thr Thr Cys Ser Ser His Pro Ser Val Val Gly Leu Tyr Tyr Gly
      115          120          125
Ala Ala Met Phe Met Tyr Met Arg Pro Ala Ser Lys His Thr Pro Asp
      130          135          140
Gln Asp Lys Met Val Ser Ala Phe Tyr Thr Asn Pro Ala
      145          150          155

```

&lt;210&gt; 2296

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M1 4726083-1-12568-18197 3361-4335)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2296

```

Thr Met Trp Ser Asn Ile Ser Ala Ala Pro Phe Leu Leu Thr Gly Phe
 1           5           10           15
Pro Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala
      20           25           30
Ile Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile
      35           40           45
Lys Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met
      50           55           60
Leu Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val
      65           70           75           80
Met Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys
      85           90           95
Phe Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly
      100          105          110
Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro
      115          120          125
Leu His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Ile Ala Ile Gly
      130          135          140
Leu Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu
      145          150          155          160
Pro Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala
      165          170          175
Phe Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr
      180          185          190

```

Phe Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu  
 195 200 205  
 Asp Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val  
 210 215 220  
 Met Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys  
 225 230 235 240  
 Val Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly  
 245 250 255  
 Leu Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His  
 260 265 270  
 Ile Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro  
 275 280 285  
 Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Val Leu His  
 290 295 300  
 Leu Leu Ser Val Xaa Asp Asp Val Asn His Tyr Ile Ile Ile Gln Arg  
 305 310 315 320  
 Ser Leu Gly Met Phe  
 325

&lt;210&gt; 2297

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M2 4726083-1-175-4296 2476-1523)

&lt;400&gt; 2297

Leu Ser Ala Met Pro Ser Met Trp Leu Asn Ile Ser Ser Ser Pro Phe  
 1 5 10 15  
 Leu Leu Thr Gly Phe Pro Gly Leu Glu Lys Ala His His Leu Ile Ser  
 20 25 30  
 Leu Pro Leu Leu Met Ala Tyr Ile Ser Ile Leu Leu Gly Asn Gly Thr  
 35 40 45  
 Leu Leu Phe Leu Ile Lys Asp Asp His Asn Leu His Glu Pro Met Tyr  
 50 55 60  
 Tyr Phe Leu Gly Met Leu Ala Ala Thr Asp Leu Gly Val Thr Leu Thr  
 65 70 75 80  
 Thr Met Pro Thr Val Leu Ser Val Leu Trp Leu Asn His Arg Glu Ile  
 85 90 95  
 Gly His Gly Ala Cys Phe Ser Gln Ala Tyr Phe Ile His Thr Leu Ser  
 100 105 110  
 Ile Val Glu Ser Gly Val Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile  
 115 120 125  
 Ala Ile Arg Asn Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asp Thr Lys  
 130 135 140  
 Val Ile Lys Ile Gly Ile Gly Leu Val Met Arg Ala Gly Leu Ser Ile  
 145 150 155 160  
 Met Pro Ile Ile Ile Arg Leu His Trp Phe Pro Tyr Cys Arg Ser His  
 165 170 175  
 Val Leu Ser His Ala Phe Cys Leu His Gln Asp Val Ile Lys Leu Ala  
 180 185 190  
 Cys Ala Asp Ile Thr Phe Asn Arg Leu Tyr Pro Val Val Val Phe  
 195 200 205  
 Ala Met Val Leu Leu Asp Phe Leu Ile Ile Phe Phe Ser Tyr Val Leu  
 210 215 220  
 Ile Leu Lys Thr Val Met Gly Ile Ala Ser Thr Asp Glu Arg Ala Lys  
 225 230 235 240  
 Ala Leu Asn Thr Cys Val Ser His Ile Cys Cys Ile Leu Val Phe Tyr  
 245 250 255  
 Val Thr Val Val Gly Leu Thr Phe Ile His Arg Phe Gly Lys Asn Val  
 260 265 270  
 Pro His Val Val His Ile Thr Met Ser Tyr Ile Tyr Phe Leu Phe Pro  
 275 280 285

Pro Phe Met Asn Pro Val Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln  
 290 295 300  
 Ser Gly Leu Leu Arg Leu Phe Ser Leu Pro Cys Ser Lys Thr  
 305 310 315

<210> 2298

<211> 351

<212> PRT

<213> Mus musculus (M3 4726083-1-26023-28273 267-1318)

<220>

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 2298

Leu Ser Pro Ser Leu Lys Pro Ser Cys Asn Cys Asp Pro Thr Met Trp  
 1 5 10 15  
 Pro Asn Ser Ser Asp Ala Pro Phe Leu Leu Thr Gly Phe Leu Gly Leu  
 20 25 30  
 Glu Met Ile His His Trp Ile Ser Ile Pro Phe Phe Val Ile Tyr Phe  
 35 40 45  
 Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp Ser Asp  
 50 55 60  
 His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu Ala Ser  
 65 70 75 80  
 Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu Gly Val  
 85 90 95  
 Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe Ile Gln  
 100 105 110  
 Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val Leu Leu  
 115 120 125  
 Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu His Tyr  
 130 135 140  
 Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu Gly Ala  
 145 150 155 160  
 Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro Leu Phe  
 165 170 175  
 Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe Cys Leu  
 180 185 190  
 His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn Leu  
 195 200 205  
 Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp Ala Leu  
 210 215 220  
 Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met Gly Ile  
 225 230 235 240  
 Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val Ser His  
 245 250 255  
 Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu Thr Phe  
 260 265 270  
 Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile Thr Met  
 275 280 285  
 Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr  
 290 295 300  
 Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu Leu Ser  
 305 310 315 320  
 Lys His Ser Arg Thr Xaa Ile Leu Ile Ile Asp Ser Gln Val Leu Tyr  
 325 330 335  
 Tyr Phe Trp Pro Phe Ile Arg Asn Lys Ser Cys Leu Lys Xaa Tyr  
 340 345 350

<210> 2299  
 <211> 339  
 <212> PRT  
 <213> Mus musculus (M4 4761596-1-24347-28106 1259-2275)

<220>  
 <221> VARIANT  
 <222> (1)...(339)  
 <223> Xaa = Any Amino Acid

<400> 2299  
 Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val Trp Tyr Val  
 1 5 10 15  
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp Ile Ala Ile  
 20 25 30  
 Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn Val Leu Leu  
 35 40 45  
 Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser Thr Ala Thr  
 65 70 75 80  
 Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg Gly Ile Ser  
 85 90 95  
 Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe Ile Phe Val  
 100 105 110  
 Ala Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ser Ser Val Ile  
 130 135 140  
 Gly Lys Ile Gly Thr Ala Val Val Arg Ser Phe Leu Ile Cys Phe  
 145 150 155 160  
 Pro Phe Ile Phe Leu Val Tyr Arg Leu Leu Tyr Cys Gly Lys His Ile  
 165 170 175  
 Ile Pro His Ser Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys  
 180 185 190  
 Asp Asn Ile Thr Val Asn Ile Ile Tyr Gly Leu Thr Met Ala Leu Leu  
 195 200 205  
 Ser Thr Gly Leu Asp Ile Leu Leu Ile Ile Ile Ser Tyr Thr Met Ile  
 210 215 220  
 Leu Arg Thr Val Phe Gln Ile Pro Ser Trp Ala Ala Arg Tyr Lys Ala  
 225 230 235 240  
 Leu Asn Thr Cys Gly Ser His Ile Cys Val Ile Leu Leu Phe Tyr Thr  
 245 250 255  
 Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Gly Lys Thr Val  
 260 265 270  
 Pro Arg His Ile His Ile Leu Val Ala Asn Leu Tyr Val Val Val Pro  
 275 280 285  
 Pro Met Leu Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gln  
 290 295 300  
 Asp Arg Val Val Phe Leu Phe Ser Ser Val Ser Thr Cys Gln His Asp  
 305 310 315 320  
 Ser Arg Cys Xaa Arg Xaa His Ile Pro Lys Glu Asn Ser Phe Lys Cys  
 325 330 335  
 His Pro Cys

<210> 2300  
 <211> 344  
 <212> PRT  
 <213> Mus musculus (M5 4761596-1-36028-37764 563-1594)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(344)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2300

```

Ile Ser Glu Leu Thr Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro
 1          5          10          15
Ser Val Leu Thr Leu Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys
          20          25          30
Trp Ile Gly Ile Pro Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly
          35          40          45
Asn Ser Leu Ile Leu Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile
          50          55          60
Pro Met Tyr Ile Phe Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu
65          70          75          80
Ser Thr Cys Ile Leu Pro Lys Met Leu Gly Ile Phe Trp Phe His Met
          85          90          95
Pro Gln Ile Ser Phe Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His
          100          105          110
Ser Phe Gln Ala Thr Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp
          115          120          125
Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser
130          135          140
Pro Gln Leu Thr Thr Cys Leu Gly Ala Gly Ala Leu Leu Arg Ala Phe
145          150          155          160
Ile Leu Val Ser Pro Ser Ile Leu Leu Ile Lys Cys Arg Leu Lys Tyr
          165          170          175
Phe Arg Thr Thr Ile Ile Ser His Ser Tyr Cys Glu His Met Ala Ile
          180          185          190
Val Lys Leu Ala Ala Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu
          195          200          205
Leu Val Ala Phe Ala Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe
210          215          220
Ser Tyr Val Arg Ile Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu
225          230          235          240
Ala Arg Phe Lys Ala Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe
          245          250          255
Leu Gln Phe Tyr Leu Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe
          260          265          270
Gly Ala His Ile Pro Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr
          275          280          285
Leu Leu Val Pro Pro Phe Leu Asn Pro Ile Val Tyr Gly Val Lys Thr
          290          295          300
Lys Gln Ile Arg Asp Gln Val Leu Lys Met Leu Phe Ser Lys Lys Pro
305          310          315          320
Leu Val Ser Leu Ser Val Glu Lys Leu Cys Gly Phe Xaa Xaa Gln Leu
          325          330          335
Xaa Xaa Val Lys Leu Phe Ile Phe
          340

```

&lt;210&gt; 2301

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M6 4761596-1-45918-48570 619-1659)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(347)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2301

```

Thr Gly Arg Phe Ser Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro
 1          5          10          15
Ser Val Leu Thr Leu Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys
          20          25          30
Trp Ile Gly Ile Pro Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly
          35          40          45
Asn Ser Leu Ile Leu Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile
          50          55          60
Pro Met Tyr Ile Phe Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu
65          70          75          80
Ser Thr Cys Ile Leu Pro Lys Met Leu Gly Ile Phe Trp Phe His Met
          85          90          95
Pro Gln Ile Ser Phe Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His
          100          105          110
Ser Phe Gln Ala Thr Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp
          115          120          125
Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser
          130          135          140
Pro Gln Leu Thr Thr Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu
145          150          155          160
Ile Thr Thr Phe Pro Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr
          165          170          175
Phe Arg Thr Thr Ile Ile Ser His Ser Tyr Cys Glu His Met Ala Ile
          180          185          190
Val Lys Leu Ala Ala Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu
          195          200          205
Leu Val Ala Phe Ala Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe
          210          215          220
Ser Tyr Val Arg Ile Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu
225          230          235          240
Ala Arg Phe Lys Ala Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe
          245          250          255
Leu Gln Phe Tyr Leu Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe
          260          265          270
Gly Ala His Ile Pro Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr
          275          280          285
Leu Leu Val Pro Pro Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr
          290          295          300
Lys Gln Ile Arg Asp Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro
305          310          315          320
Leu Xaa Thr Ser Val Thr Arg Ser Val Glu Lys Leu Cys Gly Phe Xaa
          325          330          335
Leu Glu Leu Glu Xaa Val Lys Pro Xaa Ile Phe
          340          345

```

&lt;210&gt; 2302

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M7 5051393-1-104482-107691 2444-1393)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(351)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2302

```

Val Leu Cys Thr Thr Leu Ser Xaa Gln Ser His Ser Ser Asn Xaa Ile
 1          5          10          15
Gln Met Thr Met Val Asn Gln Ser Thr Pro Val Gly Phe Leu Leu Leu
          20          25          30

```

Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Phe Val Val Val  
           35                          40                          45  
 Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile Leu Leu  
           50                          55                          60  
 Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu  
           65                          70                          75                          80  
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys Val Pro  
                           85                          90                          95  
 Gln Met Leu Phe Asn Leu Trp Gly Pro Thr Lys Thr Ile Ser Phe Leu  
                           100                          105                          110  
 Gly Cys Ser Val Gln Leu Phe Ile Phe Met Leu Leu Gly Thr Thr Glu  
                           115                          120                          125  
 Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys  
                           130                          135                          140  
 Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Arg Gln  
                           145                          150                          155                          160  
 Leu Ala Gly Val Ala Trp Ala Ile Gly Leu Val Gln Ser Ile Val Gln  
                           165                          170                          175  
 Ile Pro Pro Thr Leu Thr Leu Pro Phe Cys Ser His Arg Gln Ile Asp  
                           180                          185                          190  
 Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp  
                           195                          200                          205  
 Thr Thr Phe Asn Glu Ile Gln Leu Ser Val Ala Gly Val Ile Phe Leu  
                           210                          215                          220  
 Leu Val Pro Leu Ser Leu Ile Ile Val Ser Tyr Gly Val Ile Ala Arg  
                           225                          230                          235                          240  
 Ala Val Leu Lys Thr Asn Ser Ser Lys Gly Arg Arg Lys Ala Phe Gly  
                           245                          250                          255  
 Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser Ser Val  
                           260                          265                          270  
 Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Ser  
                           275                          280                          285  
 Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Thr Leu Asn Pro  
                           290                          295                          300  
 Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe Trp Arg  
                           305                          310                          315                          320  
 Leu Leu Gly Lys Asp Ala Ala Ser Gly Arg Asn Xaa Gly Gln Ile Leu  
                           325                          330                          335  
 Val Xaa Phe Leu Asn Tyr Lys Val Ser Ser Xaa Tyr Val Tyr Cys  
                           340                          345                          350

&lt;210&gt; 2303

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M8 5051393-1-124150-125858 1430-472)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(320)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2303

Arg Leu Asp Thr Glu Ile Met Val Asn Gln Ser Ser Pro Val Val Phe  
   1                          5                          10                          15  
 Phe Leu Leu Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Phe  
           20                          25                          30  
 Val Val Val Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu  
           35                          40                          45  
 Ile Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu His Thr Pro Met Tyr  
           50                          55                          60  
 Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr

```

65          70          75          80
Cys Val Pro Gln Met Leu Phe Asn Leu Trp Gly Pro Glu Lys Thr Ile
      85          90          95
Ser Phe Leu Gly Cys Phe Val Xaa Leu Phe Ile Phe Met Ser Leu Gly
      100        105        110
Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val
      115        120        125
Ala Val Cys Gln Pro Leu His Tyr Ala Thr Val Ile Asn Pro Arg Leu
      130        135        140
Cys Gln Gln Leu Ala Gly Ile Ala Trp Ala Ile Gly Leu Val Gln Ser
145      150      155      160
Ile Val Gln Thr Pro Pro Thr Leu Lys Leu Pro Phe Cys Ser His Arg
      165        170        175
Gln Ile Asp Asn Phe Val Cys Glu Val Pro Ser Leu Ile Gln Leu Ser
      180        185        190
Cys Gly Asp Ile Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Ile
      195        200        205
Phe Ile Val Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala
      210        215        220
Ile Ala Arg Ala Val Leu Lys Ile Ser Ser Ala Lys Gly Arg Arg Lys
225      230      235      240
Ala Phe Gly Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr
      245        250        255
Ser Ser Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg
      260        265        270
Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ile
      275        280        285
Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala
290      295      300
Phe Trp Lys Leu Leu Arg Lys Asp Glu Asp Ser Glu Glu Ser Trp Arg
305      310      315      320

```

&lt;210&gt; 2304

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M9 5051393-1-149569-151395 1755-805)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2304

```

Pro Gln Ala Asn His Ser Ser Ala Glu Arg Phe Leu Leu Leu Gly Phe
1          5          10          15
Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val Leu Leu
      20          25          30
Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ala Ala Leu Val Leu Leu Ala
      35          40          45
Ile Arg Asp Pro Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Cys His
50      55      60
Leu Ala Leu Val Asp Val Gly Phe Thr Thr Ser Val Val Pro Pro Leu
65      70      75      80
Leu Ala Ser Leu Arg Gly Ser Met Leu Gln Leu Pro Arg Ala Gly Cys
      85          90          95
Met Ala Gln Leu Cys Ser Ser Leu Ala Leu Gly Ser Ala Glu Cys Val
      100        105        110
Leu Leu Ala Val Met Ala Leu Asp Arg Ala Ala Val Cys Asn Pro
      115        120        125
Leu Arg Tyr Thr Ser Leu Ala Ser Pro Leu Leu Cys Arg Thr Leu Ala
130      135      140

```



Gly Val Ser Trp Leu Gly Gly Leu Ala Asn Ser Ala Ala Gln Thr Ala  
 145 150 155 160  
 Leu Leu Ala Ala Arg Pro Leu Cys Ala Pro Arg Cys Leu Asp His Phe  
 165 170 175  
 Ile Cys Glu Leu Pro Ala Leu Leu Gln Leu Ala Cys Arg Gly Gly Arg  
 180 185 190  
 Ser Ala Thr Glu Arg Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu  
 195 200 205  
 Val Pro Ser Ala Val Ile Leu Ala Ser Tyr Ile Ala Val Gly Arg Ala  
 210 215 220  
 Val Trp Gly Met His Ser Ser Ser Gly Trp Arg Lys Ala Ala Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Thr  
 245 250 255  
 Tyr Thr Tyr Leu Gln Pro Thr His Ser Tyr Asn Gln Gly Arg Gly Lys  
 260 265 270  
 Phe Val Ser Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Ala Leu Arg Leu  
 290 295 300  
 Leu Arg Ser Leu Gly Arg Pro Xaa Val Gly Gln Xaa Lys  
 305 310 315

&lt;210&gt; 2305

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M10 5051393-1-39874-41685 1277-235)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(348)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2305

Val Leu Cys Thr Thr Leu Ser Xaa Gln Ser His Pro Ser Asn Xaa Ile  
 1 5 10 15  
 Gln Met Thr Met Val Asn Gln Ser Ser Pro Val Gly Phe Leu Leu Leu  
 20 25 30  
 Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Ile Val Val Val  
 35 40 45  
 Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile Leu Leu  
 50 55 60  
 Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu  
 65 70 75 80  
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys Val Pro  
 85 90 95  
 Gln Met Leu Phe Asn Leu Trp Gly Pro Ala Lys Thr Ile Ser Phe Leu  
 100 105 110  
 Gly Cys Phe Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu  
 115 120 125  
 Cys Ile Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys  
 130 135 140  
 Gln Pro Leu His Tyr Ala Thr Val Ile His Pro Arg Leu Cys Cys Gln  
 145 150 155 160  
 Leu Ala Ala Val Ala Cys Thr Ile Gly Leu Val Glu Ser Val Val Gln  
 165 170 175  
 Thr Pro Ser Thr Leu Arg Leu Pro Phe Cys Pro His His Gln Val Asp  
 180 185 190  
 Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Gly Asp  
 195 200 205  
 Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu

210	215	220
Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Ala Arg		
225	230	235
Ala Val Leu Arg Ile Ser Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly		
	245	250
Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser Ser Val		
	260	265
Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg Glu Arg Gly		
	275	280
Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro		
	290	295
Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe Arg Arg		
305	310	315
Leu Leu Trp Lys Glu Val Lys Pro Ser Xaa His Thr Leu Ser Lys Leu		
	325	330
Asn Gly Lys Ser Ala Cys Leu Val Gly Leu Ser Phe		
	340	345

&lt;210&gt; 2306

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M11 5051393-1-46409-49345 2458-1419)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(347)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2306

Cys Pro Lys Ser Thr Thr Ser Gly His Ile Glu Ser Cys Met Gly Gln		
1	5	10
Tyr Phe Gln Leu Asp Ser Xaa Gln Lys Gln Thr Met Val Asn Gln Ser		
	20	25
Ser Pro Val Gly Phe Leu Leu Leu Gly Phe Ser Glu His Pro Gln Leu		
	35	40
Glu Lys Val Leu Phe Val Ile Val Leu Cys Ser Tyr Leu Leu Thr Leu		
	50	55
Leu Gly Asn Thr Leu Ile Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu		
65	70	75
His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu		
	85	90
Cys Phe Thr Thr Thr Cys Val Pro Gln Met Leu Phe Asn Leu Trp Gly		
	100	105
Pro Ala Lys Thr Ile Ser Phe Leu Gly Cys Ser Val Gln Leu Phe Ile		
	115	120
Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ser		
	130	135
Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Val		
145	150	155
Ile His Pro Arg Leu Cys Trp Lys Leu Ala Ala Val Ala Trp Met Met		
	165	170
Gly Leu Leu Gln Ser Ile Val Gln Thr Pro Pro Thr Leu Lys Leu Pro		
	180	185
Phe Cys Pro His Arg Gln Ile Asp Asp Phe Leu Cys Glu Val Pro Ser		
	195	200
Leu Ile Arg Leu Ser Cys Gly Asp Thr Thr Phe Asn Glu Ile Gln Leu		
	210	215
Ala Val Ser Ser Val Ile Leu Val Val Val Pro Leu Ser Leu Ile Leu		
225	230	235
Val Ser Tyr Gly Ala Ile Ala Arg Ala Val Met Arg Ile Asn Ser Thr		
	245	250
		255

Glu Ala Trp Lys Lys Ala Leu Arg Thr Cys Ser Ser His Leu Ile Val  
                   260                  265                  270  
 Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro Lys  
                   275                  280                  285  
 Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala  
                   290                  295                  300  
 Val Gly Thr Pro Thr Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys  
 305                  310                  315                  320  
 Glu Val Lys Arg Ala Phe Trp Arg Leu Leu Gly Lys Asp Gly Asp Ser  
                   325                  330                  335  
 Lys Asn Thr Xaa Glu Ile Asn Ser Arg Arg Thr  
                   340                  345

&lt;210&gt; 2307

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M12 5051393-1-65471-67664 1437-460)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2307

Leu Asp Thr Glu Ile Met Val Asn Gln Ser Ser Pro Val Val Phe Phe  
 1                  5                  10                  15  
 Leu Leu Gly Phe Ser Glu His Pro Gln Leu Lys Lys Val Leu Phe Val  
                   20                  25                  30  
 Val Val Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile  
                   35                  40                  45  
 Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe  
                   50                  55                  60  
 Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys  
 65                  70                  75                  80  
 Val Pro Gln Met Leu Phe Asn Leu Trp Gly Pro Ala Lys Thr Ile Ser  
                   85                  90                  95  
 Phe Leu Gly Cys Phe Val Gln Leu Phe Ile Phe Met Ser Leu Gly Thr  
                   100                  105                  110  
 Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala  
                   115                  120                  125  
 Val Cys Gln Pro Leu His Tyr Ala Thr Lys Ile Asn Pro His Leu Cys  
                   130                  135                  140  
 Arg Gln Leu Ala Gly Ile Ala Trp Ala Ile Gly Leu Val Gln Ser Ile  
 145                  150                  155                  160  
 Val Gln Thr Pro Pro Thr Leu Lys Leu Pro Phe Cys Ser His Arg Gln  
                   165                  170                  175  
 Ile Asp Asn Phe Leu Cys Glu Val Pro Ser Leu Ile Gln Leu Ser Cys  
                   180                  185                  190  
 Gly Asp Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Ile Phe  
                   195                  200                  205  
 Ile Val Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile  
                   210                  215                  220  
 Ala Arg Ala Val Leu Lys Ile Ser Ser Ala Lys Gly Arg Arg Lys Ala  
 225                  230                  235                  240  
 Phe Gly Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser  
                   245                  250                  255  
 Ser Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg Glu  
                   260                  265                  270  
 Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Thr Leu  
                   275                  280                  285  
 Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe

290                      295                      300  
 Trp Lys Leu Leu Arg Lys Asp Glu Asp Ser Glu Glu Ser Xaa Arg Arg  
 305                      310                      315                      320  
 Asn Thr Xaa His Thr Phe  
                          325

&lt;210&gt; 2308

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M13 6143913-1-1-2867 848-3)

&lt;400&gt; 2308

Leu Ile Ile Tyr Cys Leu Phe Leu Ser Phe Pro Gly Ile Met Asp His  
 1                      5                      10                      15  
 Val Asn Tyr Thr Trp Thr Arg Thr Phe Ile Leu Ala Gly Phe Thr Thr  
                          20                      25                      30  
 Ser Gly Thr Leu Gln His Leu Ala Val Phe Gly Thr Leu Cys Ile Tyr  
                          35                      40                      45  
 Leu Leu Thr Leu Ala Gly Asn Leu Phe Ile Ile Val Leu Val Gln Ala  
                          50                      55                      60  
 Asp Ser Gly Leu Ser Thr Pro Met Tyr Phe Phe Ile Ser Val Leu Ser  
 65                      70                      75                      80  
 Phe Leu Glu Leu Trp Tyr Val Ser Thr Thr Val Pro Thr Leu Leu His  
                          85                      90                      95  
 Thr Leu Leu His Gly Pro Ser Pro Ile Pro Ser Ser Ala Cys Phe Val  
                          100                      105                      110  
 Gln Leu Tyr Val Phe His Ser Leu Gly Met Thr Glu Cys Tyr Leu Leu  
                          115                      120                      125  
 Gly Val Met Ala Leu Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His  
                          130                      135                      140  
 Tyr His Ala Leu Met Ser Arg Gln Val Gln Lys Gln Leu Val Gly Val  
 145                      150                      155                      160  
 Thr Trp Leu Ala Gly Phe Ser Ala Ala Leu Val Pro Ala Gly Leu Thr  
                          165                      170                      175  
 Ala Ser Leu Pro Tyr Cys Leu Lys Glu Val Ala His Tyr Phe Cys Asp  
                          180                      185                      190  
 Leu Ala Pro Val Met Gln Leu Ala Cys Val Asp Thr Ser Trp His Ala  
                          195                      200                      205  
 Arg Leu Tyr Ile Ala Val Ile Gly Met Ile Asn Thr Cys Asn Leu Thr  
                          210                      215                      220  
 Phe Ile Leu Gly Leu Tyr Gly Gly Ile Val Arg Ala Val Leu Lys Leu  
 225                      230                      235                      240  
 Pro Ser Ala Ala Ser Arg Ala Lys Ala Phe Ser Thr Cys Ser Ser His  
                          245                      250                      255  
 Ile Thr Val Val Thr Leu Phe Phe Gly Ser Ala Phe Ile Val Tyr Val  
                          260                      265                      270  
 Gly Pro Pro Glu Ile Arg Ala Glu Gly Arg  
                          275                      280

&lt;210&gt; 2309

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M14 6143913-1-6180-10825 2950-1952)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2310

Leu Leu Leu Gly Thr Met Asp His Val Asn Tyr Thr Trp Thr Arg Thr

```

1           5           10           15
Phe Ile Leu Ala Gly Phe Thr Thr Ser Gly Ala Leu Arg Pro Leu Ala
20           25           30
Phe Leu Gly Thr Leu Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Leu
35           40           45
Phe Ile Ile Val Leu Val Gln Ala Asp Ser Gly Leu Ser Thr Pro Met
50           55           60
Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Leu Trp Tyr Val Ser
65           70           75           80
Thr Thr Val Pro Thr Leu Leu His Thr Leu Leu His Gly His Ser Pro
85           90           95
Ile Pro Ser Ser Ala Cys Phe Val Gln Leu Tyr Val Phe His Ser Leu
100          105          110
Gly Met Thr Glu Cys Tyr Leu Leu Gly Val Met Ala Leu Asp Arg Tyr
115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr His Ala Leu Met Ser Lys Gln
130          135          140
Val Gln Leu Trp Leu Ala Gly Ala Thr Trp Val Ala Gly Phe Ser Ala
145          150          155          160
Ala Leu Val Pro Ala Cys Leu Thr Ala Ser Leu Pro Tyr Cys Leu Lys
165          170          175
Glu Ile Ala His Tyr Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala
180          185          190
Cys Val Ser Thr Arg Trp His Ala Arg Val His Gly Ala Val Ile Gly
195          200          205
Val Ala Thr Gly Cys Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly
210          215          220
Ile Leu Thr Ala Val Leu Lys Leu Pro Ser Ala Ala Ser Arg Ala Lys
225          230          235          240
Ala Phe Ser Thr Cys Ser Ser His Met Thr Val Val Ala Leu Phe Tyr
245          250          255
Ala Ser Ala Phe Thr Val Tyr Val Gly Ser Pro Gln Ser Arg Pro Glu
260          265          270
Gly Thr Asp Lys Leu Ile Ala Leu Val Tyr Ala Leu Leu Thr Pro Phe
275          280          285
Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
290          295          300
Val Lys Arg Val Ser Glu Lys Ile Arg Thr Leu Leu Arg Asp Thr Xaa
305          310          315          320
Leu Ser Leu Leu Thr Leu Pro Thr Phe Arg Val Asn Ala
325          330

```

&lt;210&gt; 2311

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M15 6143913-1-66312-67763 687-330)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(120)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2311

```

Val Thr Val Gly His Cys Leu Gly Gln Met Ser Leu Ser Val Asp Thr
1           5           10           15
Asp Phe Leu Ile Glu Phe Phe Cys Leu Lys Arg Lys Glu Lys Lys Arg
20           25           30
Lys Lys Lys Asp Cys Ser Pro Leu Tyr Leu Asp Ser Xaa Phe Gln Ser
35           40           45
His Glu Ile Thr Gly Ser Phe Ser Phe Ser Val Phe His Arg Ser Leu
50           55           60

```

Leu Ser Asn Ile Ser Leu Gln Met Met Ala Tyr Phe Gln Ile Thr Leu  
 65 70 75 80  
 Pro Ser Thr Phe Cys Ile Pro Xaa Gln Arg Ser Gln Thr Ser Ala Cys  
 85 90 95  
 Ile Tyr Val Leu Asn Asn Leu Leu Ser Leu Phe His Ser Leu Ile Ser  
 100 105 110  
 Ser Leu Xaa Pro Thr Ala Ser Thr  
 115 120

&lt;210&gt; 2312

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M16 6456795-1-106495-108409 847-1815)

&lt;400&gt; 2312

Leu Ser Ser Tyr Gln Phe Leu Leu Glu Lys Lys Arg Pro Ile Met Asn  
 1 5 10 15  
 Cys Ser Lys Thr Pro Gly Phe Ile Leu Leu Gly Leu Ser Ser Asp Pro  
 20 25 30  
 Glu Lys Trp Gln Pro Leu Phe Asn Ile Phe Leu Cys Leu Tyr Leu Leu  
 35 40 45  
 Gly Leu Leu Gly Asn Leu Leu Leu Leu Ala Ile Gly Thr Asp Val  
 50 55 60  
 His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu Val  
 65 70 75 80  
 Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro Lys Met Leu Glu Ala Leu  
 85 90 95  
 Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser Gly Cys Leu Thr Gln Phe  
 100 105 110  
 Tyr Phe Phe Ala Val Phe Ala Asp Met Asp Asn Leu Leu Ala Val  
 115 120 125  
 Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Phe Tyr Pro  
 130 135 140  
 Phe Leu Met Thr Pro Cys Arg Cys Glu Val Leu Ala Ser Gly Ser Trp  
 145 150 155 160  
 Gly Ile Ala His Cys Val Ser Leu Phe Tyr Thr Leu Leu Leu Ser Gln  
 165 170 175  
 Phe Tyr Tyr His Thr Asn Gln Gly Ile Pro His Phe Phe Cys Asp Ser  
 180 185 190  
 Arg Pro Leu Leu Leu Leu Ser Cys Ser Asp Thr His Leu Ser Glu Gly  
 195 200 205  
 Leu Met Met Ala Leu Ser Gly Val Leu Gly Met Ser Ser Val Leu Cys  
 210 215 220  
 Leu Val Ser Ser Tyr Gly Cys Ile Phe Tyr Ala Val Ala Arg Val Pro  
 225 230 235 240  
 Ser Ala Gln Gly Lys Arg Lys Ser Leu Ala Thr Cys Ser Ser His Leu  
 245 250 255  
 Ser Val Val Leu Leu Phe Tyr Ser Thr Val Phe Ala Thr Tyr Leu Lys  
 260 265 270  
 Pro Pro Ser Thr Ser His Ser Ser Ala Glu Val Val Ala Ala Val Met  
 275 280 285  
 Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Ser Leu Arg  
 290 295 300  
 Asn Lys Asp Val Lys Ser Ser Leu Arg Lys Ile Leu Asn Met Asp Lys  
 305 310 315 320  
 Phe Gln Gly

&lt;210&gt; 2313

&lt;211&gt; 284

&lt;212&gt; PRT

<213> Mus musculus (M17 6456795-1-108765-110526 1744-894)

<220>

<221> VARIANT

<222> (1)...(284)

<223> Xaa = Any Amino Acid

<400> 2313

```

Cys Ile Tyr Ile Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val
1      5      10      15
Cys Ile Ser Ile Cys Thr Tyr Leu His Ile Xaa Ile His Met Cys Val
20      25      30
Gln Val Val Ile Lys Leu Lys Val Lys Xaa Val Thr Trp Lys Glu Val
35      40      45
Xaa Lys Met Ser Val Glu Lys Arg Thr Gln Ser Arg Gln Lys Ser Gly
50      55      60
Tyr Leu Ala Asn Cys Phe Leu Gln Ser Phe Ile Leu Gly Ser Val Asp
65      70      75      80
Arg Asn Ile Cys Leu Leu Ile Val Met Val Tyr Asp His Tyr Leu Thr
85      90      95
Ile Cys His His Leu Xaa Tyr Pro Phe Leu Met Gly Pro Leu Trp Gly
100     105     110
Leu Gly Phe Gly Leu Thr Thr Ser Phe Val Val Asp Glu Leu Ile Val
115     120     125
Ala Leu Met Ala Gln Leu Arg Phe Cys Val Pro Lys Gln Ile Asp His
130     135     140
Phe Tyr Tyr Asp Phe Ser Pro Leu Val Val Leu Ala Tyr Thr Asp Thr
145     150     155     160
Gly Leu Val Gln Val Thr Thr Phe Val Leu Phe Val Val Phe Leu Thr
165     170     175
Val Pro Phe Gly Leu Val Leu Ile Ser Cys Ala Gln Ile Ala Val Thr
180     185     190
Val Leu Arg Val Pro Ser Arg Thr Arg Arg Asn Lys Ala Phe Ser Thr
195     200     205
Cys Ser Ser His Leu Asp Glu Val Ser Thr Phe Tyr Gly Ser Leu Met
210     215     220
Val Trp Tyr Thr Glu Pro Ser Ala Val His Ser Gln Ile Leu Ser Lys
225     230     235     240
Val Ile Ala Leu Leu Tyr Thr Val Val Thr Thr Ile Phe Asp Pro Gly
245     250     255
Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ser Leu Arg Arg His
260     265     270
Leu Tyr Cys Lys Pro Thr Glu Met Xaa Pro Lys Arg
275     280

```

<210> 2314

<211> 312

<212> PRT

<213> Mus musculus (M18 6456795-1-142088-143512 370-1305)

<400> 2314

```

Ile Ser Pro Arg Met Asn Cys Ser Gln Ala Pro Gly Phe Ile Leu Leu
1      5      10      15
Gly Leu Pro Arg Glu Pro Glu Lys Trp Gln His Phe Phe Ile Ile Phe
20      25      30
Leu Gly Leu Tyr Leu Leu Gly Leu Leu Gly Asn Leu Leu Leu Leu
35      40      45
Ala Ile Gly Ser Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
50      55      60
Ser Gln Leu Ser Leu Val Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro
65      70      75      80

```

Lys Thr Leu Glu Thr Trp Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser  
                             85                            90                            95  
 Gly Cys Leu Thr Gln Leu Tyr Phe Phe Gly Val Phe Ala Asp Met Asp  
                             100                            105                            110  
 Asn Leu Leu Leu Ala Val Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys  
                             115                            120                            125  
 His Pro Leu Leu Tyr Pro Leu Leu Met Thr Pro Cys Arg Cys Glu Val  
                             130                            135                            140  
 Leu Val Ser Gly Ser Trp Gly Ile Ala His Cys Val Ser Leu Met Tyr  
 145                            150                            155                            160  
 Thr Leu Leu Leu Ser Gln Leu Tyr Phe His Thr Asn Gln Glu Ile Pro  
                             165                            170                            175  
 Arg Phe Phe Cys Asp Cys Arg Pro Leu Leu Leu Leu Ser Cys Ser Asp  
                             180                            185                            190  
 Thr His Leu Asn Glu Val Leu Met Met Ala Leu Ala Gly Val Leu Gly  
                             195                            200                            205  
 Val Ser Ala Val Leu Cys Ile Val Ser Ser Tyr Gly Cys Ile Phe Tyr  
                             210                            215                            220  
 Ala Val Ala Arg Val Pro Ser Ala Gln Gly Lys Arg Lys Ala Leu Thr  
 225                            230                            235                            240  
 Thr Cys Ser Ser His Leu Ser Val Val Leu Phe Tyr Ser Thr Val  
                             245                            250                            255  
 Phe Ala Thr Tyr Leu Lys Pro Pro Ser Thr Ser His Ser Ser Gly Glu  
                             260                            265                            270  
 Val Val Ala Ala Val Met Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro  
                             275                            280                            285  
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Ser Leu Arg Arg  
                             290                            295                            300  
 Val Leu Asn Ile Glu Lys Ser Gln  
 305                            310

&lt;210&gt; 2315

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M19 6456795-1-14626-16881 1501-527)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2315

Cys Pro Phe Leu Xaa Val Met Ser Asn Gln Thr Ser Val Thr Glu Phe  
   1                            5                            10                            15  
 Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe  
                             20                            25                            30  
 Val Ile Phe Phe Thr Ile Tyr Phe Val Asn Ile Thr Gly Asn Gly Ala  
                             35                            40                            45  
 Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr  
                             50                            55                            60  
 Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val  
 65                            70                            75                            80  
 Thr Leu Pro Lys Met Leu Gln Asn Leu Leu Ser Thr Asn Lys Ala Ile  
                             85                            90                            95  
 Ser Phe Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly  
                             100                            105                            110  
 Ser Thr Glu Ala Met Leu Leu Pro Val Met Ala Phe Asp Arg Phe Val  
                             115                            120                            125  
 Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn His Gln Leu  
                             130                            135                            140  
 Cys Ile His Met Thr Val Thr Ile Trp Thr Leu Gly Phe Phe His Ala



```

145          150          155          160
Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Pro Asn
          165          170          175
His Val His His Phe Phe Cys Asp Ile Lys Pro Leu Leu Asp Leu Ala
          180          185          190
Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Gly
          195          200          205
Thr Ile Ala Leu Thr Pro Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr
          210          215          220
Ile Ile Thr Tyr Leu Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His
225          230          235          240
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Ile Leu Leu
          245          250          255
Tyr Val Pro Val Leu Phe Thr Tyr Ile Arg Pro Ala Ser Gly Ser Ser
          260          265          270
Leu Asp Gln Asp Arg Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro
          275          280          285
Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser
          290          295          300
Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Xaa Phe Glu Glu Ile Xaa
305          310          315          320
Ile Thr Leu Leu Trp
          325

```

&lt;210&gt; 2316

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M20 6456795-1-147325-149242 1694-983)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(237)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2316

```

Leu Xaa Thr Tyr Ile Pro Thr His Thr His Thr His Thr His
1          5          10          15
Thr His Thr His Ile Tyr Ile Cys Asn Tyr Asn Val Gln Arg Asn Asn
          20          25          30
Gly Tyr Gln Val Asp His Tyr Leu Xaa Ile Cys His Pro Leu His Tyr
          35          40          45
Pro Leu Leu Met Gly His Gln Trp Cys Leu Gly Phe Val Leu Thr Leu
          50          55          60
Gln Leu Phe Gly Ile Thr Val Asp Gly Leu Val Val Ile Leu Val Ala
65          70          75          80
Gln Met Trp Phe Cys Gly Pro Asn Leu Ile Asp Tyr Phe Xaa Tyr Asn
          85          90          95
Phe Ser Pro Ile Met Asp Leu Ala Xaa Ser Asp Thr Gln Val Phe Gln
          100          105          110
Val Ile Thr Phe Val Leu Ser Val Val Phe Leu Thr Val Pro Phe Gly
          115          120          125
Leu Val Leu Ile Ser Tyr Ile Gln Ile Val Val Thr Val Leu Arg Val
          130          135          140
Leu Ser Gly Asp Arg Arg Thr Lys Asp Phe Ser Thr Cys Ser Ser His
145          150          155          160
Leu Ala Val Val Ser Thr Phe Tyr Arg Ser Leu Met Val Leu Tyr Thr
          165          170          175
Val Pro Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Lys Val Val
          180          185          190
Ile Pro Ile Phe Asn His Val Ile Tyr Thr Leu Arg Asn Gln Glu Val
          195          200          205

```

Pro Xaa Ala Leu Arg Arg His Leu Tyr Cys Lys Pro Thr Glu Met Xaa  
 210 215 220  
 Pro Lys Met Glu Gly Ser Lys Asp Phe Leu Phe Asn Cys  
 225 230 235

<210> 2317

<211> 237

<212> PRT

<213> Mus musculus (M21 6456795-1-153518-155435 1694-983)

<220>

<221> VARIANT

<222> (1)...(237)

<223> Xaa = Any Amino Acid

<400> 2317

Leu Xaa Thr Tyr Ile Pro Thr His Thr His Thr His Thr His  
 1 5 10 15  
 Thr His Thr His Ile Tyr Ile Cys Asn Tyr Asn Val Gln Arg Asn Asn  
 20 25 30  
 Gly Tyr Gln Val Asp His Tyr Leu Xaa Ile Cys His Pro Leu His Tyr  
 35 40 45  
 Pro Leu Leu Met Gly His Gln Trp Cys Leu Gly Phe Val Leu Thr Leu  
 50 55 60  
 Gln Leu Phe Gly Ile Thr Val Asp Gly Leu Val Val Ile Leu Val Ala  
 65 70 75 80  
 Gln Met Trp Phe Cys Gly Pro Asn Leu Ile Asp Tyr Phe Xaa Tyr Asn  
 85 90 95  
 Phe Ser Pro Ile Met Asp Leu Ala Xaa Ser Asp Thr Gln Val Phe Gln  
 100 105 110  
 Val Ile Thr Phe Val Leu Ser Val Val Phe Leu Thr Val Pro Phe Gly  
 115 120 125  
 Leu Val Leu Ile Ser Tyr Ile Gln Ile Val Val Thr Val Leu Arg Val  
 130 135 140  
 Leu Ser Gly Asp Arg Arg Thr Lys Asp Phe Ser Thr Cys Ser Ser His  
 145 150 155 160  
 Leu Ala Val Val Ser Thr Phe Tyr Arg Ser Leu Met Val Leu Tyr Thr  
 165 170 175  
 Val Pro Leu Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Lys Val Val  
 180 185 190  
 Ile Pro Ile Phe Asn His Val Ile Tyr Thr Leu Arg Asn Gln Glu Val  
 195 200 205  
 Pro Xaa Ala Leu Arg Arg His Leu Tyr Cys Lys Pro Thr Glu Met Xaa  
 210 215 220  
 Pro Lys Met Glu Gly Ser Lys Asp Phe Leu Phe Asn Cys  
 225 230 235

<210> 2318

<211> 318

<212> PRT

<213> Mus musculus (M22 6456795-1-37464-41929 1501-549)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2318

Cys Val Ile Phe Xaa Val Met Leu Asn Gln Thr Ser Val Thr Glu Phe  
 1 5 10 15  
 Ile Leu Leu Gly Val Arg Asp Ile Gln Glu Pro Gln Pro Phe Leu Phe

```

      20      25      30
Ala Ile Phe Phe Thr Ile Tyr Phe Val Asn Ile Thr Gly Asn Gly Ala
      35      40      45
Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
      50      55      60
Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Ser Tyr Ser Thr Val
65      70      75      80
Thr Val Pro Lys Met Leu Glu Asn Leu Leu Ser Thr Asn Lys Ala Ile
      85      90      95
Ser Leu Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
      100      105      110
Thr Thr Glu Ser Leu Leu Leu Ala Val Met Ala Phe Asp Arg Phe Val
      115      120      125
Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn Trp Gln Val
      130      135      140
Cys Ile Leu Met Ala Val Thr Ile Trp Thr Ile Ala Phe Leu His Ala
145      150      155      160
Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Leu Asn
      165      170      175
His Ile His His Phe Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala
      180      185      190
Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Gly
      195      200      205
Thr Ile Ala Ser Val Pro Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr
      210      215      220
Ile Ile Thr Tyr Leu Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His
225      230      235      240
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Val Leu Phe
      245      250      255
Tyr Ala Pro Val Leu Phe Thr Tyr Ile Arg Pro Thr Ser Gly Ser Ser
      260      265      270
Leu Asp Gln Asp Arg Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro
      275      280      285
Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser
      290      295      300
Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Leu Leu Glu Glu
305      310      315

```

&lt;210&gt; 2319

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M23 6456795-1-63066-65167 771-1694)

&lt;400&gt; 2319

```

Val Leu Leu Asn His Thr Leu Val Thr Glu Phe Leu Leu Leu Gly Val
1      5      10      15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Thr Val Leu Ala
      20      25      30
Met Tyr Phe Val Asn Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val
      35      40      45
Ile Ser Asp Pro Arg Leu His Leu Pro Met Tyr Phe Phe Leu Gly Asn
      50      55      60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
65      70      75      80
Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
      85      90      95
Ile Thr Gln Leu His Phe Phe Asn Phe Leu Gly Ser Thr Glu Ala Leu
      100      105      110
Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
      115      120      125
Leu His Tyr Pro Ala Ile Met Asn Ser Gln Val Cys Ile Gln Val Ala

```

```

      130              135              140
Ile Ser Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
145              150              155              160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn His Ile His His Phe
      165              170              175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
      180              185              190
Leu Asn Arg Trp Leu Leu Asn Thr Leu Thr Gly Thr Val Ala Ile Gly
      195              200              205
Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
      210              215              220
Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
225              230              235              240
Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
      245              250              255
Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
      260              265              270
Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Gly Ala Leu Asn Arg Lys
      290              295              300
Ile Arg Ile Leu
305

```

&lt;210&gt; 2320

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M24 6456795-1-750-2697 1501-527)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2320

```

Cys Pro Phe Leu Xaa Val Met Ser Asn Gln Thr Ser Val Thr Glu Phe
1      5      10      15
Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe
      20      25      30
Val Ile Phe Phe Thr Ile Tyr Phe Ile Asn Ile Thr Gly Asn Gly Ala
      35      40      45
Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
      50      55      60
Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Ser Tyr Ser Thr Val
65      70      75      80
Thr Val Pro Lys Leu Leu Gln Asn Leu Leu Ser Thr Ser Lys Ala Ile
      85      90      95
Ser Phe Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
      100      105      110
Ser Thr Glu Thr Met Leu Leu Pro Val Met Ala Phe Asp Arg Phe Val
      115      120      125
Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn His Gln Leu
      130      135      140
Cys Ile His Met Thr Val Thr Ile Trp Thr Leu Gly Phe Phe His Ala
145      150      155      160
Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Pro Asn
      165      170      175
His Val His His Phe Phe Cys Asp Ile Lys Pro Leu Leu Asp Leu Ala
      180      185      190
Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Gly
      195      200      205

```

Thr Ile Ala Leu Thr Ser Phe Phe Leu Ile Phe Leu Ser Tyr Phe Tyr  
 210 215 220  
 Ile Ile Thr Asn Leu Leu Lys Thr Arg Ser Cys Ser Met Leu His  
 225 230 235 240  
 Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Val Leu Phe  
 245 250 255  
 Tyr Ala Pro Val Leu Phe Thr Tyr Ile Arg Pro Ala Ser Gly Ser Ser  
 260 265 270  
 Leu Asp Gln Asp Thr Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro  
 275 280 285  
 Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser  
 290 295 300  
 Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Xaa Pro Glu Glu Ser Lys  
 305 310 315 320  
 Glu Val Phe Phe Ser  
 325

&lt;210&gt; 2321

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M25 6456795-1-78460-79066 2-526)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(177)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2321

Val Ser Ala His Val Cys Met Gly Cys Xaa Leu Ser Trp Pro Val Arg  
 1 5 10 15  
 Cys Glu Ile Ile Phe Gly Val Met His Thr Thr Val Asn Phe Ser Ile  
 20 25 30  
 Val Leu Cys Gly Thr Ser Val Ile His Xaa Phe Cys Asp Val Leu Leu  
 35 40 45  
 Val Leu Lys Leu Ser Cys Leu Tyr Asp His Val Ser Glu Ile Ala Ile  
 50 55 60  
 Ser Asp Phe Ser Ile Ser Leu Ala Phe Phe Cys Phe Ile Ser Pro Asn  
 65 70 75 80  
 Phe Thr Tyr Val His Ile Phe Ser Thr Glu Leu Arg Met Pro Phe Val  
 85 90 95  
 Glu Gly Lys Thr Ser Val Phe Ser Thr Cys Leu Cys His Met Thr Ser  
 100 105 110  
 Ile Leu Phe Ile Pro Thr Gly Ile Phe Glu Phe Leu Arg Ser His Thr  
 115 120 125  
 Glu Ser Ser Thr Ser Leu Asp Phe Ile Leu Asn Phe Ser Tyr Phe Ser  
 130 135 140  
 Leu Ser Thr Leu Asn Pro Gly Ile Tyr Ser Leu Arg Asn Glu Ala Val  
 145 150 155 160  
 Asp Thr Val Gln Arg Lys Ile Phe Phe Phe Lys Glu Lys Tyr Leu Phe  
 165 170 175  
 Leu

&lt;210&gt; 2322

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M26 6456795-1-84123-87238 211-1134)

&lt;400&gt; 2322

Val Leu Leu Asn His Thr Phe Ile Thr Glu Phe Leu Leu Leu Gly Val  
 1 5 10 15

Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Met Val Leu Ala  
 20 25 30  
 Met Tyr Phe Ile Asn Val Phe Gly Asn Gly Ala Ile Met Met Ile Val  
 35 40 45  
 Ile Leu Asp Ser Arg Leu Tyr Ser Pro Met Tyr Phe Phe Leu Gly Asn  
 50 55 60  
 Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met  
 65 70 75 80  
 Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys  
 85 90 95  
 Ile Thr Gln Leu His Phe Phe His Phe Leu Gly Cys Thr Asp Ala Leu  
 100 105 110  
 Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro  
 115 120 125  
 Leu His Tyr Pro Ser Ile Met Asn Arg Gln Val Cys Ile Gln Val Ala  
 130 135 140  
 Ala Thr Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile  
 145 150 155 160  
 Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe  
 165 170 175  
 Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu  
 180 185 190  
 Leu Asn Arg Trp Leu Leu Asn Thr Leu Ala Gly Thr Ile Gly Ile Gly  
 195 200 205  
 Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu  
 210 215 220  
 Phe Leu Lys Thr His Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu  
 245 250 255  
 Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg  
 260 265 270  
 Ile Ile Ala Val Met Tyr Thr Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ala Leu Arg Asn Lys Glu Val Arg Cys Ala Leu Asn Arg Lys  
 290 295 300  
 Leu Arg Ile Leu  
 305

&lt;210&gt; 2323

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M27 6456795-1-89089-90071 35-969)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2323

Ser Leu Phe Tyr Ser Gln Arg Ser Arg Met Asn Val Ala Asn Phe Thr  
 1 5 10 15  
 Ala Met Thr Ile Phe Leu Leu Leu Met Gly Phe Ser Arg Asn Ser Gln  
 20 25 30  
 Val Glu Ile Ile Phe Ser Thr Leu Ala Leu Val Val Leu Ile Gly Thr  
 35 40 45  
 Ile Ser Ile Val Ala Val Thr Ser Leu Ser Ile Arg Leu Cys Ser Leu  
 50 55 60  
 Met Pro Phe Leu Leu Ile His Leu Phe Cys Phe Asp Val Cys Tyr Ile  
 65 70 75 80  
 Ser Val Met Met Pro Lys Ser Val Cys Ser Ser Phe Met Tyr Ser Ala

```

      85              90              95
Tyr Ile Ser Leu Ile Glu Cys Thr Leu Gln Val Phe Tyr Ser Gln Ser
      100              105              110
Ser Tyr Thr Ala Met Ala Ile Leu Thr Val Met Ser Tyr Asp Cys Tyr
      115              120              125
Met Ala Val Trp His Lys Val Ile Thr Asn Val Ser Thr Cys Ile His
      130              135              140
Gly Val Leu Ala Val Leu Val Asn Gly Cys Glu Ile Ile Phe Gly Val
      145              150              155              160
Met His Thr Thr Leu Thr Phe Ser Ile Tyr Ile Cys Gly Thr Ser Thr
      165              170              175
Ile Arg Xaa Phe Cys Asp Val Leu Leu Val Leu Lys Leu Ser Phe Thr
      180              185              190
Asn Asp His Val Asn Glu Leu Glu Ser Leu Ala Phe Ser Ser Val Glu
      195              200              205
Gly Arg Thr Lys Ser Phe Ser Thr Cys Leu Gly His Val Ser Val Gly
      210              215              220
Ser Leu Phe Asn Pro Pro Gly Val Phe Glu Phe Leu Asn Pro Tyr Ser
      225              230              235              240
Glu Ser Pro Thr Ser Leu Asp Ile Ile Val Thr Val Phe Ile Leu Pro
      245              250              255
Gln Thr Leu Ser Val Glu Ile Tyr Ser Leu Ser Asn Glu Ala Ile Asp
      260              265              270
Thr Ala Xaa Arg Lys Phe Phe Phe Gln Arg Lys Thr Ser Leu Ser Ile
      275              280              285
Leu His Tyr Phe Leu Leu Gly Ser His Ile Xaa Xaa Val Leu Arg Lys
      290              295              300
Thr Thr Val Ser Met Asn Gln Leu Lys Leu
      305              310

```

&lt;210&gt; 2324

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M28 6456795-1-95949-101645 434-1360)

&lt;400&gt; 2324

```

Val Leu Leu Asn Gln Thr Leu Val Thr Glu Phe Leu Leu Leu Gly Val
      1              5              10              15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Thr Val Leu Ala
      20              25              30
Met Tyr Phe Val Asn Val Ala Gly Asn Gly Ala Ile Leu Leu Ile Val
      35              40              45
Ile Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn
      50              55              60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Ile
      65              70              75              80
Leu Asp Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
      85              90              95
Ile Thr Gln Leu Tyr Phe Phe His Leu Leu Gly Ser Thr Glu Ala Leu
      100              105              110
Leu Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
      115              120              125
Leu His Tyr Pro Ser Ile Met Asn Gly Gln Val Cys Ile Gln Val Ala
      130              135              140
Ile Ser Ile Trp Ala Ile Pro Phe Val His Ala Leu Val His Ser Ile
      145              150              155              160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Gln Ile His His Phe
      165              170              175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
      180              185              190
Leu Asn Arg Trp Leu Leu Asn Thr Phe Thr Gly Thr Phe Ala Ile Gly

```

195                      200                      205  
 Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Ile Thr Tyr Leu  
     210                      215                      220  
 Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr  
 225                      230                      235                      240  
 Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu  
                     245                      250                      255  
 Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg  
                     260                      265                      270  
 Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu  
                     275                      280                      285  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Gly Ala Leu Asn Arg Lys  
                     290                      295                      300  
 Leu Arg Ile Leu Leu  
 305

&lt;210&gt; 2325

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M29 6691272-106-1-1090 908-19)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(296)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2325

Cys Ile Phe Ile Gly Val Phe Leu Ile Ser Ser Ala Ser Gly Ala Met  
     1                      5                      10                      15  
 Pro Gly Gln Asn Tyr Ser Thr Ile Ser Glu Phe Ile Leu Phe Gly Phe  
                     20                      25                      30  
 Ser Ala Phe Pro His Gln Met Leu Pro Ala Leu Phe Leu Leu Tyr Leu  
                     35                      40                      45  
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Val Ile Met Ala Ala  
                     50                      55                      60  
 Ile Trp Thr Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu Cys  
 65                      70                      75                      80  
 Ala Leu Ser Ile Ser Glu Ile Leu Phe Thr Val Val Ile Thr Pro Arg  
                     85                      90                      95  
 Met Leu Ser Asp Met Leu Ser Thr His Arg Ser Ile Thr Phe Ile Ala  
                     100                      105                      110  
 Cys Ala Asn Gln Leu Phe Phe Ser Phe Thr Phe Gly Tyr Thr His Ser  
                     115                      120                      125  
 Phe Leu Leu Val Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
                     130                      135                      140  
 Pro Leu His Tyr His Ala Leu Met Ser Leu Gln Gly Cys Ala Arg Leu  
 145                      150                      155                      160  
 Val Ala Trp Ser Trp Ala Gly Gly Ser Leu Ile Gly Met Ala Leu Thr  
                     165                      170                      175  
 Ile Ile Ile Phe His Leu Thr Phe Cys Glu Ser Asn Val Ile His His  
                     180                      185                      190  
 Ile Leu Cys His Val Phe Ser Leu Leu Lys Leu Ala Cys Gly Glu Arg  
                     195                      200                      205  
 Thr Ala Phe Val Thr Ile Ala Val Ile Leu Val Cys Val Thr Pro Leu  
                     210                      215                      220  
 Ile Gly Cys Leu Val Phe Ile Ile Leu Ser Tyr Ile Phe Ile Val Ala  
 225                      230                      235                      240  
 Ala Ile Leu Arg Ile Pro Ser Thr Glu Gly Arg His Lys Thr Phe Ser  
                     245                      250                      255  
 Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Phe Ala  
                     260                      265                      270



Ser Leu Ile Tyr Leu Gln Gly Tyr Pro Leu Glu Ser Asp Xaa Thr Gly  
 275 280 285  
 Met Ser Ser Trp His Ala Ser Phe  
 290 295

<210> 2326

<211> 334

<212> PRT

<213> Mus musculus (M30 6691273-103-1206-2961 586-1585)

<220>

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 2326

Trp Ala Asn Gln Ser Arg Ala Arg Glu Leu Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Phe Ala His Val Pro Ser Leu Arg Pro Met Leu Ala Ala Leu Phe Leu  
 20 25 30  
 Ala Ala Phe Leu Leu Thr Met Ser Gly Asn Ser Leu Ile Val Leu Leu  
 35 40 45  
 Thr Ser Leu Asp Phe Gly Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg  
 50 55 60  
 Gln Leu Ala Leu Val Glu Ile Cys Phe Ser Leu Asp Val Ala Pro Arg  
 65 70 75 80  
 Leu Leu Val Thr Leu Leu Gln Pro Gly Arg Gly Val Ser Pro Thr Ser  
 85 90 95  
 Cys Ala Leu Gln Leu Leu Leu Val Leu Ser Cys Val Thr Ser Glu Cys  
 100 105 110  
 Phe Leu Leu Met Val Met Ala Trp Asp Arg Phe Leu Ala Ile Cys Arg  
 115 120 125  
 Pro Leu Arg Tyr Gly Ala Ile Met Ser Pro Gln Leu Cys Tyr Leu Leu  
 130 135 140  
 Ala Thr Thr Cys Trp Leu Ala Gly Ile Pro Val Ala Leu Val Phe Thr  
 145 150 155 160  
 Ile Trp Leu Phe Asn Phe Pro Phe Cys Gly Pro Arg Gly Ile Arg His  
 165 170 175  
 Phe Phe Cys Asp Ile Ala Pro Leu Leu Ser Leu Val Cys Ala Asp Thr  
 180 185 190  
 Arg Val Phe Glu Ala Asn Val Phe Val Ala Thr Val Leu Val Ile Met  
 195 200 205  
 Val Pro Phe Cys Leu Ile Ala Thr Ser Tyr Val Met Ile Leu Val Ala  
 210 215 220  
 Val Leu Arg Met Pro Ser Ala Ser Gly Arg His Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Ile Val Val Ile Leu Phe Tyr Gly Thr Thr Gly  
 245 250 255  
 Val Ile His Leu Arg Pro Lys Ala Ser Tyr Ser Pro Glu Ser Lys Gln  
 260 265 270  
 Val Val Ser Leu Ser Tyr Thr Met Val Thr Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Phe Gly Arg Val  
 290 295 300  
 Cys Cys Gly Arg Xaa Glu Ser Arg Leu His Glu Xaa Thr His Leu Leu  
 305 310 315 320  
 Cys Gln Pro Phe Ser Val Arg Xaa Leu Leu Arg Pro Thr Phe  
 325 330

<210> 2327

<211> 330

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M31 6691273-105-4369-6206 1597-608)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(330)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2327

```

Val Leu Leu Xaa Cys Tyr Xaa Arg Thr Asp Asp Asn Asn Trp Leu Val
 1           5           10           15
Ser Leu Gln Met Ala Arg Ser Leu Glu Leu Ala Asn Met Thr Arg Val
      20           25           30
Gln Lys Phe Leu Leu Leu Gly Leu Ser Thr Arg Leu Asp Ile Arg Asp
      35           40           45
Ala Leu Phe Ala Val Phe Leu Thr Leu Tyr Leu Leu Thr Leu Val Glu
      50           55           60
Asn Thr Leu Ile Ile Tyr Leu Ile Phe Ser His Lys Glu Leu His Lys
      65           70           75           80
Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Cys Leu Glu Met Cys Tyr
      85           90           95
Val Ser Val Thr Met Pro Thr Leu Leu Val Gly Leu Trp Thr Gly Pro
      100          105          110
Tyr His Ile Pro Phe Thr Leu Cys Met Thr Gln Leu Phe Phe Phe Ile
      115          120          125
Val Leu Ile Cys Thr Glu Cys Thr Leu Leu Ala Ser Met Ala Tyr Asp
      130          135          140
Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Pro Leu Leu Met Arg
      145          150          155          160
Pro Gln Val Cys Leu Gly Leu Ala Leu Ser Ser Trp Leu Gly Gly Leu
      165          170          175
Ile Val Ser Val Ala Lys Thr Thr Cys Ile Ala Ser Leu Ser Tyr Cys
      180          185          190
Gly Pro Asn Val Leu Asn Gln Phe Phe Cys Asp Val Ser Pro Leu Leu
      195          200          205
Asn Leu Ser Cys Thr His Val Ala Leu Thr Glu Leu Val Asp Phe Ile
      210          215          220
Ser Ala Ile Val Ile Phe Cys Gly Thr Leu Leu Val Ser Leu Ala Ser
      225          230          235          240
Tyr Ser Ala Ile Gly Met Ala Val Leu Arg Met Pro Ser Ala Ala Ala
      245          250          255
Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Val Val Val Gly
      260          265          270
Ile Phe Tyr Ser Ala Ala Leu Phe Ile Tyr Cys Arg Pro Ser Arg Ile
      275          280          285
Lys Ser Met Asp Leu Asn Lys Val Leu Ser Val Ile Tyr Thr Val Val
      290          295          300
Thr Pro Leu Cys Asn Pro Ile Ile Tyr Cys Leu Arg Asn Lys Glu Val
      305          310          315          320
His Thr Val Leu Lys Lys Thr Leu His Trp
      325          330

```

&lt;210&gt; 2328

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M32 6691273-108-10257-11726 1388-432)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2328

```

Leu Val Pro Ser Phe Gln Arg His Thr Met Ala Asn Leu Ser Thr Val
 1          5          10          15
Ser Val Phe Ile Leu Gln Gly Phe Ser Ala Val Pro Ala Leu Gln Leu
          20          25          30
Leu Ser Met Ala Ile Phe Leu Leu Ile Tyr Leu Ala Ala Val Leu Gly
          35          40          45
Asn Val Ser Ile Met Ile Ala Val Thr Leu Asp Ser His Leu His Thr
          50          55          60
Pro Met Tyr Phe Phe Ile Lys His Leu Ser Leu Val Asp Leu Cys Ser
65          70          75          80
Thr Ser Thr Thr Leu Pro Arg Ala Leu Val Ala Thr Met Ala Asp Thr
          85          90          95
Lys Glu Ile Ser Leu Pro Ala Cys Ala Ser Gln Leu Phe Ala Phe Val
          100          105          110
Cys Phe Gly Ser Leu Glu Cys Phe Leu Ile Thr Ala Met Ala Phe Asp
          115          120          125
Arg Cys Leu Ala Ile Tyr Arg Pro Leu Thr Tyr Gly Val Thr Met Ser
          130          135          140
Ser Gln Thr Cys Val Ser Leu Val Val Val Ala Trp Val Ser Gly Leu
145          150          155          160
Leu Phe Ser Thr Phe His Met Val Asn Thr Phe Ser Leu Pro Phe Cys
          165          170          175
Gly Pro Asn Met Ile Asp His Phe Phe Cys Asp Ile Pro Pro Leu Met
          180          185          190
His Leu Ala Cys Gly Asp Thr Gln Gly His Glu Ala Ala Gly Phe Ile
          195          200          205
Val Ser Gly Cys Val Ile Met Thr Cys Phe Ala Leu Thr Cys Leu Ser
          210          215          220
Tyr Val Leu Ile Val Tyr Thr Val Val His Ile Arg Ser Ala Ala Gly
225          230          235          240
Arg Trp Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ala Thr Val Leu
          245          250          255
Leu Phe Tyr Gly Thr Gly Ser Ser Ala Tyr Met Gln Pro Thr Ala His
          260          265          270
Tyr Ser Pro Leu Gln Gly Arg Met Ala Ala Ile Phe Tyr Ser Ile Leu
          275          280          285
Met Pro Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met
          290          295          300
Lys Ala Ala Leu Arg Lys Leu Tyr Pro Gln Val Pro Ser Xaa Ile
305          310          315

```

&lt;210&gt; 2329

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M33 6850399-12-3847-5066 800-1195)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(133)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2329

```

Thr Glu Leu Asn Ser Cys Leu Gln Trp Leu Pro Ile Leu His Arg Ser
 1          5          10          15
Thr Thr Glu Ala Ser Ser Ala Val Leu Xaa Glu Leu Leu Leu Gln Arg
          20          25          30
Pro Ala Ser Ala Leu Xaa Pro Pro Ile Gly Ser Ser Asp Leu Ala Gly
          35          40          45
Cys Phe Ser Val Tyr Ile Leu Thr Leu Thr Asp Asn Thr Thr Val Arg

```

50                      55                      60  
 Ile Asn Ser Phe Leu Asn His Lys Leu His Thr Pro Met Ser Ser Phe  
 65                      70                      75                      80  
 Cys Phe Gly Leu Ser Ile Leu Asp Leu Cys Phe Thr Pro Ser Thr Val  
                     85                      90                      95  
 Pro Pro Asp His Gln Ile Leu Gly Asn Pro Xaa Gly Pro Glu Lys Leu  
                     100                      105                      110  
 Ala Ile Leu Val Xaa Ala Ile Gln Leu Ser Val Ala Leu Gly Phe Gly  
                     115                      120                      125  
 Ser Thr Val Cys Val  
 130

<210> 2330  
 <211> 191  
 <212> PRT  
 <213> Mus musculus (M35 6850399-2-1-641 21-587)

<220>  
 <221> VARIANT  
 <222> (1)...(191)  
 <223> Xaa = Any Amino Acid

<400> 2330  
 Asp Ala Ile Ser Gln Pro Leu His Tyr Gly Ala Ile Thr His Ser Glu  
 1                      5                      10                      15  
 Ile Leu Trp Gln Leu Ala Thr Val Ala Gln Ile Ser Gly Phe Val Glu  
                     20                      25                      30  
 Phe Arg Ser Pro Ser Ile Phe Gln Leu Pro Arg Cys Gly Gly Gly Gly  
                     35                      40                      45  
 Val Val Cys Lys Ala Xaa Asn Tyr Leu Cys Arg His Asn Phe Pro Gly  
                     50                      55                      60  
 Lys Xaa Leu Ser Thr Val Thr Ala Leu Cys Val Val Thr Leu Met Gly  
 65                      70                      75                      80  
 Leu Val Leu Val Ser Tyr Val Ser Ile Val Lys Gly Val Leu Arg Gly  
                     85                      90                      95  
 Gly Pro Ile Glu Asp Met Gly Lys Ala Phe Gly Thr Cys Gly Tyr His  
                     100                      105                      110  
 Leu Ile Ala Gly Leu Leu Phe Phe Lys Ala Ile Ile Ser Val Tyr Thr  
                     115                      120                      125  
 His Pro Arg Asn Glu Phe Thr Gly Ser His Gly Lys Pro Phe Leu Leu  
                     130                      135                      140  
 Leu Tyr Pro Val Val Met Pro Ser Leu Gly Pro Leu Ile Asp Thr Leu  
 145                      150                      155                      160  
 Arg Ser Gln Glu Ser Ser Arg Val Ile Lys Arg Leu Val Ala Lys Asp  
                     165                      170                      175  
 Xaa Lys Leu Ser Arg Lys Asn Thr Xaa Cys Thr Ser Arg Ser Trp  
                     180                      185                      190

<210> 2331  
 <211> 320  
 <212> PRT  
 <213> Mus musculus (M36 7263202-1-54100-55962 166-1125)

<400> 2331  
 Ser Ser Gln Ala Pro Glu Lys Gln Gln Asp Asn Gly Thr Trp Leu Val  
 1                      5                      10                      15  
 Thr Glu Phe Leu Leu Val Gly Phe Ser Asn Leu Pro Glu Leu Arg Pro  
                     20                      25                      30  
 Thr Leu Phe Ile Leu Phe Leu Leu Thr Tyr Leu Val Thr Leu Ser Gly  
                     35                      40                      45  
 Asn Ala Thr Ile Ile Thr Ile Ile Gln Val Asp Arg Thr Leu His Thr

50	55	60
Pro Met Tyr Arg Phe Leu Ala Val Leu Ser Leu Ser Glu Thr Cys Tyr		
65	70	75
Thr Leu Val Thr Ile Pro Asn Met Leu Ala His Leu Leu Met Glu Ser		80
	85	90
Gln Ala Ile Ser Ile Ala Gly Cys Arg Ala Gln Met Phe Phe Phe Leu		95
	100	105
Gly Leu Gly Cys Ser His Cys Phe Leu Leu Thr Leu Met Gly Tyr Asp		110
	115	120
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Ser Val Ile Met Arg		125
	130	135
Pro Thr Val Cys Leu Cys Leu Gly Ala Leu Val Phe Cys Ser Gly Phe		140
	145	150
Ser Val Ala Leu Ile Glu Thr Cys Met Ile Phe Ser Ser Pro Phe Cys		155
	165	170
Gly Ala Gly His Val Glu His Phe Phe Cys Asp Ile Ala Pro Val Leu		175
	180	185
Lys Leu Ser Cys Asp Glu Ser Ser Leu Lys Gly Leu Gly Ile Phe Phe		190
	195	200
Leu Ser Ile Leu Val Val Leu Val Ser Phe Leu Phe Ile Leu Leu Ser		205
	210	215
Tyr Ala Phe Ile Val Ala Ala Ile Val Arg Ile Pro Ser Ala Ser Gly		220
	225	230
Arg Arg Lys Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile		235
	245	250
Val His Phe Gly Cys Ala Ser Ile Ile Tyr Leu Arg Pro Asp Ser Gly		255
	260	265
Ala Asn Pro Ser Gln Asp Arg Leu Val Ala Val Phe Tyr Thr Val Val		270
	275	280
Thr Pro Leu Leu Asn Pro Val Val Tyr Thr Leu Arg Asn Lys Glu Val		285
	290	295
Arg Val Ala Leu Arg Lys Asn Leu Ala Arg Gly Cys Gly Ala Phe Lys		300
	305	310
		315
		320

&lt;210&gt; 2332

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M38 7340303-58-1-1344 4-367)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(122)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2332

His Leu Ser Glu Glu Val Gly Phe Ala Val Ser Ser Cys Ile Val Met	
1	5
Ser Ser Phe Ala Leu Thr Val Val Ser Tyr Ile Gly Ile Val Ala Thr	10
	20
Val Leu Arg Ile Pro Ser Val Glu Gly Arg Trp Lys Ala Phe Ser Thr	25
	30
	35
Cys Ser Ser His Leu Thr Thr Val Ile Leu Phe Tyr Gly Thr Gly Ser	40
	45
	50
Phe Val Tyr Leu Arg Pro Ala Ser Gln Tyr Ser Pro Thr Leu Gly Pro	55
	60
65	70
Leu Ala Ser Ile Phe Tyr Ser Val Val Thr Pro Ser Leu Asn Pro Val	75
	80
	85
Val Tyr Cys Leu Arg Asn Lys Asp Met Lys Phe Ala Leu Gln Lys Leu	90
	95
	100
Tyr Cys Gly Arg Lys Tyr Xaa Asp Leu Glu	105
	110
	115
	120

&lt;210&gt; 2333

&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M41 7363372-318-7546-10891 3278-2211)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(356)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2333

```

Tyr Val Phe Phe Cys Phe Gln Tyr Ser Xaa Glu Trp Lys Thr Glu Leu
 1           5           10           15
Glu Met Asp Val Ser Asn Gln Thr Thr Val Thr Glu Phe Val Leu Leu
          20           25           30
Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile
          35           40           45
Leu Ser Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
          50           55           60
Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          65           70           75           80
Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Pro
          85           90           95
Leu Val Leu Asp Gly Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser
          100          105          110
Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu
          115          120          125
Cys Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
          130          135          140
Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala Tyr Val Pro
          145          150          155          160
Met Ala Val Ser Ser Trp Val Ala Gly Gly Ala Asn Ser Leu Val Gln
          165          170          175
Ile Ser Leu Ala Val Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn
          180          185          190
His Phe Ile Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
          195          200          205
Ile Ser Ile Asn Val Ile Ser Met Gly Val Ala Asn Val Ile Phe Leu
          210          215          220
Gly Val Pro Val Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu Ser
          225          230          235          240
Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser
          245          250          255
Thr Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile
          260          265          270
Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp
          275          280          285
Lys Gln Asp Leu Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Leu Leu
          290          295          300
Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val
          305          310          315          320
Lys Ala Ala Val Arg Asn Leu Ala Ser His Arg Cys Leu Thr Phe Xaa
          325          330          335
Trp Arg Asp Arg Ala His Asp Pro His Val Leu Met Ala Leu Thr Xaa
          340          345          350
Glu Ser Tyr Cys
          355

```

&lt;210&gt; 2334

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M42 7363372-319-4901-8603 988-1980)

&lt;400&gt; 2334

Cys Pro Leu Leu Ser Gln Asp Gly Lys Arg Thr Cys Glu Met Glu Gly  
 1 5 10 15  
 Ala Asn Gln Ser Thr Val Ala Glu Phe Val Leu Leu Gly Leu Ser Asp  
 20 25 30  
 His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile Leu Leu Met Tyr  
 35 40 45  
 Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu Val Ser Ile Leu  
 50 55 60  
 Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser  
 65 70 75 80  
 Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Leu Val Leu Asp  
 85 90 95  
 Gly Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Gly Cys Ala Val  
 100 105 110  
 Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys Val Leu Leu  
 115 120 125  
 Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg  
 130 135 140  
 Tyr Pro Val Val Met Asn Lys Ser Ala Tyr Val Pro Met Ala Val Ser  
 145 150 155 160  
 Ser Trp Val Ala Gly Gly Ala Asn Ser Leu Val Gln Ile Ser Leu Ala  
 165 170 175  
 Val Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His Phe Thr Cys  
 180 185 190  
 Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile Ser Ile Asn  
 195 200 205  
 Val Ile Ser Met Gly Val Ala Asn Val Ile Phe Leu Gly Val Pro Val  
 210 215 220  
 Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu Ser Thr Ile Leu Arg  
 225 230 235 240  
 Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ala  
 245 250 255  
 His Leu Thr Val Val Leu Val Phe Tyr Gly Thr Ile Leu Phe Met Tyr  
 260 265 270  
 Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Val  
 275 280 285  
 Ser Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Leu Thr Pro Met Leu  
 290 295 300  
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Val  
 305 310 315 320  
 Arg Asn Leu Val Gly Gln Lys Cys Leu Ile Gln  
 325 330

&lt;210&gt; 2335

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M43 7363372-320-18353-20567 840-1811)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2335

Asn Met Glu Arg Ser Asn Lys Thr Thr Pro Val Ser Ser Phe Ile Leu  
 1 5 10 15  
 Leu Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu

```

      20      25      30
Ile Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Val Val Leu Ile
      35      40      45
Leu Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
      50      55      60
Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val
65      70      75      80
Pro Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe
      85      90      95
Ser Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr
      100      105      110
Glu Cys Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Pro Val Val Met Ser Lys Ala Ala Tyr Val
      130      135      140
Pro Met Ala Ala Gly Ser Trp Val Ser Gly Ser Ile Thr Ala Thr Val
145      150      155      160
Gln Ile Ser Leu Ala Met Thr Leu Pro Phe Cys Gly Asp Asn Val Ile
      165      170      175
Asn His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala
      180      185      190
Asp Ile Ser Ile Asn Val Ile Ser Met Ala Val Ala Asn Ala Met Phe
      195      200      205
Leu Gly Val Pro Val Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu
      210      215      220
Ser Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe
225      230      235      240
Ser Thr Cys Ser Ala His Leu Thr Val Val Leu Val Phe Tyr Gly Thr
      245      250      255
Ile Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala
      260      265      270
Asp Lys Gln Asp Leu Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val
      275      280      285
Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp
      290      295      300
Val Lys Ala Ala Val Thr Asn Leu Val Gly Gln Lys His Phe Lys Trp
305      310      315      320
Xaa Trp Cys Met

```

&lt;210&gt; 2336

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M44 7363372-320-22007-23346 51-820)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(257)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2336

```

Leu Leu Phe Val Val Lys Met Lys Arg Leu Gln Thr Cys Xaa Phe Xaa
1      5      10      15
Gln Pro Ala Leu Leu Arg Gly Leu Ser Ser Leu Lys Gly Gln Arg Asp
      20      25      30
Pro Arg Leu Asn Glu Cys Cys Met Pro Leu Leu Xaa Gln Asp Pro Arg
      35      40      45
Gly Lys Ala Ser Phe Leu Val Cys Leu Val Leu Val Thr Leu Ser Cys
      50      55      60
Met Trp Gln Glu Gln Cys Pro Pro Met His Val Thr Phe Val His Ser
65      70      75      80

```



Leu Ala Val Arg Gln Leu Lys Val Ile Asn Ser Arg Ala Ala Cys Val  
                     85                    90                    95  
 Leu Arg Ser Ala Glu Leu Xaa Ala Thr Gly Ala Thr Tyr Pro Leu Ser  
                     100                    105                    110  
 Thr Asn Tyr Cys Ile Cys Lys Thr Arg Thr Ser Ala Arg Ala Asp Ile  
                     115                    120                    125  
 Ser Ile Asn Val Ile Ser Ile Gly Val Glu Leu Gly Val Pro Val Leu  
                     130                    135                    140  
 Phe Ile Phe Ile Ser Tyr Ile Phe Ile Leu Ser Thr Ile Leu Gly Ile  
                     145                    150                    155                    160  
 Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ala His  
                     165                    170                    175  
 Leu Thr Met Val Ile Ile Phe Tyr Gly Thr Ile Leu Phe Met Tyr Gly  
                     180                    185                    190  
 Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Leu Ala  
                     195                    200                    205  
 Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr Pro Met Leu Asn  
                     210                    215                    220  
 Leu Arg Thr Thr Val Arg Ala Phe Ile Phe Arg Lys Tyr Phe Ser Gln  
                     225                    230                    235                    240  
 Xaa Trp Trp Gln Gly Met Leu Trp Thr Val Thr His Arg Thr Glu Lys  
                     245                    250                    255  
 Ile

&lt;210&gt; 2337

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M45 7363372-320-7359-9353 512-1474)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2337

Asp Ser Met Glu Ile Asn Asn Gln Thr Ser Phe Pro Val Ser Ser Phe  
   1                    5                    10                    15  
 Ile Leu Leu Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe  
                     20                    25                    30  
 Met Leu Ile Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Ile  
                     35                    40                    45  
 Leu Ile Leu Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr  
                     50                    55                    60  
 Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser  
   65                    70                    75                    80  
 Ser Val Pro Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile  
                     85                    90                    95  
 Ser Phe Ser Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly  
                     100                    105                    110  
 Ala Thr Glu Cys Val Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val  
                     115                    120                    125  
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala  
                     130                    135                    140  
 Tyr Val Pro Met Ala Val Ser Ser Trp Ser Gly Gly Ile Ala Val Ser  
   145                    150                    155                    160  
 Val Val Gln Thr Ser Leu Ala Met Lys Leu Thr Phe Cys Gly Asp Asn  
                     165                    170                    175  
 Val Ile Asn His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala  
                     180                    185                    190  
 Cys Ala Asp Ile Ser Ile Asn Val Ile Ser Met Gly Val Thr Asn Ile

```

      195              200              205
Ile Phe Leu Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe
 210              215              220
Ile Leu Val Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys
 225              230              235              240
Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Leu Val Phe Tyr
      245              250              255
Gly Thr Ile Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu
      260              265              270
Gly Ala Asp Lys Gln Asp Leu Ala Asp Xaa Leu Ile Ser Leu Phe Tyr
      275              280              285
Gly Val Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn
      290              295              300
Lys Asp Val Arg Ala Ala Val Thr Asn Leu Val Val Leu Lys Lys Ser
 305              310              315              320
Phe

```

&lt;210&gt; 2338

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M50 8075174-14-7636-10544 2097-1198)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(300)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2338

```

Gln Asp Leu Val Ala Thr Gly Val Ile Gly Ala Val Leu Ser Thr Met
 1              5              10              15
Gly Val Val Gly Val Val Gly Asn Val Tyr Thr Leu Val Val Met Cys
      20              25              30
Arg Phe Leu Arg Ala Ser Ala Ser Met Tyr Val Tyr Val Val Asn Leu
      35              40              45
Ala Leu Ala Asp Leu Leu Tyr Leu Leu Ser Ile Pro Phe Ile Val Ala
      50              55              60
Thr Tyr Val Thr Lys Asp Trp His Phe Gly Asp Val Gly Cys Arg Val
      65              70              75              80
Leu Phe Ser Leu Asp Phe Leu Thr Met His Ala Ser Ile Phe Thr Leu
      85              90              95
Thr Ile Met Ser Ser Glu Arg Tyr Ala Ala Val Leu Arg Pro Leu Asp
      100              105              110
Thr Val Gln Arg Ser Lys Gly Tyr Arg Lys Leu Leu Ala Leu Gly Thr
      115              120              125
Cys Cys Trp His Cys Cys Xaa Pro Tyr Pro Xaa Cys Tyr Ala Ile Arg
      130              135              140
Leu Val Arg Arg Gly Ser Lys Ser Leu Cys Leu Pro Ala Trp Gly Pro
      145              150              155              160
Arg Ala His Arg Thr Tyr Leu Thr Leu Leu Phe Gly Thr Ser Ile Val
      165              170              175
Gly Pro Gly Leu Val Ile Gly Leu Leu Tyr Ile Arg Leu Ala Arg Ala
      180              185              190
Tyr Trp Leu Ser Gln Gln Ala Ser Phe Lys Gln Thr Arg Arg Leu Pro
      195              200              205
Asn Pro Arg Val Leu Tyr Leu Ile Leu Gly Ile Val Leu Leu Phe Trp
      210              215              220
Ala Cys Phe Leu Pro Phe Val Ala Met Ala Ala Ala Gly Pro Val Pro
      225              230              235              240
Pro Gly His Ala Thr Asp Thr Arg Ala Ala Arg Ile Ile Asn Tyr Leu
      245              250              255

```

Thr Ala Cys Leu Thr Tyr Gly Asn Ser Cys Ile Asn Pro Phe Leu Tyr  
                   260                  265                  270  
 Thr Leu Leu Thr Lys Asn Tyr Arg Glu Tyr Leu Arg Gly Arg Gln Arg  
                   275                  280                  285  
 Ser Leu Gly Ser Ser Cys Arg Gly Pro Gly Ser Ala  
                   290                  295                  300

&lt;210&gt; 2339

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M51 8076974-22-383-3835 1573-554)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(340)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2339

Cys Leu Phe Phe Pro Gln Arg Asn Leu Asp Ala Met Asn Arg Ser Ala  
 1                  5                  10                  15  
 Ala His Val Thr Glu Phe Val Leu Leu Gly Phe Pro Gly Ser Trp Lys  
                   20                  25                  30  
 Ile Gln Ile Phe Leu Phe Val Leu Phe Leu Val Phe Tyr Val Leu Thr  
                   35                  40                  45  
 Leu Leu Gly Asn Gly Ala Ile Ile Cys Ala Val Arg Cys Asp Ser Arg  
                   50                  55                  60  
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu  
 65                  70                  75                  80  
 Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Ile Leu Ala Asn Ile Leu  
                   85                  90                  95  
 Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr  
                   100                  105                  110  
 Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met  
                   115                  120                  125  
 Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr  
                   130                  135                  140  
 Ile Met Thr Arg Arg Leu Cys Cys Ile Leu Val Ser Ser Cys Trp Leu  
 145                  150                  155                  160  
 Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Ser Ile Ser Gln Leu  
                   165                  170                  175  
 Pro Phe Cys Gly Ser Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp  
                   180                  185                  190  
 Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Phe Ile  
                   195                  200                  205  
 Phe Tyr Ala Gln Ser Ser Phe Val Leu Phe Phe Thr Ile Ala Tyr Ile  
                   210                  215                  220  
 Leu Arg Ser Tyr Ile Leu Leu Arg Ala Val Phe Gln Val Pro Ser  
 225                  230                  235                  240  
 Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val  
                   245                  250                  255  
 Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro  
                   260                  265                  270  
 Thr Tyr Gly Ile Pro Ile Leu Met Gln Lys Ile Leu Thr Leu Val Tyr  
                   275                  280                  285  
 Ser Val Met Thr Pro Leu Phe Asn Pro Leu Ile Tyr Ser Leu Arg Asn  
                   290                  295                  300  
 Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Leu Gly Met Arg Ile  
 305                  310                  315                  320  
 Val Lys Asn Met Xaa Val Lys Ala Val Ser Tyr Ser His Val Leu Ile  
                   325                  330                  335  
 Lys Asn Lys Leu

340

&lt;210&gt; 2340

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M57 8218295-1-14626-16881 1501-527)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2340

Cys	Pro	Phe	Leu	Xaa	Val	Met	Ser	Asn	Gln	Thr	Ser	Val	Thr	Glu	Phe
1				5					10					15	
Leu	Leu	Leu	Gly	Val	Thr	Asp	Ile	Gln	Glu	Leu	Asn	Pro	Ile	Leu	Phe
			20					25					30		
Val	Ile	Phe	Phe	Thr	Ile	Tyr	Phe	Val	Asn	Ile	Thr	Gly	Asn	Gly	Ala
			35				40					45			
Ile	Leu	Met	Ile	Val	Ile	Leu	Asp	Pro	Arg	Leu	His	Ser	Pro	Met	Tyr
			50			55					60				
Phe	Phe	Leu	Gly	Asn	Leu	Ala	Cys	Leu	Asp	Ile	Cys	Phe	Ser	Thr	Val
65				70					75					80	
Thr	Leu	Pro	Lys	Met	Leu	Gln	Asn	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Ile
			85					90						95	
Ser	Phe	Leu	Gly	Cys	Ile	Thr	Gln	Leu	His	Phe	Phe	His	Phe	Leu	Gly
			100				105						110		
Ser	Thr	Glu	Ala	Met	Leu	Leu	Pro	Val	Met	Ala	Phe	Asp	Arg	Phe	Val
			115				120					125			
Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Ser	Val	Ile	Met	Asn	His	Gln	Leu
			130			135					140				
Cys	Ile	His	Met	Thr	Val	Thr	Ile	Trp	Thr	Leu	Gly	Phe	Phe	His	Ala
145				150					155					160	
Leu	Leu	His	Ser	Val	Met	Thr	Ser	Arg	Leu	Ser	Phe	Cys	Gly	Pro	Asn
			165					170						175	
His	Val	His	His	Phe	Phe	Cys	Asp	Ile	Lys	Pro	Leu	Leu	Asp	Leu	Ala
			180				185						190		
Cys	Gly	Asn	Thr	Glu	Leu	Asn	Leu	Trp	Leu	Leu	Asn	Thr	Val	Thr	Gly
		195				200					205				
Thr	Ile	Ala	Leu	Thr	Pro	Phe	Phe	Leu	Thr	Phe	Leu	Ser	Tyr	Phe	Tyr
		210				215					220				
Ile	Ile	Thr	Tyr	Leu	Phe	Leu	Lys	Thr	Arg	Ser	Cys	Ser	Met	Leu	His
225				230					235					240	
Lys	Ala	Leu	Ser	Thr	Cys	Ala	Ser	His	Phe	Met	Val	Val	Ile	Leu	Leu
			245					250						255	
Tyr	Val	Pro	Val	Leu	Phe	Thr	Tyr	Ile	Arg	Pro	Ala	Ser	Gly	Ser	Ser
		260					265						270		
Leu	Asp	Gln	Asp	Arg	Ile	Ile	Ala	Ile	Met	Tyr	Ser	Val	Val	Thr	Pro
		275					280				285				
Ala	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Arg	Ser
		290				295					300				
Ala	Leu	Asn	Arg	Lys	Val	Arg	Arg	Trp	Leu	Xaa	Phe	Glu	Glu	Ile	Xaa
305				310					315						320
Ile	Thr	Leu	Leu	Trp											
				325											

&lt;210&gt; 2341

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M63 8218295-1-78460-79066 2-526)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(177)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2341

Val Ser Ala His Val Cys Met Gly Cys Xaa Leu Ser Trp Pro Val Arg  
 1 5 10 15  
 Cys Glu Ile Ile Phe Gly Val Met His Thr Thr Val Asn Phe Ser Ile  
 20 25 30  
 Val Leu Cys Gly Thr Ser Val Ile His Xaa Phe Cys Asp Val Leu Leu  
 35 40 45  
 Val Leu Lys Leu Ser Cys Leu Tyr Asp His Val Ser Glu Ile Ala Ile  
 50 55 60  
 Ser Asp Phe Ser Ile Ser Leu Ala Phe Phe Cys Phe Ile Ser Pro Asn  
 65 70 75 80  
 Phe Thr Tyr Val His Ile Phe Ser Thr Glu Leu Arg Met Pro Phe Val  
 85 90 95  
 Glu Gly Lys Thr Ser Val Phe Ser Thr Cys Leu Cys His Met Thr Ser  
 100 105 110  
 Ile Leu Phe Ile Pro Thr Gly Ile Phe Glu Phe Leu Arg Ser His Thr  
 115 120 125  
 Glu Ser Ser Thr Ser Leu Asp Phe Ile Leu Asn Phe Ser Tyr Phe Ser  
 130 135 140  
 Leu Ser Thr Leu Asn Pro Gly Ile Tyr Ser Leu Arg Asn Glu Ala Val  
 145 150 155 160  
 Asp Thr Val Gln Arg Lys Ile Phe Phe Phe Lys Glu Lys Tyr Leu Phe  
 165 170 175  
 Leu

&lt;210&gt; 2342

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M65 8218295-1-89089-90071 35-969)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(314)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2342

Ser Leu Phe Tyr Ser Gln Arg Ser Arg Met Asn Val Ala Asn Phe Thr  
 1 5 10 15  
 Ala Met Thr Ile Phe Leu Leu Leu Met Gly Phe Ser Arg Asn Ser Gln  
 20 25 30  
 Val Glu Ile Ile Phe Ser Thr Leu Ala Leu Val Val Leu Ile Gly Thr  
 35 40 45  
 Ile Ser Ile Val Ala Val Thr Ser Leu Ser Ile Arg Leu Cys Ser Leu  
 50 55 60  
 Met Pro Phe Leu Leu Ile His Leu Phe Cys Phe Asp Val Cys Tyr Ile  
 65 70 75 80  
 Ser Val Met Met Pro Lys Ser Val Cys Ser Ser Phe Met Tyr Ser Ala  
 85 90 95  
 Tyr Ile Ser Leu Ile Glu Cys Thr Leu Gln Val Phe Tyr Ser Gln Ser  
 100 105 110  
 Ser Tyr Thr Ala Met Ala Ile Leu Thr Val Met Ser Tyr Asp Cys Tyr  
 115 120 125  
 Met Ala Val Trp His Lys Val Ile Thr Asn Val Ser Thr Cys Ile His  
 130 135 140  
 Gly Val Leu Ala Val Leu Val Asn Gly Cys Glu Ile Ile Phe Gly Val

```

145          150          155          160
Met His Thr Thr Leu Thr Phe Ser Ile Tyr Ile Cys Gly Thr Ser Thr
          165          170          175
Ile Arg Xaa Phe Cys Asp Val Leu Leu Val Leu Lys Leu Ser Phe Thr
          180          185          190
Asn Asp His Val Asn Glu Leu Glu Ser Leu Ala Phe Ser Ser Val Glu
          195          200          205
Gly Arg Thr Lys Ser Phe Ser Thr Cys Leu Gly His Val Ser Val Gly
          210          215          220
Ser Leu Phe Asn Pro Pro Gly Val Phe Glu Phe Leu Asn Pro Tyr Ser
225          230          235          240
Glu Ser Pro Thr Ser Leu Asp Ile Ile Val Thr Val Phe Ile Leu Pro
          245          250          255
Gln Thr Leu Ser Val Glu Ile Tyr Ser Leu Ser Asn Glu Ala Ile Asp
          260          265          270
Thr Ala Xaa Arg Lys Phe Phe Phe Gln Arg Lys Thr Ser Leu Ser Ile
          275          280          285
Leu His Tyr Phe Leu Leu Gly Ser His Ile Xaa Xaa Val Leu Arg Lys
          290          295          300
Thr Thr Val Ser Met Asn Gln Leu Lys Leu
305          310

```

&lt;210&gt; 2343

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M70 8439670-95-9581-11872 695-1697)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2343

```

His Asp His Pro Ser Ala Glu Val Gly Gly Ala Met Ala Asn Ser Thr
1          5          10          15
Thr Val Thr Glu Phe Ile Leu Leu Gly Leu Ser Asp Ala Cys Glu Leu
          20          25          30
Gln Val Leu Ile Phe Leu Gly Phe Leu Leu Thr Tyr Phe Leu Ile Leu
          35          40          45
Leu Gly Asn Phe Leu Ile Ile Phe Ile Thr Leu Val Asp Arg Arg Leu
          50          55          60
Tyr Thr Pro Met Tyr Tyr Phe Leu Arg Asn Phe Ala Met Leu Glu Ile
65          70          75          80
Trp Phe Thr Ser Val Ile Phe Pro Lys Met Leu Thr Asn Ile Ile Thr
          85          90          95
Gly His Lys Thr Ile Ser Leu Leu Gly Cys Phe Leu Gln Ala Phe Leu
          100          105          110
Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu Leu Ala Val Met Ser
          115          120          125
Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Ala Thr Ile
130          135          140
Met Ser Lys Arg Val Cys Val Gln Leu Val Phe Cys Ser Trp Met Ser
145          150          155          160
Gly Leu Leu Leu Ile Ile Val Pro Ser Ser Ile Val Phe Gln Gln Pro
          165          170          175
Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Asn Phe Pro
          180          185          190
Leu Met Glu Leu Ile Cys Ala Asp Thr Ser Leu Val Glu Phe Leu Gly
          195          200          205
Phe Val Ile Ala Asn Phe Ser Leu Leu Gly Thr Leu Ala Val Thr Ala
210          215          220

```

Thr Cys Tyr Gly His Ile Leu Tyr Thr Ile Leu His Ile Pro S r Ala  
 225 230 235 240  
 Lys Glu Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val  
 245 250 255  
 Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met Tyr Val Arg Ser Gly  
 260 265 270  
 Lys Asn Gly Gln Gly Glu Asp His Asn Lys Val Val Ala Leu Leu Asn  
 275 280 285  
 Thr Val Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn  
 290 295 300  
 Lys Gln Val Lys Gln Val Phe Arg Glu His Val Ser Lys Phe Gln Lys  
 305 310 315 320  
 Phe Ser Gln Thr Xaa Arg Lys Ala Pro Leu Gln Thr Cys Leu Thr  
 325 330 335

&lt;210&gt; 2344

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M71 8439670-97-10488-11856 213-627)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(139)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2344

Ser Ile Val Cys Ser Leu Ser Leu Ser Phe Phe Leu Ser Phe Phe Leu  
 1 5 10 15  
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Leu  
 20 25 30  
 Ser Leu Ser Leu Ser Leu Ser Leu Ser Phe Phe Leu Ser Phe Phe Leu  
 35 40 45  
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Leu Pro Thr Phe Pro Pro  
 50 55 60  
 Ser Leu Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu  
 65 70 75 80  
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu  
 85 90 95  
 Ser Phe Phe Leu Ser Ser Leu Ser Phe Leu Ser Phe Tyr Ile Tyr Xaa  
 100 105 110  
 Trp Leu Val Cys Gly Pro Leu Pro Ser Xaa Gly Thr Val Gly Lys Gln  
 115 120 125  
 Ser Cys Val Met Met Leu Ile Cys Ser Trp Leu  
 130 135

&lt;210&gt; 2345

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M72 8439916-11-1-1677 434-1425)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(331)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2345

Phe Leu Leu Ala Trp Val His Arg Phe Leu Xaa Arg Arg Met Gly Phe  
 1 5 10 15  
 Glu Asn Gly Ser Ser Val Thr Glu Phe Ile Leu Val Gly Leu Thr Lys  
 20 25 30  
 Glu Ser Asp Leu Gln Cys Pro Leu Phe Ile Leu Phe Leu Met Met Tyr

```
<210> 2346
<211> 333
<212> PRT
<213> Mus musculus (M73 8439916-12-562-4356 2317-1320)
```

```
<220>
<221> VARIANT
<222> (1)...(333)
<223> Xaa = Any Amino Acid
```

<400> 2346															
Ile	Ser	Leu	Ile	Ser	Phe	Ile	Ser	Thr	Asp	Ser	Thr	Xaa	Arg	Arg	Met
1				5					10					15	
Val	Val	Thr	Asn	Gly	Ser	Leu	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly	Leu
			20					25					30		
Thr	Asp	Asn	Pro	Asp	Leu	Gln	Ile	Pro	Leu	Phe	Leu	Val	Phe	Leu	Val
		35				40						45			
Met	Tyr	Met	Ile	Thr	Ala	Phe	Gly	Asn	Leu	Thr	Leu	Ile	Leu	Leu	Thr
	50					55					60				
Val	Leu	Asn	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe	Asn
65				70						75				80	
Leu	Ser	Phe	Ile	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Val	Thr	Pro	Lys	Leu
				85					90					95	



Leu Met Asn Phe Val Leu Lys Lys Asn Ile Ile Gly Phe Ala Gly Cys  
                   100                  105                  110  
 Met Thr Gln Leu Tyr Phe Phe Cys Phe Ph Val Ile Ser Glu Cys Tyr  
                   115                  120                  125  
 Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
                   130                  135                  140  
 Leu Met Tyr Asn Val Thr Met Ser Pro Lys Val Cys Ser Tyr Leu Met  
 145                  150                  155                  160  
 Leu Gly Ser Tyr Leu Met Gly Phe Ser Asp Ala Met Ile His Thr Gly  
                   165                  170                  175  
 Cys Ile Leu Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His Tyr  
                   180                  185                  190  
 Phe Cys Asp Leu Leu Pro Leu Met Gln Leu Ser Cys Thr Ser Thr Tyr  
                   195                  200                  205  
 Ile Asn Glu Val Glu Ile Phe Ile Val Gly Gly Lys Asp Ile Thr Val  
                   210                  215                  220  
 Pro Ser Ile Val Ile Ile Ile Ser Tyr Gly Phe Ile Leu Ser Asn Ile  
 225                  230                  235                  240  
 Leu Gln Ile Lys Ser Thr Gly Gly Arg Ser Lys Ala Phe Asn Thr Cys  
                   245                  250                  255  
 Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Cys Ala Phe  
                   260                  265                  270  
 Met Tyr Leu Lys Pro Pro Ser Ala Gly Ser Leu Asn Glu Gly Lys Val  
                   275                  280                  285  
 Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Met Asn Pro Leu Ile  
                   290                  295                  300  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Arg Lys Thr Leu  
 305                  310                  315                  320  
 Ser Arg Arg Lys Phe Xaa Xaa Xaa Ile Tyr Tyr Leu Cys  
                   325                  330

&lt;210&gt; 2347

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M74 8439916-15-1-3070 860-1887)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(343)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2347

Phe Ser Phe Ile Phe Phe Val Ser Thr Asp Ser Leu Arg Glu Asp Met  
   1                  5                  10                  15  
 Thr Phe Glu Asn Ala Ser Met Val Ile Glu Phe Ile Leu Leu Gly Ile  
                   20                  25                  30  
 Thr Asp Gln Pro Asp Leu Lys Ile Pro Phe Phe Leu Leu Phe Phe Val  
                   35                  40                  45  
 Gly Tyr Met Ile Thr Val Leu Gly Asn Leu Thr Leu Ile Ile Leu Ile  
                   50                  55                  60  
 Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe Asn  
 65                  70                  75                  80  
 Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys Met  
                   85                  90                  95  
 Leu Met Ser Phe Ile Gln Lys Lys Asn Ile Ile Ser Tyr Thr Gly Cys  
                   100                  105                  110  
 Met Ile Gln Leu Tyr Phe Phe Cys Phe Phe Val Ile Ser Glu Cys Tyr  
                   115                  120                  125  
 Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
                   130                  135                  140  
 Leu Leu Tyr Asn Val Thr Leu Ser Ser Lys Val Cys Cys Tyr Leu Met

145                      150                      155                      160  
 Leu Gly Ser Tyr Phe Met Gly Phe Ser Gly Ala Met Ile His Thr Gly  
                                  165                      170                      175  
 Cys Ile Leu Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His Tyr  
                                  180                      185                      190  
 Phe Cys Asp Leu Leu Pro Leu Leu Gln Ile Ser Cys Thr Ser Thr Tyr  
                                  195                      200                      205  
 Ile Asn Glu Ile Glu Leu Phe Ile Val Ala Gly Lys Asp Ile Ile Val  
                                  210                      215                      220  
 Pro Thr Ile Ile Ile Phe Ile Ser Tyr Gly Phe Ile Leu Phe Ser Val  
 225                      230                      235                      240  
 Leu Lys Ile Lys Ser Thr Glu Ser Arg Ser Lys Ala Phe Ser Thr Cys  
                                  245                      250                      255  
 Ser Ser His Met Leu Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe  
                                  260                      265                      270  
 Met Tyr Leu Lys Pro Thr Ser Ala Leu Ser Ile Asn Lys Gly Lys Phe  
                                  275                      280                      285  
 Ser Ser Leu Phe Tyr Thr Ile Val Val Pro Met Met Asn Pro Leu Ile  
                                  290                      295                      300  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Thr Leu  
 305                      310                      315                      320  
 Asn Arg Arg Ile Phe Ser Ser Xaa Thr Gly Tyr Leu Xaa Ala Tyr Thr  
                                  325                      330                      335  
 Xaa Thr Ile Glu Arg Leu Cys  
                                  340

&lt;210&gt; 2348

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M75 8439916-16-717-3690 2556-1594)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2348

Lys Lys Met Ala Ser Ala Asn Val Ser Leu Val Thr Glu Phe Ile Leu  
 1                      5                      10                      15  
 Val Gly Leu Thr Asn Gln Pro Asp Leu Gln Ile Pro Leu Phe Phe Val  
                                  20                      25                      30  
 Phe Leu Ile Met Tyr Ile Val Thr Ala Leu Gly Asn Leu Cys Leu Ile  
                                  35                      40                      45  
 Ile Leu Ile Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe  
 50                      55                      60  
 Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Thr Val Phe Thr  
 65                      70                      75                      80  
 Pro Lys Met Leu Met Asn Phe Ile Leu Ser Lys Asn Ala Ile Ser Tyr  
                                  85                      90                      95  
 Met Gly Cys Leu Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Ile Ser  
                                  100                      105                      110  
 Glu Cys Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile  
                                  115                      120                      125  
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro Lys Leu Cys Leu  
                                  130                      135                      140  
 Asn Leu Met Leu Gly Thr Tyr Ala Met Ala Phe Ser Gly Ala Met Ala  
 145                      150                      155                      160  
 His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile  
                                  165                      170                      175  
 Asn His Tyr Phe Cys Asp Ile Leu Pro Val Met Gln Leu Ser Cys Thr  
                                  180                      185                      190

```

Ser Thr Tyr Val Asn Glu Leu Val Val Phe Ile Val Val Gly Ile Asn
    195                200                205
Ile Ile Val Pro Ser Ile Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu
    210                215                220
Ser Ser Ile Phe His Ile Lys Ser Asn Glu Gly Arg Ser Lys Ala Phe
    225                230                235                240
Ser Thr Cys Ser Ser His Ile Ile Ala Val Cys Leu Phe Phe Gly Ser
    245                250                255
Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Ser Ser Met Asp Gln
    260                265                270
Gly Lys Thr Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Met Asn
    275                280                285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Leu Arg
    290                295                300
Lys Thr Leu Ser Arg Trp Lys Phe Xaa Lys Glu Thr Thr Cys Thr Cys
    305                310                315                320
Leu

```

&lt;210&gt; 2349

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M76 8439916-16-8665-10443 1774-1125)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(217)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2349

```

Phe Leu Thr Phe Leu Pro Leu Leu Pro Phe Leu Ser Phe Phe Leu Ser
  1              5              10              15
Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Glu Cys
    20              25              30
Cys Val Leu Thr Ser Met Ala Tyr Asp Ser Ile Cys Asn Pro Leu Leu
    35              40              45
Tyr Asn Leu Phe Met Ser Pro Lys Xaa Cys Leu Asn Leu Ile Leu Gly
    50              55              60
Ser Phe Phe Ile Ser Phe Ser Asp Ala Val Ala His Ser Thr Cys Arg
    65              70              75              80
Leu Lys Leu Thr Phe Cys Asp Cys Asp Ile Pro Pro Leu Leu Gln Leu
    85              90              95
Cys Cys Thr Ser Thr Tyr Val Asn Glu Leu Val Ile Phe Phe Val Val
    100             105             110
Gly Cys Ile Asn Ile Ile Val Pro Ser Ser Thr Ile Leu Ile Ser Tyr
    115             120             125
Asp Phe Ile Leu Ser Ser Met Phe Cys Ile Lys Ser Ser Glu Gly Arg
    130             135             140
Ser Lys Ala Phe Ser Thr Tyr Ser Ser His Val Ile Ser Leu Ser Leu
    145             150             155             160
Phe Phe Asp Ser Ser Ala Phe Val Tyr Phe Lys Ser Ser Ser Ala Gly
    165             170             175
Ser Leu Gly Glu Glu Asn Ile Ser Ser Val Phe Tyr Ser Asn Val Val
    180             185             190
Leu Ile Val Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Ser Leu
    195             200             205
Arg Lys Thr Leu Thr Arg Lys Asn Phe
    210             215

```

&lt;210&gt; 2350

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M77 8439916-17-1-2001 619-1618)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2350

```

Ile Ile Leu Xaa Tyr Asn Ser Phe Phe Leu Ser Leu Xaa Ile Pro Leu
1           5           10           15
Lys Arg Met Asp Ser Val Asn Val Ser Leu Val Thr Glu Phe Leu Leu
          20           25           30
Val Gly Leu Thr His Gln Pro Asp Arg Gln Ile Pro Leu Phe Leu Leu
          35           40           45
Phe Leu Ala Met Tyr Leu Val Thr Ala Leu Gly Asn Leu Gly Leu Ile
          50           55           60
Ile Leu Val Leu Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe
65           70           75           80
Leu Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Phe Thr
          85           90           95
Pro Lys Met Leu Met Asn Phe Ile Leu Arg Gln Asn Ala Ile Ser Tyr
          100          105          110
Met Gln Cys Met Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Val Ser
          115          120          125
Glu Cys Phe Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
          130          135          140
Cys Asn Pro Leu Leu Tyr Asn Val Met Ile Ser Pro Gln Val Cys Leu
145          150          155          160
Asn Leu Met Ile Gly Ser Tyr Leu Met Ala Phe Ser Glu Ala Val Ala
          165          170          175
Leu Thr Val Cys Met Leu Thr Leu Thr Phe Cys Asp Gly Asn Ile Asn
          180          185          190
His Tyr Phe Cys Asp Ile Leu Ala Leu Phe Gln Leu Ser Cys Ser Ser
          195          200          205
Thr Tyr Val Asn Lys Leu Val Ala Tyr Val Ile Val Val Ile Asn Ile
          210          215          220
Leu Phe Ser Thr Pro Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
225          230          235          240
Ser Ile Phe Arg Ile Ser Ser Ser Lys Gly Arg Ser Lys Ala Phe Ser
          245          250          255
Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
          260          265          270
Ala Phe Val Tyr Phe Lys Pro Ser Ser Pro Gly Ser Met Glu Trp Ala
          275          280          285
Lys Ile Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Met Asn Pro
          290          295          300
Leu Ile Tyr Ser Leu Lys Asn Lys Asp Val Lys Ile Ala Leu Arg Lys
305          310          315          320
Ser Leu Ala Arg Xaa Arg Phe Asp Trp Ile His Met Tyr
          325          330

```

&lt;210&gt; 2351

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M78 8439916-17-6970-9135 1261-2156)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(299)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2351

```

Thr Asp Ser Pro Xaa Arg Arg Met Asp Xaa Val Asn Ile Ser Leu Val
 1          5          10          15
Thr Glu Phe Ile Val Val Gly Xaa Ala Glu Gln Pro Asp Leu Gln Ile
          20          25          30
Pro Met Phe Phe Gly Phe Leu Ala Met Tyr Thr Val Thr Ala Leu Glu
          35          40          45
Asn Leu Phe Leu Ile Ile Leu Thr Val Leu Asn Ser His Val His Thr
          50          55          60
Thr Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Val Val Leu Cys Tyr
65          70          75          80
Ser Ser Val Phe Thr Pro Gln Met Leu Met Asn Phe Ile Ile Arg Lys
          85          90          95
Asn Thr Ile Ser Tyr Met Glu Cys Ile Thr Xaa Leu Phe Phe Leu Ser
          100          105          110
Phe Phe Leu Ile Phe Leu Cys Phe Phe Leu Ser Ser Phe Phe Leu Ser
          115          120          125
Phe Phe Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe
          130          135          140
Phe Leu Ser Ser Phe Leu Pro Ser Leu Leu Pro Ser Phe Leu Ser Phe
145          150          155          160
Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Leu Ser Phe
          165          170          175
Leu Ser Ala Ala Tyr Xaa Leu Gln Cys Ala Met Ile Ser Ile Cys Asn
          180          185          190
Ser Leu Val Tyr Asn Leu Phe Met Arg Pro Xaa Val Leu Ser Glu Pro
          195          200          205
Tyr Ser Trp Val Ile Leu Xaa Phe Ile Tyr Xaa Cys Val Asn Thr Leu
          210          215          220
Ser Ser Gly Ile Glu Thr Asp Thr Val Arg Arg Glu Thr Ser Cys Leu
225          230          235          240
Arg Val Arg Pro Ala Ala Pro Gly His Met Ser Val Ser Leu Glu Phe
          245          250          255
Phe Phe Cys Ser Gly Arg Val Tyr Leu Trp Gly Leu Pro Gln Thr Glu
          260          265          270
Leu Ile Pro Tyr Ala Xaa Leu Pro Val Gln Arg Pro Pro Val Leu Glu
          275          280          285
Glu Ser Leu Glu Gly Arg Arg Ala Arg Asn Val
          290          295

```

&lt;210&gt; 2352

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M80 8439916-20-13750-16634 2033-1016)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(339)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2352

```

Cys His Ser Phe Phe Leu Leu Leu Ile His Arg Leu Phe Xaa Arg Arg
 1          5          10          15
Met Gly Val Glu Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Gln Gly
          20          25          30
Leu Thr Ser Asp Pro Asp Leu Gln Leu Pro Leu Phe Leu Phe Leu
          35          40          45
Leu Ile Tyr Thr Thr Thr Ala Leu Gly Asn Leu Ser Leu Ile Thr Leu
          50          55          60
Ile Ala Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu

```

```

65          70          75          80
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
      85          90          95
Met Leu Met Asn Phe Leu Val Ser Lys Asn Phe Ile Ser Tyr Val Gly
      100         105         110
Cys Met Thr Gln Leu Tyr Leu Phe Val Phe Phe Ala Val Ser Glu Cys
      115         120         125
Cys Val Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      130         135         140
Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro Gln Val Cys Ser Tyr Leu
145         150         155         160
Met Leu Gly Ser Tyr Ile Met Gly Phe Ser Gly Ala Met Ile His Thr
      165         170         175
Gly Trp Met Leu Arg Leu Thr Phe Cys Asp Arg Ser Ile Ile Asn His
      180         185         190
Tyr Phe Cys Asp Leu Leu Pro Leu Leu Gln Leu Ser Cys Thr Asn Thr
      195         200         205
Tyr Ala Asn Glu Ile Glu Ile Ile Ile Val Gly Gly Ile Asp Ile Ile
      210         215         220
Val Pro Ser Ile Ile Ile Phe Thr Ser Tyr Gly Phe Val Leu Ser Asn
225         230         235         240
Ile Phe Gln Met Arg Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
      245         250         255
Cys Ser Ser His Ile Val Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
      260         265         270
Phe Met Tyr Leu Gln Pro Ser Ser Pro Glu Ser Met Asp Gln Gly Lys
      275         280         285
Arg Ser Ser Val Phe Tyr Thr Ile Leu Val Pro Met Met Asn Pro Leu
290         295         300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Leu Lys Lys Thr
305         310         315         320
Phe Ser Thr Gln Ser Val Xaa Xaa Glu Ile Asn Val Tyr His Tyr Thr
      325         330         335
Tyr Ala Asn

```

&lt;210&gt; 2353

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M82 8439916-21-1-3132 1296-290)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2353

```

Asn Phe Ile Phe Phe Leu Pro Ile Asp Ser Leu Arg Glu Asp Met Ala
1          5          10          15
Leu Glu Asn Ala Ser Leu Val Thr Glu Phe Ile Leu Met Gly Leu Thr
      20          25          30
Asn Arg Pro Asp Leu Gln Ile Pro Leu Phe Leu Leu Phe Leu Val Met
      35          40          45
Tyr Val Ile Ala Thr Leu Gly Asn Leu Ala Leu Ile Met Leu Ile Ile
      50          55          60
Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu Asn Leu
65         70         75         80
Ser Cys Ile Asp Leu Phe Tyr Cys Ser Val Ile Thr Pro Lys Met Leu
      85          90          95
Met Asn Phe Val Leu Lys Lys Asn Val Ile Ser Tyr Glu Gly Cys Met
      100         105         110

```

Ala Gln Phe Tyr Phe Phe Ala Phe Phe Ala Ile Ser Glu Cys Tyr Val  
 115 120 125  
 Leu Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu  
 130 135 140  
 Leu Tyr Asn Ile Val Met Ser Pro Lys Leu Cys Ser Tyr Leu Met Met  
 145 150 155 160  
 Gly Thr Tyr Leu Met Gly Phe Ser Gly Ala Met Ile His Thr Gly Cys  
 165 170 175  
 Ile Leu Arg Leu Thr Phe Cys Asp Lys Asn Thr Ile Asn His Tyr Phe  
 180 185 190  
 Cys Asp Ile Leu Pro Leu Leu Gln Ile Ser Cys Thr Ser Thr Tyr Val  
 195 200 205  
 Asn Glu Ile Glu Leu Phe Ile Val Ala Gly Lys Asp Ile Ile Val Pro  
 210 215 220  
 Thr Val Ile Ile Phe Thr Ser Tyr Gly Phe Ile Leu Ser Ser Ile Leu  
 225 230 235 240  
 Lys Ile Ser Ser Thr Ala Gly Met Ser Lys Ala Phe Ser Thr Cys Ser  
 245 250 255  
 Ser His Ile Ile Ala Leu Cys Leu Phe Phe Gly Ser Cys Thr Phe Met  
 260 265 270  
 Tyr Leu Lys Pro Ser Ser Val Glu Ser Met Asp Gln Gly Lys Ile Ser  
 275 280 285  
 Ser Val Phe Tyr Asn Ile Val Val Pro Leu Met Asn Pro Leu Ile Tyr  
 290 295 300  
 Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Ile Lys Lys Thr Ile Thr  
 305 310 315 320  
 Lys Gly Lys Phe Xaa Ser Glu Phe Val Ile Leu Phe Thr Phe Ser Tyr  
 325 330 335

&lt;210&gt; 2354

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M84 8439916-22-16651-22211 2487-1540)

&lt;400&gt; 2354

Met Ala Leu Ala Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Thr Asp Gln Pro Asp Leu Gln Met Pro Leu Phe Leu Ile Phe Leu  
 20 25 30  
 Ile Ile Tyr Leu Ile Thr Ala Phe Gly Asn Leu Thr Leu Ile Ile Leu  
 35 40 45  
 Ile Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Leu Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Met Asn Phe Val Leu Glu Lys Asn Ile Ile Ser Tyr Met Gly  
 85 90 95  
 Cys Met Thr Gln Phe Tyr Phe Phe Gly Phe Phe Ala Ile Ser Glu Cys  
 100 105 110  
 Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Ser Val Ala Met Ser Pro Lys Met Cys Ser Tyr Phe  
 130 135 140  
 Ile Leu Gly Ser Tyr Phe Met Gly Phe Ser Gly Ala Met Ile His Thr  
 145 150 155 160  
 Gly Cys Val Met Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His  
 165 170 175  
 Tyr Phe Cys Asp Leu Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr  
 180 185 190  
 Tyr Val Asn Glu Ile Glu Leu Phe Ile Val Thr Gly Lys Asp Ile Ile  
 195 200 205

Val Pro Thr Val Ile Ile Phe Ala Ser Tyr Gly Phe Ile Leu Ser Asn  
 210 215 220  
 Ile Leu Lys Ile Arg Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Ile Ile Ala Val Ser Met Phe Phe Gly Ser Ser Ala  
 245 250 255  
 Phe Met Tyr Leu Lys Pro Ser Ser Ala Val Ser Met Asn Glu Ala Lys  
 260 265 270  
 Phe Ser Ser Ile Phe Tyr Ser Ile Val Val Pro Met Met Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Gly Leu Lys Lys Thr  
 290 295 300  
 Leu Ser Arg Met Phe Ser His Asn Leu Ile Ser Leu  
 305 310 315

&lt;210&gt; 2355

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M90 8567804-15-6071-7402 605-1319)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(239)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2355

Asn Thr Glu Gly His Ser Leu Ile Leu Thr Tyr Asn Val Ser Asn Thr  
 1 5 10 15  
 Gln Ile Asn Cys Phe Cys Leu Ile Tyr Thr Xaa Tyr Asn Leu Leu Xaa  
 20 25 30  
 Phe Leu Glu Ile Tyr Phe Cys Pro Leu Leu Ile Pro Cys Val Ala Glu  
 35 40 45  
 Trp Ser Arg Gly Asp Cys Ile Glu Ile Leu Glu Tyr Asn Ile Cys Ile  
 50 55 60  
 Phe Ile Lys Leu Met Val Pro Thr Met Ser Ser Leu His Tyr Leu Met  
 65 70 75 80  
 Asn Ser Ser Val Xaa Tyr Leu Lys Ile Phe His Val Ser Lys Glu Leu  
 85 90 95  
 Tyr Gly Ser Phe Leu Gly Gly Ile Phe Phe Leu Ala Asn His Cys Arg  
 100 105 110  
 Glu Ile Glu Ile Ser Asn Arg Thr Thr Glu Met Arg Ile Lys Ala Leu  
 115 120 125  
 Gln Lys Gly Leu Arg Asp Ile Ser Phe Ile Thr Asn Ser Val Gly Ile  
 130 135 140  
 Val Ile Leu Ile Ile Ile Tyr Ala Arg Leu Gln Lys Ser Thr Glu Gly  
 145 150 155 160  
 Thr Val Lys Thr Ser Ser Asn Cys Gly Tyr His Ile Ile Ser Ile Tyr  
 165 170 175  
 Leu Phe Phe Leu Lys Phe Ala Phe Leu Tyr Ile Phe Lys Tyr Val Ser  
 180 185 190  
 Arg Met His Gln Gly Ser Val Ser Ser Val Phe Tyr Thr Asn Val Val  
 195 200 205  
 Pro Ile Cys Asn Thr Leu Ile Tyr Ser Leu Xaa Asn Asp Val Thr Ile  
 210 215 220  
 Ala Trp Met Asn Val Leu Met Lys Phe Gln Arg His Leu Phe Tyr  
 225 230 235

&lt;210&gt; 2356

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M96 8567804-8-3023-3783 759-153)



&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(202)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2356

```

Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe
 1           5           10           15
Phe Gln Phe Leu Gly Ile Tyr Val Val Ser Ile Val Gly Asn Leu Gly
      20           25           30
Leu Ile Val Leu Ile Val Leu Asn Pro His Leu His Thr Pro Met Tyr
      35           40           45
Tyr Phe Leu Phe Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Ala
      50           55           60
Ile Thr Pro Lys Met Leu Val Gly Phe Val Asn Gln Asn Ile Ile Ala
      65           70           75           80
His Ala Glu Cys Leu Thr Gln Leu Phe Phe Cys Phe Phe Val Leu
      85           90           95
Asp Glu Cys Tyr Ile Cys Thr Glu Met Ala Tyr Asp Arg Tyr Ala Ala
      100          105          110
Ile Cys Lys Thr Leu Leu Asn Gln Val Thr Met Ser His Gln Val Cys
      115          120          125
Leu Glu Ile Thr Lys Gly Trp Ile Ile Leu Tyr Ser Glu Met Glu Lys
      130          135          140
Ser Lys Lys Ser Phe Xaa Met Tyr Ile Ser Ile Leu Leu Phe Phe Ser
      145          150          155          160
Leu Phe Gly Asp Ile Ile Ser Leu Lys Ser Phe Met Leu Ser Lys Cys
      165          170          175
Leu Thr Thr Asp Leu His Leu Lys Ser Arg His Ile Cys Lys Phe Cys
      180          185          190
Val Ala Val Ser Asp Asn Val Leu Leu Leu
      195          200

```

&lt;210&gt; 2357

&lt;211&gt; 123

&lt;212&gt; PRT.

&lt;213&gt; Mus musculus (M98 8570471-14-891-2711 1429-1795)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(123)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2357

```

Leu Cys Gly Ser Gly Thr Leu Ile Phe Ser Ser Glu Met Leu Phe Ile
 1           5           10           15
Phe Leu Gly Lys Xaa Phe Phe Gly Xaa Xaa Asp Leu Ile Val Ala Ile
      20           25           30
Phe Cys Ile Phe Asn Phe Leu Lys Leu Ser Leu Leu Thr Lys Val Pro
      35           40           45
Glu Cys Asp Phe Xaa Asn Lys Leu Ser Xaa Xaa Asn Glu Tyr Ile Xaa
      50           55           60
Asn Ile Val Pro Asp Ser Tyr Xaa Tyr Arg Asn Leu Tyr Trp Gly Asn
      65           70           75           80
Gly Asn Met Ser Ser Thr Gly Cys Met Leu Arg Leu Thr Ser Trp Asp
      85           90           95
Gly Asn Thr Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Phe Leu Gln
      100          105          110
Leu Ser Cys Thr Ser Thr Tyr Val His Tyr Thr
      115          120

```

<210> 2358  
 <211> 179  
 <212> PRT  
 <213> Mus musculus (M99 8570471-17-1-2939 17-553)

<220>  
 <221> VARIANT  
 <222> (1)...(179)  
 <223> Xaa = Any Amino Acid

<400> 2358  
 Ile Cys Leu Asn Leu Met Leu Val Ser Tyr Phe Ile Ala Phe Ser Glu  
 1 5 10 15  
 Ser Val Ala His Thr Ala Cys Met Leu Arg Leu Thr Phe Cys Asp Ala  
 20 25 30  
 Asn Thr Ile Asn Tyr Tyr Phe Cys Asp Ile Pro Pro Leu Leu Gln Leu  
 35 40 45  
 Ser Cys Thr Thr Thr Arg Val Asn Glu Val Val Ile Phe Val Val Gly  
 50 55 60  
 Ser Ile Asn Ile Ile Ile Pro Thr Ser Thr Ile Phe Val Ser Tyr Gly  
 65 70 75 80  
 Phe Ile Leu Ser Ser Ile Phe Leu Ile Thr Ala Ser Glu Gly Arg Ser  
 85 90 95  
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Ala Phe Leu Phe  
 100 105 110  
 Phe Gly Ser Gly Ala Ile Arg Tyr Phe Lys Pro Ser Ser Asp Gly Ser  
 115 120 125  
 Met Asp Glu Gly Lys Ile Ser Ser Val Phe Tyr Thr Asn Val Ile Pro  
 130 135 140  
 Met Ile Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Ile Lys Val  
 145 150 155 160  
 Ala Leu Arg Arg Thr Leu Arg Lys Arg Asn Phe Xaa Leu Ser Ser Val  
 165 170 175  
 Val Cys Val

<210> 2359  
 <211> 324  
 <212> PRT  
 <213> Mus musculus (M100 8570471-17-6599-8104 424-1396)

<220>  
 <221> VARIANT  
 <222> (1)...(324)  
 <223> Xaa = Any Amino Acid

<400> 2359  
 Ile Phe Cys Val Tyr Arg Phe Ser Gln Arg Arg Met Asp Ser Val Asn  
 1 5 10 15  
 Ile Ser Leu Val Thr Glu Phe Ile Leu Val Gly Leu Thr Asp Lys Pro  
 20 25 30  
 Tyr Leu Gln Ile Pro Leu Phe Phe Ile Phe Leu Ala Met Tyr Leu Val  
 35 40 45  
 Thr Ala Leu Gly Asn Leu Ser Leu Ile Ile Leu Thr Val Leu Asn Ser  
 50 55 60  
 His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Val  
 65 70 75 80  
 Asp Phe Cys Tyr Ser Ser Val Phe Thr Pro Gln Met Leu Met Asn Phe  
 85 90 95  
 Ile Thr Arg Lys Asn Thr Ile Ser Tyr Met Glu Cys Met Ser Gln Leu

```

      100      105      110
Tyr Phe Phe Cys Phe Phe Val Ile Ser Glu Cys Tyr Val Leu Thr Ser
      115      120      125
Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Asn
      130      135      140
Leu Val Met Ser Ser Lys Leu Cys Leu Asn Leu Met Leu Val Ser Tyr
145      150      155      160
Phe Ile Ala Phe Ser Glu Ser Val Ala His Thr Val Cys Ile Met Arg
      165      170      175
Leu Asn Phe Cys Asp Ala Ser Lys Ile Asn His Tyr Phe Cys Asp Ile
      180      185      190
Pro Pro Leu Leu Gln Leu Ser Cys Thr Thr Thr Tyr Ile Asn Lys Leu
      195      200      205
Val Val Phe Val Ala Ser Ser Ile Asn Ile Ile Val Pro Ile Ser Thr
      210      215      220
Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser Ile Phe His Ile His
225      230      235      240
Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Ile
      245      250      255
Ile Ala Ala Phe Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr Phe Gln
      260      265      270
Pro Ser Ser Ala Glu Ser Met Asp Glu Gly Lys Ile Ser Ser Val Phe
      275      280      285
Tyr Thr Asn Val Ile Pro Met Met Asn Pro Leu Leu Tyr Ser Leu Arg
      290      295      300
Asn Lys Asp Ile Lys Val Ala Leu Arg Lys Thr Leu Ser Lys Arg Asn
305      310      315      320
Ile Xaa Leu Tyr

```

&lt;210&gt; 2360

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M101 8570471-19-17517-20152 1114-134)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2360

```

Leu Phe Ile Phe His Lys Ile Ser Tyr Arg Ser Met Ala Leu Ile Asn
1      5      10      15
Gly Ser Val Val Thr Glu Phe Ile Leu Leu Gly Leu Thr Asp Gln Pro
      20      25      30
Asp Leu Gln Val Pro Leu Phe Leu Val Phe Leu Leu Met Tyr Met Ile
      35      40      45
Thr Ala Leu Gly Asn Leu Thr Leu Ile Ile Leu Ile Val Leu Asn Ser
      50      55      60
His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Val
      65      70      75      80
Asp Phe Cys Tyr Ser Ser Val Ile Ile Pro Lys Met Leu Met Asn Phe
      85      90      95
Ile Leu Lys Lys Asn Phe Ile Ser Tyr Val Gly Cys Met Thr Gln Phe
      100      105      110
Tyr Leu Phe Gly Phe Cys Val Ile Leu Glu Cys Tyr Ile Leu Thr Ser
      115      120      125
Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Asn
      130      135      140
Ile Val Met Ser Pro Lys Met Cys Ser Tyr Leu Met Leu Gly Ser Tyr
145      150      155      160

```

Leu Met Gly Phe Ser Gly Ala Met Ile His Thr Gly Cys Val Leu Arg  
 165 170 175  
 Leu Ser Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Phe Cys Asp Leu  
 180 185 190  
 Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn Glu Ile  
 195 200 205  
 Glu Val Leu Ile Val Ala Gly Lys Asp Ile Ile Val Pro Thr Val Ile  
 210 215 220  
 Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser Ile Phe Gln Met Lys  
 225 230 235 240  
 Ser Thr Lys Gly Met Ser Lys Ala Phe Ser Thr Cys Ser Ser His Ile  
 245 250 255  
 Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys  
 260 265 270  
 Pro Asn Ser Thr Gly Thr Met Asn Asn Gly Lys Ile Pro Ser Ile Ile  
 275 280 285  
 Tyr Thr Ile Leu Ile Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg  
 290 295 300  
 Asn Lys Asp Val Lys Val Ala Leu Arg Lys Thr Leu Arg Lys Lys Ile  
 305 310 315 320  
 Leu Xaa Ser Glu Thr Val Ile  
 325

&lt;210&gt; 2361

&lt;211&gt; 341

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M104 8570471-3-1-2271 2172-1151)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(341)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2361

Asn Phe Ala Ile Phe Phe Ser Val His Arg Phe Ser Xaa Arg Arg Met  
 1 5 10 15  
 Ala Leu Val Asn Gly Ser Thr Val Thr Glu Phe Ile Leu Leu Gly Leu  
 20 25 30  
 Thr Asp Gln Pro Gly Leu Gln Met Pro Leu Phe Leu Leu Phe Leu Leu  
 35 40 45  
 Met Tyr Met Ile Thr Val Phe Gly Asn Leu Thr Leu Ile Phe Leu Ile  
 50 55 60  
 Leu Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu Asn  
 65 70 75 80  
 Leu Ser Phe Val Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys Met  
 85 90 95  
 Leu Met Asn Phe Ile Leu Lys Lys Asn Leu Ile Ser Tyr Met Gly Cys  
 100 105 110  
 Met Ser Gln Leu Tyr Phe Phe Cys Phe Phe Ile Ile Ser Glu Cys Tyr  
 115 120 125  
 Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro  
 130 135 140  
 Leu Leu Tyr Asn Thr Ala Met Ser Pro Arg Val Cys Ser Tyr Leu Met  
 145 150 155 160  
 Leu Gly Thr Tyr Leu Met Gly Phe Phe Asp Ala Met Ile His Thr Gly  
 165 170 175  
 Cys Met Leu Arg Leu Ser Phe Cys Asp Gly Asn Ile Ile Asn His Tyr  
 180 185 190  
 Phe Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr  
 195 200 205  
 Val Asn Glu Thr Glu Ile Phe Ile Val Gly Gly Lys Asp Ile Ile Leu

210	215	220
Pro Ser Ala Ile Ile Ph	Phe Ser Tyr Gly Phe	Ile Leu Ser Asn Ile
225	230	235
Phe Gln Ile Arg Ser	Thr Leu Gly Arg Ser	Lys Ala Phe Ser Thr Cys
245	250	255
Ser Ser His Ile Ile Ala	Val Ser Leu Phe Phe	Gly Ser Cys Gly Phe
260	265	270
Met Tyr Leu Lys Pro Ser	Ser Ala Val Ser Ile	Asp Gln Gly Lys Ile
275	280	285
Ser Ser Ile Phe Tyr Thr	Ile Val Val Pro Met	Met Asn Pro Leu Ile
290	295	300
Tyr Ser Leu Arg Asn Lys	Asp Val Lys Val Ala	Leu Arg Lys Thr Leu
305	310	315
Ser Arg Arg Lys Phe Leu	Lys Val Xaa Leu Gln	Ser Arg His Phe Leu
325	330	335
Cys Xaa Cys Thr Tyr		
340		

&lt;210&gt; 2362

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M106 8570471-9-3672-5945 1670-660)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(337)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2362

Ile Asn Ile Phe Phe Leu	Leu Pro Thr Xaa Asn Met	Gln Val Gln Met
1	5	10
Ala Asp Thr Asn His Ser	Thr Val Thr Glu Phe Ile	Leu Ala Gly Leu
20	25	30
Thr Asp Lys Pro Glu Leu	Gln Leu Pro Leu Phe	Leu Leu Phe Leu Gly
35	40	45
Ile Tyr Leu Leu Thr Val	Leu Gly Asn Leu Gly	Met Ile Ile Leu Ile
50	55	60
Leu Leu Ser Ser His Leu	His Thr Pro Met Tyr	Phe Phe Leu Ser Ser
65	70	75
Leu Ser Phe Ile Asp Leu	Cys Tyr Ser Thr Val	Ile Thr Pro Lys Met
85	90	95
Leu Val Asn Phe Val Ala	Lys Lys Asn Val Ile	Ser Tyr Glu Glu Cys
100	105	110
Met Thr Gln Leu Tyr Phe	Phe Leu Ala Phe Val	Ile Ser Glu Cys His
115	120	125
Met Leu Ala Ala Met Ala	Tyr Asp Arg Tyr Val	Ala Ile Cys Asn Pro
130	135	140
Leu Leu Tyr Asn Val Thr	Met Ser Tyr Gln Ile	Cys Ser Trp Met Val
145	150	155
Gly Gly Val Tyr Gly Met	Gly Leu Ile Gly Ala	Ala Val His Thr Leu
165	170	175
Cys Met Leu Arg Val Val	Phe Cys Lys Ala Asn	Ile Ile Asn His Tyr
180	185	190
Phe Cys Asp Leu Phe Pro	Leu Met Glu Leu Ala	Cys Ser Ser Thr Tyr
195	200	205
Val Asn Glu Val Val Leu	Leu Cys Leu Ser Ala	Phe Asn Ile Phe Ile
210	215	220
Pro Thr Leu Thr Ile Leu	Gly Ser Tyr Ile Phe	Ile Ile Ile Ser Ile
225	230	235
Leu Arg Ile Lys Ser Thr	Glu Gly Arg Phe Lys	Ala Phe Ser Thr Cys
245	250	255

Ser Ser His Phe Ser Ala Val Ser Val Phe Phe Gly Ser Leu Ala Phe  
                   260                  265                  270  
 Met Tyr Leu Gln Pro Phe Ser Val Ser Ser Lys Asp Lys Gly Lys Val  
                   275                  280                  285  
 Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met Leu Asn Pro Met Ile  
                   290                  295                  300  
 Tyr Ser Leu Arg Asn Arg Asp Val Lys Leu Ala Leu Asn Lys Leu Phe  
 305                  310                  315                  320  
 Gln Lys Lys Phe His Val Xaa Arg Ser Ile Tyr Leu Arg Lys Thr Ile  
                   325                  330                  335  
 Gln

&lt;210&gt; 2363

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M107 8571727-11-1262-2044 781-16)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(256)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2363

Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe  
 1                  5                  10                  15  
 Phe Gln Phe Leu Gly Ile Tyr Val Val Ser Ile Val Gly Asn Leu Gly  
                   20                  25                  30  
 Leu Ile Val Leu Ile Val Leu Asn Pro His Leu His Thr Pro Met Tyr  
                   35                  40                  45  
 Tyr Phe Leu Phe Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Ala  
                   50                  55                  60  
 Ile Thr Pro Lys Met Leu Val Gly Phe Val Asn Gln Asn Ile Ile Ala  
 65                  70                  75                  80  
 His Ala Glu Cys Leu Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Leu  
                   85                  90                  95  
 Asp Glu Cys Tyr Ile Cys Thr Glu Met Ala Tyr Asp Arg Tyr Ala Ala  
                   100                  105                  110  
 Ile Cys Lys Thr Leu Leu Asn Gln Val Thr Met Ser His Gln Val Cys  
                   115                  120                  125  
 Leu Gly Asn His Lys Arg Leu Asp Tyr Ile Ile Phe Arg Asn Gly Lys  
                   130                  135                  140  
 Ile Lys Lys Ile Phe Leu Asn Val His Ile Tyr Phe Ile Ile Phe Xaa  
 145                  150                  155                  160  
 Phe Val Cys Gly Thr Ser Tyr Pro Xaa Ser Leu Ser Cys Xaa Ala Ser  
                   165                  170                  175  
 Val Xaa Pro Leu Thr Tyr Ile Leu Arg Val Gly Thr Phe Val Ser Phe  
                   180                  185                  190  
 Val Trp Leu Ser Gln Thr Met Ser Tyr Tyr Phe Ile Ile Ala Asn Leu  
                   195                  200                  205  
 Trp Asp Asn Leu Xaa Glu Ser Ser Phe Xaa Arg Leu Ile Cys Cys Ser  
                   210                  215                  220  
 Lys Gly Xaa Ser Lys Glu Gly Lys Xaa Lys Leu Leu Ser Phe Trp Ser  
 225                  230                  235                  240  
 Phe Phe Ile Val Leu Lys Gln Phe Arg Lys Glu Gly Leu Thr Ser Tyr  
                   245                  250                  255

&lt;210&gt; 2364

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M111 8571727-21-4956-7261 1151-153)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2364

```

Ile Leu Met Leu Xaa Leu Leu Leu Phe Leu Gln Glu Arg Met Val Leu
 1           5           10           15
Glu Asn Ser Ser Ser Val Lys Glu Phe Ile Leu Leu Gly Leu Thr Gln
          20           25           30
Gln Pro Glu Leu Gln Met Pro Leu Phe Phe Leu Phe Leu Gly Ile Tyr
      35           40           45
Ile Val Ser Met Val Gly Asn Leu Gly Leu Thr Val Leu Ile Val Leu
      50           55           60
Asn Pro His Leu His Asn Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser
      65           70           75           80
Phe Thr Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro Arg Met Leu Val
          85           90           95
Gly Phe Val Lys Gln Asn Thr Ile Ser His Ala Glu Cys Met Thr Gln
          100          105          110
His Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr Ile Leu Thr
          115          120          125
Ala Val Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Lys Pro Leu Leu Tyr
          130          135          140
Gln Val Thr Met Ser His Gln Val Cys Leu Leu Met Thr Val Gly Val
          145          150          155          160
Tyr Val Met Gly Phe Leu Glu Ala Ile Ala His Thr Gly Ser Met Val
          165          170          175
Ser Leu Thr Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Ala Cys Asp
          180          185          190
Ile Leu Pro Leu Leu Lys Leu Ser Cys Thr Ser Thr Thr Ile Asn Glu
          195          200          205
Leu Val Val Phe Ile Val Val Gly Val Asn Val Ile Val Pro Thr Leu
          210          215          220
Thr Ile Phe Ile Ser Tyr Thr Leu Ile Leu Ser Asn Ile Leu Ser Ile
          225          230          235          240
His Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Gly Ser His
          245          250          255
Val Ile Ala Val Ser Leu Phe Phe Gly Ala Ala Ala Phe Met Tyr Leu
          260          265          270
Lys Pro Ser Ser Ala Ser Glu Asp Asp Asp Lys Val Ser Thr Ile Phe
          275          280          285
Tyr Thr Ile Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg
          290          295          300
Asn Lys Asp Val Tyr Leu Ala Leu Arg Lys Thr Leu Met Lys Arg Ser
          305          310          315          320
Phe Thr Xaa Val Glu Ser Ile Phe Val Met Glu Leu Lys
          325          330

```

&lt;210&gt; 2365

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M112 8571727-22-3043-8090 3092-2061)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(344)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 2365

```

Ile Val Cys Phe Ile Ser Leu Phe Xaa Val Met Ser Gln Lys Arg Met
 1          5          10          15
Ala Pro Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly Phe
 20          25          30
Ser Asn Gln Pro Ala Leu Gln Leu Pro Leu Phe Phe Val Phe Leu Gly
 35          40          45
Ile Tyr Val Leu Thr Val Ile Gly Asn Leu Gly Leu Ile Thr Leu Ile
 50          55          60
Gly Leu Asn Ser Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn
 65          70          75          80
Leu Ser Phe Ile Asp Phe Cys Tyr Ser Cys Val Phe Thr Pro Lys Met
 85          90          95
Leu Ser Asp Phe Val Ser Glu Asn Ile Ile Ser Tyr Met Gly Cys Met
 100          105          110
Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr Val
 115          120          125
Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
 130          135          140
Leu Tyr Thr Val Thr Met Ser Pro Gln Val Cys Thr Leu Leu Met Phe
 145          150          155          160
Cys Ser Tyr Val Ile Gly Phe Ala Gly Ala Met Ala His Thr Gly Ser
 165          170          175
Met Leu Thr Leu Thr Phe Cys Asp Ser Asn Met Ile His His Tyr Leu
 180          185          190
Cys Glu Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Ala
 195          200          205
Asn Glu Leu Val Phe Phe Ile Val Val Gly Val Val Ile Thr Ala Ser
 210          215          220
Ser Ile Ser Ile Phe Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile Leu
 225          230          235          240
Lys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Gly Thr Trp Gly
 245          250          255
Ser His Val Val Ala Val Ala Leu Phe Phe Gly Ser Gly Ala Phe Thr
 260          265          270
Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Glu Glu Gly Arg Phe Ala
 275          280          285
Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile Tyr
 290          295          300
Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Asn Lys Thr Leu Lys
 305          310          315          320
Arg Val Leu Phe Xaa Xaa Val Trp Cys Tyr His Trp Asn Xaa Ile Leu
 325          330          335
Gly Lys His Thr Gln Ile His Phe
 340

```

&lt;210&gt; 2366

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M113 8571727-23-1650-2708 1059-589)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(157)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2366

```

Ile Arg Phe Ala Gly Ser Ser Val His Thr Gly Cys Val Ph Leu Xaa
 1          5          10          15
Gly His Ala Ile Asn His Xaa Leu Phe Asn Ile Leu Thr Leu Leu Gln
 20          25          30
Leu Ser Xaa Ala Thr Thr Tyr Val Asn Val Val Ile Leu Ile Gly Val

```



```

      35      40      45
Tyr Ile Thr Val Pro Ser Phe Thr Ile Leu Ile Ser Tyr Val Phe Ile
  50      55      60
Phe Ile Asn Ile Leu Asn Ile Lys Ser Met Gln Arg Ile Ser Lys Asp
  65      70      75      80
Phe Ser Ile Cys Arg Phe His Ile Ala Ser Ile Tyr Val Phe Ile Glu
      85      90      95
Phe Thr Ala Phe Lys Cys Phe Lys Tyr Ser Tyr Gly Ser Ile Asp Gln
      100      105      110
Gly Phe Tyr Ser Ser Val Phe Tyr Thr Asp Val Ile Leu Ile Leu Asn
      115      120      125
Ile Ile Ile Tyr Ser Met Cys Ile Met Asp Val Glu Met Ala Leu Met
      130      135      140
Asp Ala Leu Met Lys Phe Gln Arg Asn Val Phe His Leu
  145      150      155

```

&lt;210&gt; 2367

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M114 8571727-23-3031-3453 387-9)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(127)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2367

```

His Ser Ile Gln Tyr Leu Asn Leu Ile Asn Leu Ser Tyr Ile Asp Leu
  1      5      10      15
Cys Tyr Ser Ser Val Pro Arg Ser Lys Met Leu Met Asn Phe Val Phe
      20      25      30
Glu Lys Asn Ala Ile Ser Phe Val Gly Cys Asp Ser Ile Gln Phe Ser
      35      40      45
Leu Val Pro Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe
      50      55      60
Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Val Ile Phe
      65      70      75      80
Xaa Tyr Tyr Thr Leu Thr Ser Met Ala Tyr Asp Phe Tyr Val Ala Ile
      85      90      95
Cys Ser Ser Leu Val His Xaa Val Thr Pro Leu Leu Gln Val Cys Phe
      100      105      110
Phe Ser Phe Leu Leu Leu Phe Phe Phe Cys Pro Leu Phe Pro Met
      115      120      125

```

&lt;210&gt; 2368

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M115 8571727-24-1-1404 400-2)

&lt;400&gt;2368

```

Cys Asn Val Ile Thr Phe Thr Val Leu Thr Asp Met Asn Trp Gly Arg
  1      5      10      15
Met Ala Leu Gly Asn Asp Ser Ser Val Lys Glu Phe Ile Leu Leu Gly
      20      25      30
Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe Phe Phe Phe Leu
      35      40      45
Gly Val Tyr Ile Phe Ser Val Val Gly Asn Leu Gly Leu Ile Val Leu
      50      55      60
Ile Val Leu Asn Pro His Leu Gln Thr Pro Met Tyr Tyr Phe Leu Phe
      65      70      75      80
Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys

```

```

      85      90      95
Met Leu Val Ser Phe Val Lys Gln Asn Ile Ile Ser His Ala Glu Cys
      100      105      110
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr
      115      120      125
Ile Leu Thr Ala Met
      130

```

&lt;210&gt; 2369

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M117 8571727-26-4808-6724 1497-715)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(262)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2369

```

Ser Ser Leu His Ala Ser His Ser His Glu Leu Xaa Lys Gly Ile Val
 1      5      10      15
Gly Leu Phe Xaa Ala Ala Ser Tyr Ser Thr Val Lys Leu Pro Lys Met
      20      25      30
Leu Val Ser Phe Val Lys Gln Asn Thr Ile Ser Tyr Ala Glu Cys Met
      35      40      45
Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr Ile
      50      55      60
Leu Thr Ala Met Ala Tyr Asp Met Phe Ala Ala Ile Ser Lys Pro Leu
      65      70      75      80
Leu Tyr Gln Val Thr Met Ser His Trp Val Cys Leu Leu Met Ile Val
      85      90      95
Gly Val Tyr Val Ile Gly Phe Ser Gly Ser His Tyr Thr Ser Met Pro
      100      105      110
Asp Leu Xaa Trp Gln Arg His Tyr Met Cys Asp Ile Leu Leu Leu Leu
      115      120      125
Gln Leu Ser Cys Glu Ser Thr Ser Ile Asn Glu Leu Val Ile Tyr Arg
      130      135      140
Val Gly Phe Asn Val Thr Val Pro Ser Leu Thr Ile Phe Ile Ser Tyr
      145      150      155      160
Thr Leu Ile Leu Ser Asn Ile Pro Ser Ile His Ser Thr Glu Gly Arg
      165      170      175
Asn Cys Gly Ser His Val Ile Ala Leu Ser Leu Leu Tyr Gly Ile Val
      180      185      190
Ala Phe Thr Tyr Leu Lys Pro Ser Ser Val Ser Val Asp Asp Ala Asn
      195      200      205
Val Ser Thr Ile Phe Phe Tyr Thr Val Val Gly Pro Met Leu Asn Pro
      210      215      220
Phe Leu His Ser Ile Arg Asn Lys Asp Val His Thr Ala Leu Arg Lys
      225      230      235      240
Thr Leu Asn Lys Ser Ser Phe Thr Xaa Val Xaa Val Cys Ile Cys Tyr
      245      250      255
Glu Ser Lys Ile Leu Gly
      260

```

&lt;210&gt; 2370

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M119 8573058-17-2172-5249 1514-528)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2370

Val	Met	Leu	Leu	Ala	Phe	Leu	Leu	Pro	Thr	Asp	Asp	Thr	Ile	Met	His
1				5					10				15		
Met	Ala	Met	Glu	Asn	Asp	Ser	Ser	Val	Thr	Glu	Phe	Val	Phe	Met	Gly
		20					25					30			
Leu	Thr	Glu	Gln	Pro	Glu	Leu	Arg	Leu	Pro	Leu	Phe	Phe	Val	Phe	Leu
	35					40					45				
Leu	Asn	Tyr	Thr	Ala	Thr	Val	Met	Gly	Asn	Leu	Ser	Leu	Met	Val	Leu
	50					55				60					
Ile	Cys	Leu	Asn	Ser	His	Leu	His	Asn	Pro	Met	Tyr	Phe	Phe	Leu	Phe
65					70				75					80	
Asn	Leu	Ser	Leu	Val	Asp	Phe	Cys	Tyr	Ser	Phe	Val	Cys	Thr	Pro	Lys
			85					90						95	
Met	Leu	Met	Gly	Phe	Val	Ser	Glu	Lys	Ser	Ile	Ile	Ser	Tyr	Thr	Gly
		100					105					110			
Cys	Met	Thr	Gln	Leu	Phe	Phe	Phe	Cys	Phe	Phe	Val	Asn	Ser	Glu	Cys
	115					120					125				
Tyr	Val	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys
	130					135					140				
Pro	Leu	Val	Tyr	Ala	Ile	Leu	Met	Ser	Pro	Arg	Met	Cys	Ser	Leu	Leu
145					150					155				160	
Met	Ile	Gly	Ser	Tyr	Leu	Met	Gly	Phe	Ala	Ser	Ala	Met	Ala	His	Thr
			165					170						175	
Gly	Cys	Met	Ile	Arg	Leu	Lys	Phe	Cys	Asp	Ser	Asn	Ile	Ile	Asn	His
		180						185				190			
Tyr	Met	Cys	Glu	Ile	Phe	Pro	Leu	Leu	Gln	Leu	Ser	Cys	Ser	Ser	Thr
	195					200					205				
Tyr	Ala	Asn	Glu	Leu	Val	Ser	Ser	Leu	Ile	Ala	Cys	Ile	Val	Val	Ile
	210					215					220				
Val	Ser	Gly	Leu	Val	Ile	Leu	Met	Ser	Tyr	Ala	Ser	Ile	Leu	Leu	Asn
225					230					235				240	
Val	Val	Gln	Met	Ser	Ser	Ala	Thr	Gly	Trp	Ser	Lys	Ala	Met	Gly	Thr
			245						250				255		
Cys	Gly	Ser	His	Ile	Ile	Thr	Val	Ser	Leu	Phe	Tyr	Gly	Ser	Gly	Leu
		260						265					270		
Leu	Thr	Tyr	Val	Lys	Pro	Ala	Ser	Ala	Glu	Ser	Val	Asp	Gln	Gly	Lys
	275					280					285				
Phe	Phe	Ser	Val	Phe	Tyr	Thr	Leu	Met	Val	Pro	Met	Leu	Asn	Pro	Leu
	290					295					300				
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala	Ala	Lys	Arg	Thr
305					310				315					320	
Met	Asn	Arg	Ile	Thr	Ile	Xaa	Gly	Lys							
				325											

&lt;210&gt; 2371

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M122 8573058-3-1-3007 1710-2714)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(335)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2371

Val	Leu	Ile	Leu	Pro	Leu	His	Leu	Phe	Leu	Gln	Met	Ser	Leu	Asn	Ala
1				5					10				15		
Gln	Lys	Thr	Met	Glu	Asn	Asp	Ser	Ser	Val	Ser	Glu	Phe	Ile	Leu	Met

```

      20      25      30
Gly Leu Thr Asp Gln Pro Glu Leu Gln Leu Pro Leu Phe Val Leu Phe
      35      40      45
Leu Val Asn Tyr Thr Val Thr Val Met Gly Asn Leu Ser Leu Met Asn
      50      55      60
Leu Ile Cys Leu Asn Ser Asn Leu His Thr Pro Met Tyr Phe Phe Ile
65      70      75      80
Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Met Val Phe Thr Pro
      85      90      95
Lys Met Leu Met Gly Phe Val Val Glu Lys Asn Ile Ile Ser Phe Arg
      100      105      110
Gly Cys Met Thr Gln Leu Phe Phe Leu Phe Phe Val Asn Ser Glu
      115      120      125
Ser Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      130      135      140
Gln Pro Leu Leu Tyr Lys Ala Val Met Ser Pro Gly Ile Cys Phe Leu
145      150      155      160
Leu Ile Phe Cys Thr Tyr Leu Met Gly Leu Val Ser Ala Leu Phe His
      165      170      175
Thr Gly Phe Met Ile Arg Leu Asn Phe Cys Asp Ser Asn Val Ile Asn
      180      185      190
His Tyr Met Cys Asp Ile Phe Pro Leu Phe Arg Leu Ser Cys Ser Ser
      195      200      205
Thr Tyr Leu Thr Glu Leu Val Ser Ser Ala Val Val Gly Thr Ala Ile
      210      215      220
Ile Leu Cys Cys Leu Ile Leu Ile Ser Tyr Gly Met Ile Leu Tyr
225      230      235      240
Asn Ile Ile His Met Ser Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly
      245      250      255
Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Val Thr Gly
      260      265      270
Met Leu Ala Tyr Val Lys Pro Ser Ser Ala Glu Thr Val Gly Gln Gly
      275      280      285
Lys Ile Phe Ser Val Phe Tyr Thr Phe Leu Val Pro Met Leu Asn Pro
      290      295      300
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Val Lys Lys
305      310      315      320
Thr Trp Lys Arg Leu Thr Cys Xaa Ile Thr His Ser Asn Val Pro
      325      330      335

```

&lt;210&gt; 2372

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M123 8573058-5-4486-4920 411-18)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(131)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2372

```

Leu Gly Gly Glu Asp Arg Phe Ser Leu Asn Asn Glu Ser Leu Ile Asn
1      5      10      15
Asn Ser Gly Leu Val Pro Cys Thr Phe His Ile Leu Thr Ser Phe Cys
      20      25      30
Lys Ser Arg Ser Xaa Thr Phe Arg Thr Cys Gly Ser His Phe Ile Ala
      35      40      45
Val Ser Leu Phe Tyr Gly Ala Ser Ala Phe Met Tyr Leu Lys Pro Ser
50      55      60
Ser Ala Ser Val Asp Asp Lys Ile Ser Thr Ile Phe Tyr Thr Ile
65      70      75      80

```

Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp  
                   85                  90                  95  
 Val His Ile Ala Leu Arg Lys Tyr Phe Glu Glu Lys Ser Phe Ile Xaa  
                   100                  105                  110  
 Glu Glu Leu Xaa Leu Ile Xaa Met Glu Asn Leu Met Val Cys Gln Ile  
                   115                  120                  125  
 Tyr Asn Phe  
                   130

&lt;210&gt; 2373

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M124 8573058-8-1-894 16-516)

&lt;400&gt;2373

Leu Thr His Gly Ser Thr Pro Thr Gly Pro Ile Thr Ala Pro Ala Leu  
   1                  5                  10                  15  
 Thr Val Cys Met Val Trp Leu Gln Phe Leu Asp Ser Pro Leu Thr Thr  
                   20                  25                  30  
 Pro Tyr Met Cys His Ile Phe Pro Leu Leu Gln Val Ser Cys Ser Ser  
                   35                  40                  45  
 Pro Tyr Val Asn Gln Leu Met Ser Tyr Ile Ala Val Gly Thr Ala Ile  
                   50                  55                  60  
 Ile Leu Cys Ser Leu Ile Ile Leu Val Ser Tyr Ala Met Ile Leu Phe  
 65                  70                  75                  80  
 Asn Ile Ile His Ile Ser Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly  
                   85                  90                  95  
 Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly  
                   100                  105                  110  
 Leu Leu Ala Tyr Val Asn Pro Ser Ser Ala Glu Thr Val Gly Gln Ala  
                   115                  120                  125  
 Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu Val Pro Met Leu Asn Pro  
                   130                  135                  140  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Met Lys Lys  
 145                  150                  155                  160  
 Ser Trp Lys Arg Ile Thr Ser  
                   165

&lt;210&gt; 2374

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M126 8574266-10-448-5833 4192-5202)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(337)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2374

Leu Phe Ser Ser Cys Tyr His Lys Phe Ile Cys Lys Met Thr Ala Arg  
   1                  5                  10                  15  
 Asn Met Thr Thr Met Ser Gly Phe Leu Leu Met Gly Phe Ser Asp Asn  
                   20                  25                  30  
 His Glu Leu Gln Ile Leu Gln Ala Leu Leu Phe Leu Leu Thr Tyr Leu  
                   35                  40                  45  
 Leu Gly Ser Ala Gly Asn Phe Ile Ile Ile Thr Ile Thr Thr Leu Asp  
                   50                  55                  60  
 Pro Gln Leu Gln Ser Pro Met Tyr Tyr Phe Leu Lys Gln Leu Ser Thr  
 65                  70                  75                  80  
 Leu Asp Leu Ser Ser Leu Ser Val Thr Val Pro Gln Tyr Val Ala Ser  
                   85                  90                  95

Ser Leu Ala Arg Ser Gly Tyr Ile Ser Tyr Gly Gln Cys Met Leu Gln  
 100 105 110  
 Ile Phe Phe Phe Thr Gly Leu Ala Trp Ser Glu Met Ala Thr Leu Thr  
 115 120 125  
 Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His Tyr  
 130 135 140  
 Glu Val Ile Met Ser Pro Arg Lys Cys Thr Trp Ala Val Ala Ala Val  
 145 150 155 160  
 Trp Leu Ser Gly Gly Ile Ser Gly Thr Leu Phe Thr Ala Ser Thr Leu  
 165 170 175  
 Ser Ile Arg Phe Cys Gly Asp Lys Ile Ile His Gln Phe Phe Cys Asp  
 180 185 190  
 Ile Pro Gln Leu Leu Lys Leu Ser Cys Ser Asn Asp Tyr Phe Gly Val  
 195 200 205  
 Leu Glu Val Ser Thr Phe Met Ser Val Met Ala Phe Ala Cys Phe Val  
 210 215 220  
 Gly Ile Ala Phe Ser Tyr Gly Gln Ile Phe Ser Thr Val Leu Arg Met  
 225 230 235 240  
 Pro Ser Ala Glu Gly Arg Ser Lys Val Phe Ser Thr Cys Leu Pro His  
 245 250 255  
 Leu Phe Val Val Ser Phe Phe Leu Ser Thr Gly Ile Cys Ala Tyr Leu  
 260 265 270  
 Lys Pro Thr Ser Asp Ser Pro Thr Ala Leu Asp Leu Met Leu Ser Ile  
 275 280 285  
 Phe Tyr Thr Leu Leu Pro Pro Thr Leu Asn Pro Val Ile Tyr Ser Leu  
 290 295 300  
 Arg Asn Glu Ser Leu Lys Arg Ala Leu Lys Lys Leu Leu Leu Ser Glu  
 305 310 315 320  
 Glu Phe Ile Arg Lys Lys Cys Leu Phe Tyr Phe Xaa Cys Leu Leu Thr  
 325 330 335  
 Leu

&lt;210&gt; 2375

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M127 8574266-13-1078-2817 1563-564)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(333)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2375

Leu Ser Phe Leu Ser Gly Asp Glu Tyr Gln Leu Leu Ser Val Gln Glu  
 1 5 10 15  
 Asn Ser Leu Ser Val Lys Arg Phe Ala Phe Ser Lys Phe Ser Glu Val  
 20 25 30  
 Pro Gly Glu Cys Phe Leu Leu Phe Thr Leu Ile Leu Leu Met Phe Leu  
 35 40 45  
 Val Ser Leu Thr Gly Asn Glu Leu Ile Val Ile Ala Ile Cys Thr Ser  
 50 55 60  
 Pro Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Leu  
 65 70 75 80  
 Leu Glu Ile Gly Tyr Thr Cys Ser Val Ile Pro Lys Met Leu Gln Ser  
 85 90 95  
 Leu Val Ser Glu Ala Arg Glu Ile Ser Arg Glu Gly Cys Ala Thr Gln  
 100 105 110  
 Met Phe Phe Phe Thr Phe Phe Gly Ile Thr Glu Cys Cys Leu Leu Ala  
 115 120 125  
 Ala Met Ala Tyr Asp Arg Cys Met Ala Ile Cys Ser Pro Leu His Tyr

```

      130              135              140
Ala Thr Arg Met Ser His Gly Val Cys Ala His Leu Ala Ile Val Ser
145              150              155              160
Trp Gly Met Gly Cys Ile Val Gly Leu Gly Gln Thr Asn Phe Ile Phe
      165              170              175
Ser Leu Asn Phe Cys Gly Pro Cys Glu Ile Asp His Phe Phe Cys Asp
      180              185              190
Leu Pro Pro Val Leu Ala Leu Ala Cys Gly Asp Thr Ser Gln Asn Glu
      195              200              205
Ala Ala Ile Phe Val Ala Ala Ile Leu Cys Ile Ser Ser Pro Phe Leu
      210              215              220
Leu Ile Ile Tyr Ser Tyr Val Arg Ile Leu Val Ala Val Leu Val Met
225              230              235              240
Pro Ser Pro Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser His
      245              250              255
Leu Leu Val Val Thr Leu Phe Phe Gly Ser Gly Ser Ile Thr Tyr Leu
      260              265              270
Arg Pro Lys Ser Ser His Leu Pro Gly Met Asp Lys Leu Leu Ala Leu
      275              280              285
Phe Tyr Thr Ala Val Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser Leu
      290              295              300
Arg Asn Lys Glu Val Lys Thr Ala Leu Arg Lys Thr Leu Ser Leu Lys
305              310              315              320
Thr Ser Arg Ala Ile Asn Arg Xaa Gln Asn Leu Ala Glu
      325              330

```

&lt;210&gt; 2376

&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M129 8574266-7-9797-11994 2006-942)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(356)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2376

```

Asn Phe Phe Leu Gln Ile Xaa Ser Gln Asn Tyr Gln Xaa Gly Xaa Leu
1      5      10      15
Lys Glu Ile Met Thr Lys Ser Asn Phe Ser Ser Pro Ile Cys Phe Arg
      20      25      30
Leu Pro Gly Phe Ser Asp His Leu Xaa Leu Asp Xaa Thr Leu Phe Leu
      35      40      45
Ala Thr Ser Val Ile Asp Ile Val Met Leu Thr Gln Asn Thr Met Ile
      50      55      60
Ile Leu Val Ser Phe Leu Asn Ser Arg Leu Gln Thr Pro Met Tyr Phe
65      70      75      80
Phe Leu Ser Asn Phe Phe Phe Leu Asp Leu Cys Phe Met Thr Asn Val
      85      90      95
Leu Xaa Ile Val Xaa Thr Ser Lys Gly Pro Glu Lys Ile Ile Ser Cys
      100      105      110
Cys Ala Ile His Val Tyr Ile Val Leu Xaa Leu Asp Phe Thr Lys Cys
      115      120      125
Val Leu Leu Thr Met Met Ala Tyr Asn Pro Val Thr Pro Ile Cys Trp
130      135      140
Pro Leu Xaa Tyr Pro Thr Thr His Pro Lys Phe Val Asp Ile His Pro
145      150      155      160
Lys Phe Pro Xaa Lys Pro Ala Ala Leu Ala Trp Ile Cys Ser Phe Met
      165      170      175
Val Phe Thr Ile Gln Thr Thr Leu Val Phe Gln Leu Ser Leu Cys Ser
      180      185      190

```

His His Arg Met Asn Asp Phe Leu Cys Val Arg Asn Pro Pro Leu Val  
 195 200 205  
 Lys Ile Thr Phe Met Asp Thr Thr Ser Leu Glu Lys His Ile Ser Val  
 210 215 220  
 Phe Thr Phe Leu Xaa Ala Val Ile Pro Cys Gly Glu Tyr Ser Ile Ile  
 225 230 235 240  
 Tyr Leu Leu Val Leu Leu Lys Val Trp Leu Lys Ile Lys Phe Thr Gly  
 245 250 255  
 Arg Met Lys Thr Phe Gly Ser Cys Gly Phe His Leu Met Ala Ile Val  
 260 265 270  
 Leu Phe Phe Gly Asn Glu Ser Ser Val Tyr Met Val Tyr Met Tyr Pro  
 275 280 285  
 Arg Ala Asn Ala Cys Gln Tyr Arg Lys Phe Ser Val Phe Tyr Met Ile  
 290 295 300  
 Val Thr Pro Ser Ile Asn Pro Leu Ile Tyr Leu Arg Asn Lys Glu Phe  
 305 310 315 320  
 Arg Trp Ala Val Gln Arg Leu Val Thr Arg Asp Pro Ser Xaa Gly Lys  
 325 330 335  
 Ile Arg Gln Ser Leu Thr Ile Phe Gln Ala Phe Gly Ile Gly Arg His  
 340 345 350  
 Tyr Ile Tyr Cys  
 355

&lt;210&gt; 2377

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M130 8574266-9-11171-19240 5578-6546)

&lt;400&gt;2377

Val Arg Ile Leu Thr Val Asn Thr Asn Met Trp Ile Asn Asn Gln Ser  
 1 5 10 15  
 Ser Val Asp Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro Trp Leu  
 20 25 30  
 Glu Thr Pro Leu Phe Val Ile Phe Leu Val Ala Tyr Ile Phe Ala Leu  
 35 40 45  
 Phe Gly Asn Ile Ser Ile Ile Leu Val Ser Arg Leu Asp Pro Gln Leu  
 50 55 60  
 Asp Ser Pro Met Tyr Phe Phe Val Ser Asn Leu Ser Leu Leu Asp Leu  
 65 70 75 80  
 Cys Tyr Thr Thr Ser Thr Val Pro Gln Met Leu Val Asn Leu Arg Gly  
 85 90 95  
 Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys Val Ala Gln Leu Tyr Ile  
 100 105 110  
 Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile Leu Leu Ala Ile Met Ala  
 115 120 125  
 Phe Asp Arg Phe Ala Ala Ile Cys Arg Pro Leu His Tyr Pro Ile Ile  
 130 135 140  
 Met Asn Gln Lys Arg Cys Ile His Met Ala Thr Gly Thr Trp Ile Ser  
 145 150 155 160  
 Gly Phe Ala Asn Ser Leu Val Gln Ser Thr Leu Thr Val Val Ala Pro  
 165 170 175  
 Arg Cys Gly Gln Arg Val Ile Asp His Phe Phe Cys Glu Val Pro Ala  
 180 185 190  
 Leu Leu Lys Leu Ala Cys Thr Asp Thr Ser Val Asn Glu Ala Glu Leu  
 195 200 205  
 Asn Val Leu Gly Ala Leu Leu Leu Val Pro Leu Ser Leu Ile Leu  
 210 215 220  
 Gly Thr Tyr Val Phe Ile Ala Gln Ala Val Leu Lys Leu Arg Ser Ala  
 225 230 235 240  
 Glu Ser Arg Arg Lys Ala Phe Asn Thr Cys Ala Ser His Leu Leu Val  
 245 250 255



Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser Met Tyr Val Gln Pro Pro  
 260 265 270  
 Ser Ser Tyr Ser His Glu Arg Gly Lys Ile Met Ala Leu Phe Tyr Gly  
 275 280 285  
 Ile Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys  
 290 295 300  
 Asp Val Lys Ala Ala Leu Arg Arg Ala Leu Thr Lys Glu Phe Trp Val  
 305 310 315 320  
 Lys Ala Arg

&lt;210&gt; 2378

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M131 8574266-9-30686-36974 2322-3308)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2378

Leu Leu Ser Val Val Phe Phe Xaa Leu Phe Leu Asn Arg Val Ser Arg  
 1 5 10 15  
 Val Ile Ile Met Asn Val Ser Phe Lys Thr Gly Phe Leu Leu Met Gly  
 20 25 30  
 Phe Ser Asp Glu Arg Asn Leu Gln Ile Leu His Ala Val Leu Phe Leu  
 35 40 45  
 Ile Thr Tyr Leu Leu Ala Ile Met Gly Asn Leu Leu Ile Ile Thr Ile  
 50 55 60  
 Ile Thr Leu Asp Gln Arg Leu His Ser Pro Met Tyr Tyr Phe Leu Lys  
 65 70 75 80  
 His Leu Ser Phe Leu Asp Leu Cys Phe Ile Ser Val Thr Val Pro Gln  
 85 90 95  
 Ser Ile Ala Asn Ser Leu Met Asn Asn Gly Phe Ile Ser Leu Gly Gln  
 100 105 110  
 Cys Met Leu Gln Val Phe Phe Phe Ile Ala Leu Ala Ser Ser Glu Val  
 115 120 125  
 Ala Ile Leu Thr Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 130 135 140  
 Pro Leu Gln Tyr Glu Thr Ile Met Asp Pro His Ala Cys Lys Cys Ala  
 145 150 155 160  
 Val Ile Ala Val Trp Met Ala Gly Gly Leu Ser Gly Leu Leu His Thr  
 165 170 175  
 Gly Val Asn Phe Ser Ile Pro Leu Cys Gly Lys Arg Ile Ile His Gln  
 180 185 190  
 Phe Phe Cys Asp Ile Pro Gln Met Leu Lys Leu Ala Cys Ser Tyr Glu  
 195 200 205  
 Phe Ile Asn Glu Ile Ala Val Ala Ala Phe Thr Thr Ser Thr Ala Phe  
 210 215 220  
 Val Cys Leu Ile Ala Ile Val Phe Ser Tyr Thr Gln Ile Phe Ser Thr  
 225 230 235 240  
 Val Met Arg Ile Pro Ser Ala Asp Ser Arg Thr Lys Val Phe Ser Thr  
 245 250 255  
 Cys Leu Pro His Leu Phe Val Val Met Phe Phe Leu Ser Ala Ala Gly  
 260 265 270  
 Phe Glu Phe Leu Arg Pro Pro Ser Asp Ser Leu Ser Ala Met Asp Leu  
 275 280 285  
 Val Phe Ser Ile Phe Tyr Thr Val Ile Pro Pro Thr Leu Asn Pro Leu  
 290 295 300  
 Ile Tyr Ser Leu Arg Asn Glu Ala Met Lys Ala Ala Leu Arg Lys Val

```
<210> 2379
<211> 324
<212> PRT
<213> Mus musculus (M132 8574266-9-4118-8767 2921-3891)

<220>
<221> VARIANT
<222> (1)...(324)
<223> Xaa = Any Amino Acid
```

```
<210> 2380
<211> 341
<212> PRT
```

<213> Mus musculus (M133 8574277-10-1-1870 1597-577)

<220>

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400>2380

```

Val Leu Leu Asn His Thr Phe Ile Thr Glu Phe Leu Leu Leu Gly Val
 1           5           10           15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Met Val Leu Ala
          20           25           30
Met Tyr Phe Ile Asn Val Phe Gly Asn Gly Ala Ile Met Met Ile Val
          35           40           45
Ile Leu Asp Ser Arg Leu Tyr Ser Pro Met Tyr Phe Phe Leu Gly Asn
          50           55           60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
          65           70           75           80
Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
          85           90           95
Ile Thr Gln Leu His Phe Phe His Phe Leu Gly Cys Thr Asp Ala Leu
          100          105          110
Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
          115          120          125
Leu His Tyr Pro Ser Ile Met Asn Arg Gln Val Cys Ile Gln Val Ala
          130          135          140
Ala Thr Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
          145          150          155          160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe
          165          170          175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
          180          185          190
Leu Asn Arg Trp Leu Leu Asn Thr Leu Ala Gly Thr Ile Gly Ile Gly
          195          200          205
Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
          210          215          220
Phe Leu Lys Thr His Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
          225          230          235          240
Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
          245          250          255
Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
          260          265          270
Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
          275          280          285
Ile Tyr Ala Leu Arg Asn Lys Glu Val Arg Cys Ala Leu Asn Arg Lys
          290          295          300
Leu Arg Ile Leu Ile Xaa Leu Gly Arg Asn Leu Val Ser Tyr Phe Val
          305          310          315          320
Ile Ser Gln His Lys Gln Leu Leu Xaa Lys Ser Met Cys Glu Ile Ser
          325          330          335
Xaa Phe Xaa Ile Cys
          340

```

<210> 2381

<211> 284

<212> PRT

<213> Mus musculus (M136 8574277-13-1-992 974-124)

<220>

<221> VARIANT

<222> (1)...(284)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2381

Cys Ile Tyr Ile Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val  
 1 5 10 15  
 Cys Ile Ser Ile Cys Thr Tyr Leu His Ile Xaa Ile His Met Cys Val  
 20 25 30  
 Gln Val Val Ile Lys Leu Lys Val Lys Xaa Val Thr Trp Lys Glu Val  
 35 40 45  
 Xaa Lys Met Ser Val Glu Lys Arg Thr Gln Ser Arg Gln Lys Ser Gly  
 50 55 60  
 Tyr Leu Ala Asn Cys Phe Leu Gln Ser Phe Ile Leu Gly Ser Val Asp  
 65 70 75 80  
 Arg Asn Ile Cys Leu Leu Ile Val Met Val Tyr Asp His Tyr Leu Thr  
 85 90 95  
 Ile Cys His His Leu Xaa Tyr Pro Phe Leu Met Gly Pro Leu Trp Gly  
 100 105 110  
 Leu Gly Phe Gly Leu Thr Thr Ser Phe Val Val Asp Glu Leu Ile Val  
 115 120 125  
 Ala Leu Met Ala Gln Leu Arg Phe Cys Val Pro Lys Gln Ile Asp His  
 130 135 140  
 Phe Tyr Tyr Asp Phe Ser Pro Leu Val Val Leu Ala Tyr Thr Asp Thr  
 145 150 155 160  
 Gly Leu Val Gln Val Thr Thr Phe Val Leu Phe Val Val Phe Leu Thr  
 165 170 175  
 Val Pro Phe Gly Leu Val Leu Ile Ser Cys Ala Gln Ile Ala Val Thr  
 180 185 190  
 Val Leu Arg Val Pro Ser Arg Thr Arg Arg Asn Lys Ala Phe Ser Thr  
 195 200 205  
 Cys Ser Ser His Leu Asp Glu Val Ser Thr Phe Tyr Gly Ser Leu Met  
 210 215 220  
 Val Trp Tyr Thr Glu Pro Ser Ala Val His Ser Gln Ile Leu Ser Lys  
 225 230 235 240  
 Val Ile Ala Leu Leu Tyr Thr Val Val Thr Thr Ile Phe Asp Pro Gly  
 245 250 255  
 Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ser Leu Arg Arg His  
 260 265 270  
 Leu Tyr Cys Lys Pro Thr Glu Met Xaa Pro Lys Arg  
 275 280

&lt;210&gt; 2382

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M143 8574277-22-875-4053 855-1796)

&lt;400&gt;2382

Tyr Pro Met Gly Ile Leu Ser Thr Gly Asn Gln Thr Val Thr Glu Phe  
 1 5 10 15  
 Val Leu Leu Gly Phe His Glu Val Pro Gly Leu His Leu Leu Phe Phe  
 20 25 30  
 Ser Val Phe Thr Ile Leu Tyr Ala Ser Ile Ile Thr Gly Asn Met Leu  
 35 40 45  
 Ile Ala Val Val Val Val Ser Gln Arg Leu His Thr Pro Met Tyr  
 50 55 60  
 Phe Phe Leu Val Asn Leu Ser Phe Ile Glu Ile Val Tyr Thr Ser Thr  
 65 70 75 80  
 Val Val Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser  
 85 90 95  
 Val Ala Gly Cys Leu Leu Gln Phe Phe Val Phe Gly Ser Leu Ala Thr  
 100 105 110  
 Asp Glu Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala

```

      115      120      125
Ile Cys His Pro Leu Arg Tyr Pro His Leu Met Gly Pro Gln Trp Cys
 130      135      140
Leu Gly Leu Val Leu Thr Val Trp Leu Ser Gly Phe Met Val Asp Gly
145      150      155      160
Leu Val Val Ala Leu Met Ala Gln Leu Arg Phe Cys Gly Pro Asn Leu
      165      170      175
Val Asp His Phe Tyr Cys Asp Phe Ser Pro Leu Met Val Leu Ala Cys
      180      185      190
Ser Asp Thr Gln Val Ala Gln Val Thr Thr Phe Val Leu Ser Val Val
      195      200      205
Phe Leu Thr Val Pro Phe Gly Leu Val Leu Ile Ser Tyr Ala Gln Ile
      210      215      220
Val Val Thr Val Leu Arg Val Pro Ser Gly Thr Arg Arg Thr Lys Ala
225      230      235      240
Phe Ser Thr Cys Ser Ser His Leu Ala Val Val Ser Thr Phe Tyr Gly
      245      250      255
Thr Leu Met Val Leu Tyr Ile Val Pro Ser Ala Val His Ser Gln Leu
      260      265      270
Leu Ser Lys Val Ile Ala Leu Leu Tyr Thr Val Val Thr Pro Ile Phe
      275      280      285
Asn Pro Val Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ala Leu
      290      295      300
Arg Arg Leu Leu Tyr Cys Lys Pro Thr Glu
305      310

```

&lt;210&gt; 2383

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M144 8574277-30-676-1123 424-104)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(107)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2383

```

Ser Gly Val Leu Gly Asn Lys Leu Ser Leu Cys Leu Xaa Val Xaa Arg
 1      5      10      15
Val Phe Phe Ser Cys Gly Xaa Val Pro Ser Ala Gln Gly Lys Arg Lys
      20      25      30
Ser Leu Ala Thr Cys Ser Ser His Leu Ser Val Val Leu Leu Phe Tyr
      35      40      45
Ser Thr Val Phe Ala Thr Tyr Leu Lys Pro Pro Ser Thr Ser His Ser
      50      55      60
Ser Ala Glu Val Val Ala Ala Val Met Tyr Thr Leu Val Thr Pro Thr
      65      70      75      80
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Ser
      85      90      95
Leu Arg Lys Ile Leu Asn Met Asp Lys Phe Gln
      100      105

```

&lt;210&gt; 2384

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M148 8574277-5-2944-4486 2-698)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(232)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2384

```

Lys Ser Leu Ala Thr Leu Ala Gly Cys Leu Leu Gln Phe Leu Thr Phe
 1           5           10           15
Thr Ser Leu Asp Ala Asp Glu Tyr Phe Leu Leu Thr Leu Met Ala His
          20           25           30
Asp His Cys Leu Ala Ile Phe Tyr Ser Leu Xaa Tyr Pro Arg Leu Met
          35           40           45
Arg Pro Gln Trp Cys Leu Gly Leu Val Ile Ile Val Trp Leu Ser Gly
          50           55           60
Phe Met Glu Ala Gly Leu Val Val Ala Leu Thr Ala Gln Leu Arg Phe
65           70           75           80
Cys Gly Pro Asn Leu Ile Asp His Phe Tyr Cys Asp Phe Ser Pro Leu
          85           90           95
Met Ile Leu Ala Cys Ser Asp Thr Xaa Val Ala Gln Met Thr Thr Phe
          100          105          110
Val Leu Phe Val Val Phe Leu Pro Val Leu Ser Gly Leu Ile Leu Met
          115          120          125
Ser Tyr Ala Gln Phe Val Val Ile Val Leu Arg Ile Pro Ser Gly Ala
          130          135          140
Arg Arg Thr Lys Ala Phe Phe Thr Cys Ser Ser His Leu Ala Met Met
145          150          155          160
Phe Thr Phe Tyr Gly Ser Leu Met Val Trp Tyr Thr Ala Pro Ser Ala
          165          170          175
Val Leu Ser Leu Gln Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Thr
          180          185          190
Val Phe Ala Pro Ile Phe Asn Ser Val Ile Tyr Thr Leu Arg Asn Leu
          195          200          205
Asp Met Gln Lys Ala Leu Arg Arg Leu Leu Tyr Cys Lys Ser Thr Glu
210          215          220
Met Xaa Pro Lys Lys Glu Gly Ser
225          230

```

&lt;210&gt; 2385

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M149 8574277-6-4252-5644 1059-82)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2385

```

Tyr Ile Val Phe Thr Pro Ile Ser Ser Xaa Asn Thr Arg Pro Thr Met
 1           5           10           15
Asn Cys Ser Gln Ala Pro Thr Phe Ile Leu Leu Gly Leu Ser Ser Asp
          20           25           30
Ala Glu Lys Trp Gln Pro Leu Phe Ser Ile Phe Leu Val Leu Tyr Leu
          35           40           45
Leu Gly Leu Leu Gly Asn Leu Leu Leu Leu Leu Ala Ile Gly Thr Asp
          50           55           60
Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu
65           70           75           80
Val Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro Lys Met Leu Glu Ala
          85           90           95
Leu Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser Gly Cys Leu Thr Gln
          100          105          110
Leu Tyr Phe Phe Ala Val Phe Ala Asp Met Asp Asn Leu Leu Leu Ala
          115          120          125
Val Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu Tyr

```

130		135		140
Pro Leu Leu Met Thr	Pro Cys Arg Cys Arg	Val Leu Val Ser Gly Ser		
145	150	155	160	
Trp Gly Val Ala His	Cys Val Ser Leu Thr His	Thr Leu Leu Phe Ser		
	165	170	175	
Lys Leu Tyr Phe His	Asn Asn Gln Glu Ile Pro	His Phe Phe Cys Asp		
	180	185	190	
Phe Gly Pro Leu Leu Leu	Ser Cys Ser Asp Thr Tyr	Leu Asn Glu		
	195	200	205	
Ser Leu Met Met Ala Leu	Ser Gly Leu Leu Ala Ile	Ser Ala Phe Leu		
	210	215	220	
Cys Ile Val Ser Ser Tyr	Gly Cys Ile Phe Tyr Ala	Val Ala Lys Val		
225	230	235	240	
Pro Ser Ala Gln Gly Lys	Arg Lys Ala Leu Ala Thr	Cys Ser Ser His		
	245	250	255	
Leu Ser Val Val Leu Leu	Phe Tyr Ser Thr Val Phe	Ala Thr Tyr Leu		
	260	265	270	
Lys Pro Pro Ser Ser Ser	His Ser Ser Gln Glu Val	Val Ala Ala Val		
	275	280	285	
Met Tyr Thr Leu Val Thr	Pro Thr Leu Asn Pro Phe	Ile Tyr Ser Leu		
	290	295	300	
Arg Asn Lys Asp Val Lys	Ser Ser Leu Arg Arg Ile	Leu Asn Met Val		
305	310	315	320	
Lys Ser Gln Asp Xaa Gly				
	325			

&lt;210&gt; 2386

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M152 8574277-7-18987-20418 1032-73)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(321)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2386

Cys Gly Leu Ser Cys Ser	Gln Arg Ser Arg Arg	Asn Val Leu Ile Ser
1	5	10
Leu Xaa Xaa Leu Asn Phe	Phe Leu Met Gly Phe	Ser Arg Lys Leu Glu
	20	25
Val Glu His Asn Phe Ile	Leu Ala Leu Gly Leu Val	Ile Leu Ile Ala
	35	40
Asn Val Phe Ile Ile Ala	Ala Ile Ser Leu Glu Tyr	His Leu Cys Ser
	50	55
Leu Arg His Phe Leu Leu	Glu Gln Leu Phe Cys	Leu Asp Leu Cys Tyr
65	70	75
Ile Ser Met Ile Val Leu	Ser Thr Ile Lys Ser	Ile Cys Arg Ser Phe
	85	90
Met Tyr Ser Ala Tyr Ile	Ser Leu Ile Glu Cys Thr	Leu Gln Gly Phe
	100	105
Ala Phe Thr Leu Cys Ser	Tyr Thr Ser Met Ala Ile	Leu Thr Val Met
	115	120
Ser Cys His Cys Tyr Val	Ile Met Cys Tyr Lys	Val Ile Ile Ser Val
	130	135
Ser Leu Cys Met His Lys	Val Leu Ala Val Trp	Ala Ser Gly Cys Gly
145	150	155
Ile Asn Phe Gly Val Met	His Thr Ala Val Asn	Phe Ser Ile Ser Leu
	165	170
Cys Gly Ala Ser Val Ile	His Xaa Phe Cys	Asn Val Leu Leu Val Leu
	180	185
		190

Lys Leu Ser Cys Ser Asn Asp Cys Val Ser Glu Leu Ser Ile Ile Gly  
           195                          200                          205  
 Phe Pro Thr Cys Arg His Phe Ile Ser Ile Ser Phe Ala Tyr Glu His  
           210                          215                          220  
 Ile Leu Ser Pro Glu Leu Arg Met Pro Ser Val Lys Gly Arg Thr Arg  
 225                          230                          235                          240  
 Val Phe Ser Thr Cys Leu Cys His Ile Ser Val Val Ile Leu Phe Ile  
                           245                          250                          255  
 Pro Thr Gly Val Phe Glu Phe Leu Asn Pro His Ser Lys Ser Pro Thr  
                           260                          265                          270  
 Xaa Ile Leu His Xaa Thr Leu Phe Leu Val Phe His Thr Phe Leu Ser  
                           275                          280                          285  
 Ser Thr Leu Asn Pro Glu Ile Asn Ser Leu Arg Asn Glu Ala Thr Glu  
                           290                          295                          300  
 His His Ser Lys Glu Asn Val Ser Leu Phe Ile Ser Thr Ile Ser Ser  
 305                          310                          315                          320  
 Leu

<210> 2387

<211> 327

<212> PRT

<213> Mus musculus (M154 8575572-1-103679-105172 492-1471)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2387

His Xaa Met Gly Ala Leu Asn Gln Thr Arg Val Thr Glu Phe Ile Phe  
   1                          5                          10                          15  
 Leu Gly Leu Thr Asp Asn Trp Val Leu Glu Ile Leu Phe Phe Val Pro  
                           20                          25                          30  
 Phe Thr Val Thr Tyr Met Leu Thr Leu Leu Gly Asn Phe Leu Ile Val  
                           35                          40                          45  
 Val Thr Ile Val Phe Thr Pro Arg Leu His Asn Pro Met Tyr Phe Phe  
                           50                          55                          60  
 Leu Ser Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val  
 65                          70                          75                          80  
 Pro Lys Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe  
                           85                          90                          95  
 Asp Asn Cys Ile Ala Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ser  
                           100                          105                          110  
 Glu Ile Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile  
                           115                          120                          125  
 Cys Ile Pro Leu His Tyr Ser Asn Val Met Asn Met Lys Val Cys Val  
                           130                          135                          140  
 Gln Leu Val Phe Ala Leu Trp Leu Gly Gly Thr Ile His Ser Leu Val  
 145                          150                          155                          160  
 Gln Thr Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile  
                           165                          170                          175  
 Asp Ser Tyr Phe Cys Asp Val Pro Pro Val Ile Lys Leu Ala Cys Thr  
                           180                          185                          190  
 Asp Thr Tyr Leu Thr Gly Ile Leu Ile Val Ser Asn Ser Gly Thr Ile  
                           195                          200                          205  
 Ser Leu Val Cys Phe Leu Ala Leu Val Thr Ser Tyr Thr Val Ile Leu  
                           210                          215                          220  
 Phe Ser Leu Arg Lys Lys Ser Ala Glu Gly Arg Arg Lys Ala Leu Ser  
 225                          230                          235                          240  
 Thr Cys Ser Ala His Phe Met Val Val Thr Leu Phe Phe Gly Pro Cys



```

                245                250                255
Ile Phe Leu Tyr Thr Arg Pro Asp Ser Ser Phe Ser Ile Asp Lys Val
                260                265                270
Val Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu Ile
                275                280                285
Tyr Thr Leu Arg Asn Glu Glu Val Lys Thr Ala Met Lys His Leu Arg
                290                295                300
Gln Arg Arg Ile Cys Ser Xaa Asn His Val Cys Val Trp Leu Val Xaa
305                310                315                320
Cys Cys Asp Asn Ser His Gly
                325

```

&lt;210&gt; 2388

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M157 8575572-1-144835-147600 2426-1439)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(330)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2388

```

Met Glu Lys Ala Val Leu Ile Asn Gln Thr Ser Val Met Ser Phe Arg
 1                5                10                15
Leu Thr Gly Leu Ser Thr Asn Pro Lys Val Gln Met Ala Ile Phe Phe
                20                25                30
Ile Phe Leu Ile Phe Tyr Val Leu Thr Leu Val Gly Asn Ile Leu Ile
                35                40                45
Val Val Thr Ile Ile His Asp His Arg Leu His Thr Pro Met Tyr Phe
                50                55                60
Phe Leu Ser Asn Leu Ser Phe Ile Asp Val Cys His Ser Thr Val Thr
65                70                75                80
Val Pro Lys Met Leu Ser Asp Thr Phe Ser Glu Glu Lys Leu Ile Ser
                85                90                95
Phe Asp Asp Cys Val Val Gln Ile Phe Phe Leu His Leu Phe Ala Cys
                100                105                110
Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala
                115                120                125
Ile Cys Lys Pro Leu Arg Tyr Met Thr Ile Met Asn Trp Lys Val Cys
130                135                140
Met Val Leu Gly Gly Ala Met Trp Thr Ala Gly Thr Ile His Ser Ile
145                150                155                160
Ser Phe Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro Asn Glu
                165                170                175
Leu Asp Ser Phe Phe Cys Asp Val Pro Gln Val Ile Glu Leu Ala Cys
                180                185                190
Thr Asp Thr Arg Ile Thr Glu Ile Leu Val Val Ser Asn Ser Gly Met
                195                200                205
Ile Ser Met Val Cys Phe Val Ile Ile Val Val Ser Tyr Ala Val Ile
210                215                220
Leu Val Ser Leu Arg Gln Gln Ile Ser Asp Gly Lys Arg Lys Ala Leu
225                230                235                240
Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu Gly His
                245                250                255
Cys Ile Phe Ile Tyr Ser Arg Pro Ala Ile Ser Leu Pro Glu Asp Lys
                260                265                270
Ile Val Ser Ala Phe Phe Thr Ala Ile Thr Pro Leu Leu Asn Pro Ile
                275                280                285
Ile Tyr Thr Phe Arg Asn Glu Asp Met Lys Ser Ala Leu Lys Lys Leu
290                295                300

```

Ile Arg Arg Lys Glu Gly Lys Glu Lys Xaa Lys Cys Ile Ser Ser Leu  
 305 310 315 320  
 Gly Phe Leu Val Ile Xaa Ile Lys Glu Ala  
 325 330

<210> 2389

<211> 331

<212> PRT

<213> Mus musculus (M158 8575572-1-18114-22131 1498-507)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400>2389

Cys Leu Ser Ala Ser Leu Asp Ile Ser Lys Met Glu Arg Ile Asn Tyr  
 1 5 10 15  
 Thr Val Leu Thr Glu Phe Ile Leu Thr Gly Val Pro His Pro Pro Arg  
 20 25 30  
 Leu Arg Thr Phe Leu Phe Val Phe Phe Leu Leu Ile Tyr Ile Leu Thr  
 35 40 45  
 Gln Leu Gly Asn Ala Leu Ile Leu Ile Thr Val Cys Ala Asp Thr Gln  
 50 55 60  
 Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Ala Leu Ser Val Ile  
 65 70 75 80  
 Asp Met Gly Ile Ser Thr Ile Ile Val Pro Arg Leu Met Met Asn Phe  
 85 90 95  
 Thr Pro Gly Ile Lys Pro Ile Pro Phe Gly Gly Cys Val Ala Gln Leu  
 100 105 110  
 Tyr Phe Tyr His Phe Leu Gly Ser Ser Gln Cys Phe Leu Tyr Thr Thr  
 115 120 125  
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro  
 130 135 140  
 Val Leu Met Ser Ala Lys Leu Ser Ile Leu Leu Val Ala Gly Ala Trp  
 145 150 155 160  
 Val Ala Gly Ser Ile His Gly Ala Ile Gln Ala Ile Leu Thr Phe Arg  
 165 170 175  
 Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile  
 180 185 190  
 Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Val Asn Glu Leu  
 195 200 205  
 Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser Cys Phe Ser Leu  
 210 215 220  
 Ile Leu Leu Ser Tyr Ile Tyr Ile Ile Arg Ala Ile Leu Arg Ile Arg  
 225 230 235 240  
 Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys Gly Ala His Val  
 245 250 255  
 Thr Ile Val Thr Val Tyr Tyr Val Pro Cys Ala Phe Ile Tyr Leu Arg  
 260 265 270  
 Pro Asp Ser His Ser Ile Leu Asp Gly Ala Ala Ala Leu Phe Pro Thr  
 275 280 285  
 Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln  
 290 295 300  
 Glu Val Lys Leu Ala Leu Arg Arg Met Val Gly Ser Gln Ser Thr Lys  
 305 310 315 320  
 Ser Glu Val Xaa Ala Pro Leu Leu Phe Xaa Gly  
 325 330

<210> 2390

<211> 324

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M160 8575572-1-54180-57203 1450-479)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2390

```

Ile Leu Thr Asp Xaa Asp Met Arg Arg Thr Arg Asn Thr Ser Leu Asp
 1           5           10           15
Ala Val Val Thr Asp Phe Leu Leu Leu Gly Leu Ala His Pro Pro Asn
 20           25           30
Leu Arg Ala Phe Leu Phe Leu Val Phe Phe Leu Ile Tyr Ile Leu Thr
 35           40           45
Gln Leu Gly Asn Leu Leu Ile Leu Leu Thr Val Trp Ala Asp Pro Lys
 50           55           60
Leu His Ala Arg Pro Met Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu
 65           70           75           80
Asp Met Trp Leu Ser Ser Val Ile Val Pro Arg Leu Ile Leu Asn Phe
 85           90           95
Thr Pro Ala Ser Lys Ala Ile Pro Phe Gly Gly Cys Val Ala Gln Leu
100           105           110
Tyr Phe Phe His Phe Leu Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu
115           120           125
Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro
130           135           140
Val Leu Met Asn Gly Lys Leu Cys Thr Ile Leu Val Ser Gly Ala Trp
145           150           155           160
Val Ala Gly Ser Ile His Gly Ser Ile Gln Thr Thr Leu Thr Phe Arg
165           170           175
Leu Pro Tyr Cys Gly Pro Asn Gln Ile Asp Tyr Phe Ile Cys Asp Ile
180           185           190
Pro Ala Val Leu Arg Leu Ala Cys Ala Asp Thr Thr Val Asn Glu Leu
195           200           205
Val Thr Phe Val Asp Ile Gly Val Val Ala Ala Ser Cys Phe Met Leu
210           215           220
Ile Leu Leu Ser Tyr Ala Asn Ile Val His Ala Ile Leu Lys Ile Arg
225           230           235           240
Thr Ala Asp Gly Arg Lys Arg Ala Phe Ser Thr Cys Gly Ser His Leu
245           250           255
Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg
260           265           270
Ala Gly Ser Lys Ser Pro Phe Asp Gly Ala Val Ala Val Phe Tyr Thr
275           280           285
Val Val Thr Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln
290           295           300
Glu Val Lys Ser Ala Leu Lys Arg Leu Thr Ala Gly Arg Arg Asp Val
305           310           315           320
Gly Gly Glu Lys

```

&lt;210&gt; 2391

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M162 8576192-11-46369-50310 3151-2165)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(329)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2391

```

Phe Ser Xaa Ser His Tyr Arg Gln Asn Met Thr Gly Asn Asn Gln Thr
 1           5           10           15
Leu Ile Ser Lys Phe Leu Leu Leu Gly Leu Pro Ile Leu Ser Glu Tyr
 20           25           30
His Phe Leu Phe Tyr Ala Leu Phe Leu Ala Met Tyr Leu Thr Thr Ile
 35           40           45
Leu Gly Asn Leu Leu Ile Ile Ala Leu Val Arg Leu Asp Ser His Leu
 50           55           60
His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu
 65           70           75           80
Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln Asn Met Gln Ser
 85           90           95
Gln Val Pro Ser Ile Ser Tyr Val Gly Cys Leu Thr Gln Leu Tyr Phe
 100          105          110
Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu Val Val Met Ala
 115          120          125
Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Ile
 130          135          140
Met Ser Thr Lys Phe Cys Thr Ser Leu Val Leu Leu Trp Met Leu
 145          150          155          160
Thr Thr Ser Asn Ala Leu Met His Thr Leu Leu Met Ala Arg Leu Ser
 165          170          175
Phe Cys Glu Lys Asn Val Ile Leu Arg Phe Phe Cys Asp Ile Ser Ala
 180          185          190
Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Val Asn Glu Leu Met Ile
 195          200          205
Phe Ile Met Gly Gly Ile Ile Ile Ile Ile Pro Phe Leu Leu Ile Val
 210          215          220
Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys Val Pro Ser Thr
 225          230          235          240
Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245          250          255
Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser
 260          265          270
Ser Asn Asn Ser Thr Val Lys Glu Ser Ala Met Ala Met Met Tyr Thr
 275          280          285
Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290          295          300
Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys Ser Lys Lys Ile Ser
 305          310          315          320
Leu Xaa Trp Lys Tyr Phe Arg Met Ile
 325

```

&lt;210&gt; 2392

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M163 8576192-5-7971-9031 1060-236)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(275)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2392

```

Ile Ile Ile Leu Ile Ile Leu Asp Phe His Leu His Thr Pro Ile Tyr
 1           5           10           15
Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
 20           25           30
Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Thr Thr Ile

```

```

      35      40      45
Ser Tyr Val Gly Cys Leu Thr Gln Met Tyr Phe Pro Asn Val Phe Ala
  50      55      60
Asn Leu Glu Asn Phe Leu Leu Met Phe Met Ala Tyr Asp Arg Tyr Val
  65      70      75      80
Ala Ile Cys Tyr Pro Leu Arg Tyr Thr Ser Ile Met Ser Pro Ile Leu
      85      90      95
Cys Val Cys Met Val Phe Met Ser Trp Leu Leu Thr Met Leu Asn Ser
      100      105      110
Thr Leu His Thr Val Leu Ile Val Lys Leu Ser Phe Cys Glu Asp Asn
      115      120      125
Val Ile Pro His Phe Phe Cys Asp Ile Ser Ala Val Leu Lys Leu Ala
      130      135      140
Cys Ser Asp Ile Tyr Ile Asn Glu Leu Thr Ile Phe Ile Thr Gly Ala
      145      150      155      160
Phe Ile Ile Val Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Gln
      165      170      175
Ile Val Cys Ser Ile Leu Lys Phe Ser Ser Thr Arg Gly Ile Ala Lys
      180      185      190
Ile Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
      195      200      205
Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Thr Asn Asn Ser Thr
      210      215      220
Val Lys Asp Thr Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met
      225      230      235      240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala
      245      250      255
Leu Ile Arg Val Leu Cys Lys Lys Glu Ile Ser Leu Xaa Trp Gln Tyr
      260      265      270
Leu His Leu
      275

```

&lt;210&gt; 2393

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M165 8576192-7-12279-14147 678-1658)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2393

```

Trp Arg Ile Arg Met Ile Ile Asn Asn Gln Thr Ala Ile Pro Gln Phe
  1      5      10      15
Ile Leu Leu Gly Leu Pro Ile Leu Pro Glu Gln Gln Met Phe Tyr
      20      25      30
Ala Leu Phe Leu Ala Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile
      35      40      45
Ile Ile Ile Leu Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr
      50      55      60
Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
      65      70      75      80
Thr Met Pro Lys Leu Leu Gln Asn Ile Gln Ser Gln Asp Pro Ser Ile
      85      90      95
Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Met Val Phe Ala
      100      105      110
Asn Thr Glu Asn Val Leu Leu Val Met Ala Tyr Asp Arg Tyr Val
      115      120      125
Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Lys Leu
      130      135      140

```

Cys Val Ser L u Val Val Leu Thr Trp Val Phe Thr Val Leu Tyr Ser  
 145 150 155 160  
 Met Leu His Thr Leu L u Leu Ala Arg Leu Ser Phe Cys Glu Asp Asn  
 165 170 175  
 Val Ile Thr His Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala  
 180 185 190  
 Cys Ser Asp Thr Tyr Ile Asn<sup>n</sup> Glu Leu Met Ile Phe Ile Leu Gly Thr  
 195 200 205  
 Leu Asp Thr Val Val Pro Phe Leu Leu Ile Val Val Ser Tyr Val Gln  
 210 215 220  
 Ile Val Cys Ser Ile Leu Lys Phe Ser Thr Lys Gln Gly Ile Ala Lys  
 225 230 235 240  
 Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr  
 245 250 255  
 Gly Thr Ile Ile Gly Val Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr  
 260 265 270  
 Val Lys Glu Ile Val Met Ala Leu Met Tyr Thr Val Val Thr Pro Met  
 275 280 285  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Glu Ala  
 290 295 300  
 Leu Ile Arg Val Leu Cys Lys Lys Gln Ile Pro Leu Xaa Cys Leu Tyr  
 305 310 315 320  
 Trp Asn Phe Xaa Ile Xaa Ile  
 325

&lt;210&gt; 2394

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M166 8576192-8-1-1469 247-1198)

&lt;400&gt;2394

Arg Gly Arg Met Val Met Asn Asn Gln Thr Val Ile Ser Gln Leu Leu  
 1 5 10 15  
 Leu Val Gly Leu His Ile Pro Pro Asp His Gln Gln Gly Phe Tyr Thr  
 20 25 30  
 Leu Phe Leu Ala Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile  
 35 40 45  
 Ile Pro Leu Ile Ile Met Asp Ser Pro Phe Pro Thr His Pro Met Tyr  
 50 55 60  
 Leu Phe Leu Ile Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val  
 65 70 75 80  
 Thr Val Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Thr Ser Ile  
 85 90 95  
 Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Met Val Phe Gly  
 100 105 110  
 Asp Met Glu Ser Phe Leu Leu Val Met Ala Tyr Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Thr Met Ser Pro Lys Phe  
 130 135 140  
 Cys Val Cys Val Gly Ala Leu Ser Trp Val Phe Thr Ile Met Tyr Ser  
 145 150 155 160  
 Met Val His Thr Leu Leu Ser Arg Leu Ser Phe Cys Glu Asp Asn  
 165 170 175  
 Val Ile Pro His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala  
 180 185 190  
 Cys Ser Asp Ile Phe Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Gly  
 195 200 205  
 Pro Val Val Ala Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg  
 210 215 220  
 Ile Val Ser Ser Ile Leu Lys Val Ser Ser Ser Gln Gly Ile His Lys  
 225 230 235 240

```

<210> 2395
<211> 244
<212> PRT
<213> Mus musculus (M167 8576192-8-6530-9303 730-2)

<220>
<221> VARIANT
<222> (1)...(244)
<223> Xaa = Any Amino Acid

```

```
<210> 2396
<211> 338
<212> PRT
<213> Mus musculus (M168 8576195-11-1440-4165 2456-1443)
<220>
```

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(338)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2396

Cys Xaa Xaa His Phe Ile Leu Ser Leu Leu Gln Met Lys Val Met Lys  
 1 5 10 15  
 Gln Met Val Thr Glu Ser Asn Ser Ser Val Thr Glu Phe Ile Leu Met  
 20 25 30  
 Gly Leu Thr Val Gln Lys Glu Leu Gln Leu Pro Leu Phe Ile Leu Phe  
 35 40 45  
 Leu Leu Asn Tyr Thr Ala Thr Val Val Gly Asn Leu Ser Leu Met Asn  
 50 55 60  
 Leu Ile Cys Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Ile  
 65 70 75 80  
 Phe Asn Leu Ser Cys Ile Asp Phe Cys Tyr Ser Phe Val Ser Asn Pro  
 85 90 95  
 Thr Met Leu Arg Ser Phe Val Thr Glu Gln Asn Thr Ile Ser Tyr Glu  
 100 105 110  
 Gly Cys Met Ser Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu  
 115 120 125  
 Cys Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 130 135 140  
 His Pro Leu Lys Tyr Thr Thr Val Met Ser Pro Lys Ile Cys Cys Leu  
 145 150 155 160  
 Leu Val Phe Gly Ser Tyr Leu Met Gly Phe Ala Gly Ala Leu Thr His  
 165 170 175  
 Thr Gly Phe Met Ile Arg Leu Ser Phe Cys Asn Ser Asn Ile Ile Asn  
 180 185 190  
 His Tyr Met Cys Asp Ile Phe Pro Leu Leu Gln Leu Ser Cys Thr Ser  
 195 200 205  
 Thr Tyr Val Asn Glu Leu Val Ser Ser Ala Val Val Gly Thr Ile Ile  
 210 215 220  
 Ile Leu Ser Ser Ile Ile Ile Leu Val Ser Tyr Ala Met Ile Leu Ser  
 225 230 235 240  
 Asn Ile Leu His Met Ser Ser Ser Lys Gly Trp Ser Lys Ala Leu Gly  
 245 250 255  
 Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly  
 260 265 270  
 Leu Leu Ala Tyr Ile Lys Pro Thr Ser Ala Glu Thr Val Asp Gln Gly  
 275 280 285  
 Lys Phe Leu Ser Ile Phe Tyr Thr Leu Val Val Pro Met Leu Asn Pro  
 290 295 300  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Arg  
 305 310 315 320  
 Thr Met Lys Arg Val Thr Thr Xaa Met Asn Ser Cys Ala Phe Ile Val  
 325 330 335  
 Leu Pro

&lt;210&gt; 2397

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M169 8576195-13-2329-4897 1250-2268)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(340)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2397



Ile Ser Cys Leu Val Val Ser Pro S r Ile Leu Gln Thr Ser His Thr  
 1 5 10 15  
 Lys Gln Ile Thr Met Glu Asn Asp Ser Phe Val Ser Glu Phe Ile Leu  
 20 25 30  
 Met Gly Leu Thr Asp His Pro Glu Leu Gln Leu Ser Leu Phe Val Leu  
 35 40 45  
 Phe Leu Met Asn Tyr Thr Ala Ile Val Met Gly Asn Leu Ser Leu Met  
 50 55 60  
 Ile Leu Ile Phe Leu Asn Ser Asn Leu His Thr Pro Met Tyr Phe Phe  
 65 70 75 80  
 Ile Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Phe Val Phe Thr  
 85 90 95  
 Pro Lys Met Leu Met Ser Phe Phe Leu Glu Lys Asn Thr Ile Ser Phe  
 100 105 110  
 Arg Gly Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser  
 115 120 125  
 Glu Ser Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile  
 130 135 140  
 Cys Lys Pro Leu Leu Tyr Lys Thr Ile Met Val Pro Arg Ile Cys Cys  
 145 150 155 160  
 Leu Leu Met Phe Val Ser Tyr Leu Ile Gly Phe Thr Ser Ala Met Ile  
 165 170 175  
 Leu Thr Gly Leu Met Phe Arg Leu Asn Phe Cys Asn Asn His Ile Ile  
 180 185 190  
 Asn His Tyr Met Cys Asp Ile Phe Pro Val Ile Gln Ile Ser Cys Ser  
 195 200 205  
 Asp Thr Tyr Leu Asn Glu Leu Val Ser Thr Ala Val Val Gly Thr Gly  
 210 215 220  
 Ile Ile Leu Cys Ser Leu Leu Ile Leu Met Ser Tyr Ala Leu Ile Leu  
 225 230 235 240  
 Phe Asn Ile Leu Asn Met Ser Ser Gly Lys Gly Trp Ser Lys Ala Met  
 245 250 255  
 Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser  
 260 265 270  
 Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala Glu Thr Val Gly Gln  
 275 280 285  
 Gly Lys Phe Phe Ser Leu Phe Tyr Thr Phe Leu Val Pro Met Leu Asn  
 290 295 300  
 Pro Leu Ile Tyr Ser Leu Gln Asn Lys Asp Val Lys Val Ala Val Lys  
 305 310 315 320  
 Lys Thr Leu Lys Arg Ile Ser Asn Xaa Leu Glu Pro Leu Ala Leu His  
 325 330 335  
 Arg Thr Leu Ser  
 340

&lt;210&gt; 2398

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M171 8576195-15-1361-3546 1172-2177)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(336)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2398

Phe Xaa Leu Met Leu Leu Gln Met Gln His Met Lys Gln Met Ile Met  
 1 5 10 15  
 Glu Asn Asp Ser Ser Val Ser Glu Phe Ile Leu Met Gly Leu Thr Tyr  
 20 25 30  
 Gln Pro Glu Leu Trp Trp Pro Leu Phe Val Leu Ph Leu Val Asn Tyr

```

      35              40              45
Thr Ala Thr Val Met Gly Asn Leu Ser Leu Met Thr Leu Ile Cys Leu
  50              55              60
Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Ile Leu Asn Leu Ser
  65              70              75              80
Phe Ile Asp Phe Cys Tyr Ser Phe Val Phe Thr Pro Lys Met Leu Met
      85              90              95
Gly Phe Val Ser Glu His Asn Thr Ile Ser Phe Thr Gly Cys Met Thr
      100              105              110
Gln Leu Phe Phe Phe Cys Leu Phe Val Asn Ser Glu Cys Tyr Val Leu
      115              120              125
Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu Leu
      130              135              140
Tyr Thr Val Val Met Ser Pro Arg Ala Cys Ser Leu Leu Met Leu Ala
      145              150              155              160
Ala His Leu Met Gly Val Ser Ser Ala Val Val His Thr Gly Cys Ile
      165              170              175
Ile Gln Leu Arg Phe Cys Gly Ser Lys Val Ile Asn His Tyr Met Cys
      180              185              190
Asp Thr Phe Pro Leu Leu Glu Leu Ser Cys Gly Ser Ser His Val Asn
      195              200              205
Glu Leu Val Ser Ser Val Ser Val Ala Val Val Val Val Ile Ser Ser
      210              215              220
Leu Ile Ile Val Ser Ser Tyr Ala Leu Ile Leu Val Asn Val Ile His
      225              230              235              240
Leu Ser Ser Ser Lys Gly Trp Ser Lys Ala Val Ser Thr Cys Ser Ser
      245              250              255
His Ile Ile Thr Val Ala Leu Phe Tyr Gly Phe Gly Leu Leu Ala His
      260              265              270
Ile Lys Pro Ser Ser Ala Glu Ser Val Val Gln Arg Lys Phe Phe Ser
      275              280              285
Val Val Tyr Thr Phe Val Leu Pro Leu Leu Asn Pro Leu Ile Tyr Ser
      290              295              300
Ser Gly Asn Lys Asp Phe Lys Leu Leu Gly Thr Ile Asp Arg Leu Ala
      305              310              315              320
Gly Ser Asn Leu Ala Ser Phe Phe Phe Leu Ser Pro Leu Leu Ser Lys
      325              330              335

```

&lt;210&gt; 2399

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M172 8576195-20-3387-5132 199-1176)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2399

```

Ile Leu Thr Asp Met Thr Xaa Glu Gly Met Ala Ser Gly Asn Asp Ser
  1              5              10              15
Thr Thr Val Lys Glu Phe Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu
      20              25              30
Leu Gln Leu Pro Phe Phe Phe Leu Phe Leu Gly Ile Tyr Val Val Ser
      35              40              45
Ile Val Gly Asn Leu Gly Leu Ile Val Leu Ile Val Leu Asn Pro His
      50              55              60
Leu His Thr Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp
      65              70              75              80
Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys Met Leu Val Gly Phe Val
      85              90              95

```

Lys Gln Asn Ile Ile Ser His Ala Glu Cys Met Thr Gln Leu Phe Phe  
 100 105 110  
 Phe Ala Phe Phe Val Ile Asp Glu Cys Cys Ile Leu Thr Ala Met Ser  
 115 120 125  
 Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Lys Val Thr  
 130 135 140  
 Met Ser Tyr Gln Val Cys Phe Met Met Thr Val Ser Val Tyr Met Met  
 145 150 155 160  
 Gly Phe Val Gly Ala Ile Ala His Thr Ile Cys Met Leu Arg Leu Thr  
 165 170 175  
 Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Met Cys Asp Ile Pro Pro  
 180 185 190  
 Leu Leu Lys Leu Ser Cys Thr Asn Thr Ser Val Asn Glu Leu Val Val  
 195 200 205  
 Phe Ile Val Val Gly Val Asn Val Ile Gly Pro Thr Leu Ile Ile Phe  
 210 215 220  
 Thr Ser Tyr Thr Leu Ile Ile Phe Asn Ile Ser His Ile Arg Ser Thr  
 225 230 235 240  
 Glu Gly Arg Ser Lys Ala Ile Ser Thr Cys Ser Ser His Ile Ile Ala  
 245 250 255  
 Val Ser Ile Phe Phe Gly Ala Ser Ala Phe Met Tyr Leu Lys Pro Ser  
 260 265 270  
 Pro Val Gly Ser Val Gly Glu Asp Lys Val Ser Thr Val Phe Tyr Thr  
 275 280 285  
 Ile Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys  
 290 295 300  
 Asp Val His Ile Ala Leu His Lys Thr Leu Lys Lys Ser Met Leu Ile  
 305 310 315 320  
 Xaa Ile Glu Thr Phe Phe  
 325

&lt;210&gt; 2400

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M174 8576195-24-446-3721 1969-959)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(337)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2400

Leu Leu Phe Leu Gln Arg Pro Ser Met Lys Gln Met Ala Thr Lys Asn  
 1 5 10 15  
 Asp Ser Ser Val Ser Glu Phe Ile Leu Met Gly Leu Thr Asp Gln Pro  
 20 25 30  
 Glu Leu Gln Leu Pro Leu Phe Phe Leu Phe Leu Leu Asn His Thr Val  
 35 40 45  
 Ile Val Val Gly Asn Leu Ser Leu Met Ser Leu Ile Ile Leu Asn Ser  
 50 55 60  
 Asn Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Ile  
 65 70 75 80  
 Asp Phe Cys Tyr Ser Phe Val Phe Thr Pro Lys Met Leu Met Ser Phe  
 85 90 95  
 Val Ser Glu Lys Asn Ile Ile Pro Phe Thr Gly Cys Met Thr Gln Leu  
 100 105 110  
 Phe Phe Phe Cys Phe Phe Ala His Ser Glu Ser Trp Val Leu Thr Val  
 115 120 125  
 Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Lys  
 130 135 140  
 Ala Ile Met Leu Pro Arg Ile Cys Cys Leu Leu Met Phe Val Ser Tyr

```

145          150          155          160
Leu Ile Gly Phe Ala Ser Ala Met Val Leu Ala Gly Leu Met Ile Arg
          165          170          175
Leu Asn Phe Cys Asn Asn Asn Ile Ile Asn His Tyr Met Cys Asp Ile
          180          185          190
Phe Pro Val Leu Arg Ile Ser Cys Ser Asn Thr Tyr Leu Asn Glu Leu
          195          200          205
Val Ser Thr Ala Val Val Gly Thr Ala Ile Ile Leu Cys Ser Leu Ile
          210          215          220
Ile Phe Ile Ser Tyr Ala Met Ile Leu Phe Asn Ile Val His Met Ser
225          230          235          240
Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile
          245          250          255
Ile Thr Val Ser Phe Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys
          260          265          270
Pro Ser Ser Ala Glu Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe
          275          280          285
Tyr Thr Phe Leu Val Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          290          295          300
Asn Lys Asp Val Lys Val Ala Val Lys Lys Thr Ile Lys Arg Ile Thr
305          310          315          320
Ser Xaa Leu Lys Gln Phe Glu Leu Val Cys Phe His Phe Leu Ser Ile
          325          330          335
Ile

```

&lt;210&gt; 2401

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Mus musculus (M175 8576195-26-1-5230 3083-4056)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(325)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2401

```

Leu Phe Ser Ser Arg Phe Ser Met Ile Ser Met Leu Ala Gly Asn Gly
1          5          10          15
Ser Ser Val Thr Glu Phe Val Leu Ala Gly Leu Thr Asp Arg Pro Glu
          20          25          30
Leu Gln Leu Pro Leu Phe Tyr Leu Phe Leu Ile Ile Tyr Ile Ile Thr
          35          40          45
Val Val Gly Asn Leu Gly Leu Ile Ile Leu Ile Gly Leu Asn Pro His
          50          55          60
Leu His Thr Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp
65          70          75          80
Leu Cys Tyr Ser Ser Val Phe Ser Pro Lys Met Leu Ile Asn Phe Val
          85          90          95
Ser Glu Lys Asn Ser Ile Ser Tyr Ala Gly Cys Met Thr Gln Leu Phe
          100          105          110
Leu Phe Leu Phe Phe Val Ile Ser Glu Cys Tyr Met Leu Thr Ser Met
          115          120          125
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val
          130          135          140
Thr Met Ser Pro Gln Ile Cys Ser Val Ile Ser Phe Ala Ala Tyr Gly
145          150          155          160
Met Gly Phe Ala Gly Ser Ser Ala His Thr Gly Cys Met Leu Arg Leu
          165          170          175
Thr Phe Cys Asn Val Asn Val Ile Asn His Tyr Leu Cys Asp Ile Leu
          180          185          190

```

```

Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val
   195                               200                               205
Val Leu Ile Val Val Gly Ile Asn Ile Thr Val Pro Ser Phe Thr Ile
   210                               215                               220
Leu Ile Ser Tyr Val Phe Ile Leu Ala Asn Ile Leu Asn Ile Lys Ser
  225                               230                               235                               240
Thr Gln Gly Arg Ala Lys Ala Phe Ser Thr Cys Ser Ser His Ile Met
                               245                               250                               255
Ala Ile Ser Leu Phe Phe Gly Ser Ala Ala Phe Met Tyr Leu Lys Tyr
                               260                               265                               270
Ser Ser Gly Ser Met Glu Gln Gly Lys Ile Ser Ser Val Phe Tyr Thr
                               275                               280                               285
Asn Val Gly Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
   290                               295                               300
Asp Val Lys Val Ala Leu Arg Lys Ser Leu Ile Lys Ile Gln Arg Lys
  305                               310                               315                               320
Asp Arg Phe Xaa Leu
                               325

```

&lt;210&gt; 2402

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Unknown (p124-dir-0-7 conceptual translation of range 2-613)

&lt;400&gt;2402

```

Phe Leu Glu Phe Ala Phe Thr Pro Ala Cys Ile Leu Arg Phe Pro Val
  1                               5                               10                               15
Thr Ile Val Thr Gly Asp Arg Thr Ile Ser Phe Ser Asn Cys Phe Phe
   20                               25                               30
Phe Gln Leu Phe Phe Ile Phe Leu Gly Val Met Glu Phe Phe Leu Leu
   35                               40                               45
Ala Pro Thr Ser Tyr Asp Cys Tyr Val Ala Ile Cys Arg Pro Leu His
   50                               55                               60
His Ser Thr Val Met Thr Arg Gly Val Cys Thr Leu Leu Val Leu Ser
   65                               70                               75                               80
Ser Phe Leu Ser Thr Tyr Leu Asn Leu Phe Pro Pro Val Val Met Asp
   85                               90                               95
Phe Trp Leu Asp Cys Cys Asp Pro Asn Ile Leu Lys His Phe Ile Cys
  100                               105                               110
Asp Ser Ser Ser Val Met Glu Leu Cys Thr Asp Thr Arg Phe Leu
  115                               120                               125
Glu Leu Met Thr Phe Pro Leu Ser Leu Val Leu Met Thr Ala Ser Tyr
  130                               135                               140
Thr Ala Ile Ile Cys Ala Ile Leu Arg Leu Pro Tyr Ala Gln Gln Arg
  145                               150                               155                               160
Arg Lys Val Phe Ser Ile Cys Ser Ser His Arg Val Gly Phe Ser Ile
   165                               170                               175
Thr Tyr Gly Ser Cys Ile Phe Met Tyr Ile Asn Thr Val Ala Asp Lys
   180                               185                               190
Asp Arg Val Gly Val Arg Gln Gly Leu Gly Gly Pro
   195                               200

```

&lt;210&gt; 2403

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (OR2B8)

&lt;400&gt;2403

```

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
  1                               5                               10                               15
Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Phe Leu

```

```
<210> 2404
<211> 315
<212> PRT
<213> Unknown (0B12D3)
```

Met	Glu	Asn	Val	Thr	Thr	Met	Asn	Glu	Phe	Leu	Leu	Leu	Gly	Leu	Thr
1				5					10					15	
Gly	Val	Gln	Glu	Leu	Gln	Pro	Phe	Phe	Phe	Gly	Ile	Phe	Leu	Ile	Ile
			20					25					30		
Tyr	Leu	Ile	Asn	Leu	Ile	Gly	Asn	Gly	Ser	Ile	Leu	Val	Met	Val	Val
		35					40					45			
Leu	Glu	Pro	Gln	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn	Leu
	50					55					60				
Ser	Cys	Leu	Asp	Ile	Ser	Tyr	Ser	Ser	Val	Thr	Leu	Pro	Lys	Leu	Leu
65					70					75					80
Val	Asn	Leu	Val	Cys	Ser	Arg	Arg	Ala	Ile	Ser	Phe	Leu	Gly	Cys	Ile
				85					90					95	
Thr	Gln	Leu	His	Phe	Phe	His	Phe	Leu	Gly	Ser	Thr	Glu	Ala	Ile	Leu
			100					105					110		
Leu	Ala	Ile	Met	Ala	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	Asn	Pro	Leu
		115					120					125			
Arg	Tyr	Thr	Val	Ile	Met	Asn	Pro	Gln	Val	Cys	Ile	Leu	Leu	Ala	Ala

```

      130              135              140
Ala Ala Trp Leu Ile Ser Phe Phe Tyr Ala Leu Met His Ser Val Met
145              150              155              160
Thr Ala His Leu Ser Phe Cys Gly Ser Gln Lys Leu Asn His Phe Phe
      165              170              175
Tyr Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Ser Asp Thr Leu Leu
      180              185              190
Asn Gln Trp Leu Leu Ser Ile Val Thr Gly Ser Ile Ser Met Gly Ala
      195              200              205
Phe Phe Leu Thr Leu Leu Ser Cys Phe Tyr Val Ile Gly Phe Leu Leu
      210              215              220
Phe Lys Asn Arg Ser Cys Arg Ile Leu His Lys Ala Leu Ser Thr Cys
225              230              235              240
Ala Ser His Phe Met Val Val Cys Leu Phe Tyr Gly Pro Val Gly Phe
      245              250              255
Thr Tyr Ile Arg Pro Ala Ser Ala Thr Ser Met Ile Gln Asp Arg Ile
      260              265              270
Met Ala Ile Met Tyr Ser Ala Val Thr Pro Val Leu Asn Pro Leu Ile
      275              280              285
Tyr Thr Leu Arg Asn Lys Glu Val Met Met Ala Leu Lys Lys Ile Phe
      290              295              300
Gly Arg Lys Leu Phe Lys Asp Trp Gln Gln His
305              310              315

```

&lt;210&gt; 2405

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Unknown (3273654-dir-0-5 conceptual translation of range 1-345)

&lt;400&gt;2405

```

Leu Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ser Cys Ser Asn Thr
1      5      10      15
Phe Ser Asp Asn Ile Val Lys Tyr Phe Leu Gly Ala Leu Tyr Gly Leu
      20      25      30
Phe Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Ile Ser Ser
      35      40      45
Ile Leu Arg Ile Pro Ser Leu Gly Gly Lys Tyr Lys Ala Phe Ser Thr
      50      55      60
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Leu Val Thr Ala Ser
65      70      75      80
Thr Val Tyr Leu Gly Ser Val Ala Ser His Ser Pro Arg Asn Asp Val
      85      90      95
Val Ala Ser Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      100      105      110
Ile Cys Ser
      115

```

&lt;210&gt; 2406

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Unknown (3810857-dir-0-6 conceptual translation of range 1-417)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(139)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2406

```

Met Ala Xaa Asp Arg Phe Val Ala Ile Cys His Pro Leu Asn Tyr Thr
1      5      10      15
Val Ile Met Asn Pro Arg Ile Cys Gly Leu Leu Val Leu Leu Ser Trp

```

```

      20      25      30
Ile Ile Met Phe Trp Val Ser Leu Ile His Met Leu Leu Met Lys Gln
      35      40      45
Leu Asn Phe Ser Thr Ser Thr Glu Ile Pro His Phe Phe Cys Glu Leu
      50      55      60
Thr Glu Leu Leu Arg Val Gly Arg Ser Asp Thr Phe Thr Gln Asn Ile
65      70      75      80
Phe Leu Tyr Leu Gly Tyr Cys Arg Ala Gly Met Phe Pro Val Ile Gly
      85      90      95
Ile Ala Phe Ser Tyr Phe His Ile Val Ser Ala Leu Met Lys Met Ser
      100      105      110
Ser Ile Lys Asn Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
      115      120      125
Cys Val Val Ser Met Phe Tyr Gly Thr Gly Leu
      130      135

```

&lt;210&gt; 2407

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Unknown (p106-dir-0-8 conceptual translation of range 2-633)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(211)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2407

```

Leu Val Asp Leu Cys Leu Val Thr Thr Leu Val Pro Lys Met Leu Val
1      5      10      15
Asn Leu Leu Thr His Ser Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
      20      25      30
Gln Met Phe Phe Phe Met Val Phe Ala Cys Ser Asn Thr Leu Leu Leu
      35      40      45
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Pro Leu Ser
      50      55      60
Tyr Val Thr Ile Met Arg Pro Gln Phe Cys Gly Leu Leu Ala Leu Leu
65      70      75      80
Ser Trp Thr Ile Ser Leu Leu Asn Ala Val Leu His Ser Pro Leu Val
      85      90      95
Met Arg Leu Leu Phe Cys Thr Glu Arg Glu Ile Pro Leu Phe Tyr His
      100      105      110
Asp Leu Thr Xaa Val Leu Arg Leu Ser Cys Thr Asp Met Leu Ile Asn
      115      120      125
Asp Ile Leu Val Tyr Leu Leu Thr Ala Leu Leu Ser Ile Phe Pro Phe
      130      135      140
Thr Gly Ile Leu Phe Ser Tyr Thr Gln Ile Cys Ser Ser Ile Val Lys
145      150      155      160
Ile Pro Ser Thr Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
Tyr Leu Cys Val Val Leu Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
      180      185      190
Leu Ser Ser Ser Val Thr Lys Ser Ser Trp Lys Ser Ser Val Ala Ser
      195      200      205
Val Ile Cys
      210

```

&lt;210&gt; 2408

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Unknown (4877338-dir-0-6 conceptual translation of range 2-478)



&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(159)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2408

```

Ile Cys His Pro Leu Arg Tyr Thr Val Ser Met Asn Pro Arg Leu Cys
 1          5          10          15
Val Gln Leu Ile Leu Leu Ser Leu Phe Ile Ser Ile Ala Asp Ala Leu
          20          25          30
Leu His Ser Leu Met Val Leu Gln Leu Ser Phe Cys Thr Asp Leu Glu
          35          40          45
Ile Ser Leu Phe Cys Glu Val Val Gln Val Ile Lys Arg Ala Cys Ser
          50          55          60
Asp Thr Leu Ile Asn Asn Ile Leu Val Tyr Phe Ala Ala Gly Ile Phe
          65          70          75          80
Ala Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ile Gln Ile Val
          85          90          95
Ser Ser Ile Leu Xaa Met Pro Ser Ser Gly Arg Lys Xaa Lys Ala Phe
          100          105          110
Ser Thr Cys Glu Ser His Leu Ser Val Val Ser Phe Phe Tyr Gly Thr
          115          120          125
Ala Phe Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser Ser Arg Lys
          130          135          140
Thr Ala Val Ala Ser Leu Met Tyr Thr Val Val Thr Pro Val Met
          145          150          155

```

&lt;210&gt; 2409

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (p22-dir-0-11 conceptual translation of range 1-930)

&lt;400&gt;2409

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
          35          40          45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
          65          70          75          80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
          145          150          155          160
Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
          165          170          175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
          180          185          190
His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Thr Leu Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
          210          215          220

```

Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala  
 245 250 255  
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val  
 260 265 270  
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu  
 290 295 300  
 Trp Arg Pro Phe Gln Arg  
 305 310

&lt;210&gt; 2410

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (p23-dir-0-11 conceptual translation of range 1-930)

&lt;400&gt;2410

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn  
 100 105 110  
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Cys  
 115 120 125  
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu  
 130 135 140  
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr  
 145 150 155 160  
 Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr  
 165 170 175  
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr  
 180 185 190  
 His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu  
 195 200 205  
 Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr  
 210 215 220  
 Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala  
 245 250 255  
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val  
 260 265 270  
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu  
 290 295 300  
 Trp Arg Pro Phe Gln Arg  
 305 310

&lt;210&gt; 2411

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (p139-dir-0-8 conceptual translation of range 2-646)

&lt;400&gt;2411

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1           5           10           15
Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
      20           25           30
Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
      35           40           45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
      50           55           60
Cys Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Ser Leu
      65           70           75           80
Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr Phe Leu Leu
      85           90           95
Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Leu Phe Cys
      100          105          110
Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr His Ile Ile
      115          120          125
His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
      130          135          140
Gly Phe Met Thr Lys Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
      145          150          155          160
Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr Cys Ala Ser
      165          170          175
His Leu Gly Val Val Ser Leu Phe Tyr Gly Met Leu Ala Met Val Tyr
      180          185          190
Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
      195          200          205
Met Tyr Ala Val Val Thr Pro
      210          215

```

&lt;210&gt; 2412

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p182-dir-0-11 conceptual translation of range 1-936)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2412

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
      20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65           70           75           80
Met Leu Val Asn Pro Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
      85           90           95
Cys Leu Thr Gln Leu Xaa Phe Leu Val Ser Leu Val Thr Leu Asp Asn
      100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
      115          120          125

```

Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu  
 130 135 140  
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr  
 145 150 155 160  
 Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr  
 165 170 175  
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr  
 180 185 190  
 His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu  
 195 200 205  
 Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Cys Ile Val Arg Thr  
 210 215 220  
 Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala  
 245 250 255  
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val  
 260 265 270  
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu  
 290 295 300  
 Arg Arg Leu Phe Gln Arg Pro Lys  
 305 310

&lt;210&gt; 2413

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p184-dir-0-11 conceptual translation of range 1-936)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2413

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Pro Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Leu Xaa Phe Leu Val Ser Leu Val Thr Leu Asp Asn  
 100 105 110  
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys  
 115 120 125  
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu  
 130 135 140  
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr  
 145 150 155 160  
 Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His His  
 165 170 175  
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr  
 180 185 190  
 His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu

195	200	205
Thr Pro Leu Gly Phe Met Thr Thr Ser His Val Cys Ile Val Arg Thr		
210	215	220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala		
	245	250
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val		
	260	265
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
	275	280
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu		
290	295	300
Arg Arg Leu Phe Gln Arg Pro Lys		
305	310	

&lt;210&gt; 2414

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p183-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2414

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly		
1	5	10
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu		
	20	25
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala		
	35	40
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala		
	50	55
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys		
65	70	75
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly		
	85	90
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn		
	100	105
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys		
	115	120
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu		
	130	135
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr		
145	150	155
Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr		
	165	170
Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr		
	180	185
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu		
	195	200
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Cys Ile Val Arg Thr		
210	215	220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala		
	245	250
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val		
	260	265
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
	275	280
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu		
290	295	300
Arg Arg Leu Phe Gln Arg Pro Lys		

305

310

&lt;210&gt; 2415

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p186-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2415

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
          35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Phe Tyr Gly Leu Leu Leu Thr
          145          150          155          160
Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
          165          170          175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
          180          185          190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
          210          215          220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
          245          250          255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
          260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
          275          280          285
His Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu
          290          295          300
Arg Arg Leu Phe Gln Arg Pro Lys
305          310

```

&lt;210&gt; 2416

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (p140-dir-0-8 conceptual translation of range 2-646)

&lt;400&gt;2416

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1          5          10          15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
          20          25          30
Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
          35          40          45

```

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His  
 50 55 60  
 Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Ser Leu  
 65 70 75 80  
 Cys Trp Gly Leu Ser Val Phe Tyr Gly Leu Leu Leu Thr Leu Leu  
 85 90 95  
 Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Phe Phe Cys  
 100 105 110  
 Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Ile  
 115 120 125  
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu  
 130 135 140  
 Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln  
 145 150 155 160  
 Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser  
 165 170 175  
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala Met Val Cys  
 180 185 190  
 Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val  
 195 200 205  
 Met Tyr Ala Val Val Thr Pro  
 210 215

&lt;210&gt; 2417

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (p141-dir-0-8 conceptual translation of range 2-646)

&lt;400&gt;2417

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Asn Met Leu Val  
 1 5 10 15  
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Lys Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His  
 50 55 60  
 Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Ser Leu  
 65 70 75 80  
 Gly Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr Leu Leu Met  
 85 90 95  
 Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Leu Phe Cys  
 100 105 110  
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Ile  
 115 120 125  
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu  
 130 135 140  
 Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln  
 145 150 155 160  
 Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr Cys Ala Ser  
 165 170 175  
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala Met Val Tyr  
 180 185 190  
 Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val  
 195 200 205  
 Met Tyr Ala Val Val Thr Pro  
 210 215

&lt;210&gt; 2418

&lt;211&gt; 312

&lt;212&gt; PRT

<213> Unknown (p187-dir-0-11 conceptual translation of range 1-936)

<400>2418

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65           70           75           80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Glu
 85           90           95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145          150          155          160
Leu Leu Met Asn Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165          170          175
Leu Phe Cys Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr
 180          185          190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195          200          205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val His Ile Val Arg Thr
 210          215          220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225          230          235          240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245          250          255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Val Leu Gly Arg Val Leu
 290          295          300
Gly Arg Pro Phe Gln Arg Pro Lys
 305          310

```

<210> 2419

<211> 211

<212> PRT

<213> Unknown (p167-dir-0-8 conceptual translation of range 2-634)

<400>2419

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1           5           10           15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
 20           25           30
Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
 35           40           45
Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr
 50           55           60
Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Cys Leu Cys
 65           70           75           80
Trp Ser Val Leu Tyr Gly Leu Leu Leu Thr Leu Leu Met Thr Thr Val

```



Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly  
1 5 10 15

```

Ile Ser Glu Ser Pro Glu Gln Gln Gln Met Leu Phe Trp Met Phe Leu
      20      25      30
Val Arg Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35      40      45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50      55      60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65      70      75      80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly
      85      90      95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
      100      105      110
Leu Asn Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
      115      120      125
Pro Leu His Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu
      130      135      140
Leu Ser Leu Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
      145      150      155      160
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
      165      170      175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
      180      185      190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
      195      200      205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala
      210      215      220
Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly
      245      250      255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
      260      265      270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Ile Asn Pro Phe Ile
      275      280      285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Arg
      290      295      300
Gln Gly Lys Ala Phe Gln Lys Leu Thr
305      310

```

&lt;210&gt; 2422

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Unknown (3831606-dir-0-8 conceptual translation of range 2-642)

&lt;400&gt;2422

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
1      5      10      15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
      20      25      30
Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
      35      40      45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
      50      55      60
Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Ser Leu
      65      70      75      80
Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
      85      90      95
Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
      100      105      110
Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
      115      120      125

```

His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu  
 130 135 140  
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln  
 145 150 155 160  
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser  
 165 170 175  
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr  
 180 185 190  
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val  
 195 200 205  
 Met His Ala Val Val Thr  
 210

&lt;210&gt; 2423

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (p35-dir-0-11 conceptual translation of range 1-954)

&lt;400&gt;2423

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu  
 20 25 30  
 Val Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Ser Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Met Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn  
 100 105 110  
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg  
 115 120 125  
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu  
 130 135 140  
 Leu Ser Leu Cys Trp Gly Phe Ser Ala Leu Tyr Gly Leu Ile His Ile  
 145 150 155 160  
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr  
 165 170 175  
 Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile  
 180 185 190  
 His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu  
 195 200 205  
 Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala His Ile Val Arg Ala  
 210 215 220  
 Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Ser Ala Ser His Leu Ala Val Val Phe Leu Phe Tyr Gly Thr Leu Gly  
 245 250 255  
 Met Val Tyr Leu Gln Pro Leu His Asn Leu Gln Pro Leu Gln Thr Tyr  
 260 265 270  
 Ser Met Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro  
 275 280 285  
 Met Ile Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met His Gly  
 290 295 300  
 Ala Leu Gly Arg Leu Arg Gln Gly Lys Ala Phe Gln Lys Leu Thr  
 305 310 315

&lt;210&gt; 2424

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p34-dir-0-11 conceptual translation of range 1-937)

&lt;400&gt;2424

```

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20           25           30
Val Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65           70           75           80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85           90           95
Cys Leu Met Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
145          150          155          160
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
          165          170          175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
          180          185          190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala His Ile Val Arg Ala
          210          215          220
Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ala Val Val Phe Leu Phe Tyr Gly Thr Val Gly
          245          250          255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
          260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Ile Asn Pro Phe Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Arg
          290          295          300
Gln Gly Lys Ala Phe Gln Lys Leu Thr
305           310

```

&lt;210&gt; 2425

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p87-dir-0-11 conceptual translation of range 1-937)

&lt;400&gt;2425

```

Met Asp Gly Asp Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Arg Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Phe Ile Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
 50           55           60
Asn Phe Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys

```

65					70					75				80	
Met	Pro	Val	Asn	Leu	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ser	Tyr	Ala	Gly
				85					90					95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Ala	Leu	Asp	Asn
			100					105					110		
Leu	Ile	Pro	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Arg
		115					120					125			
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Ile	Leu	Leu
		130				135					140				
Leu	Ser	Met	Cys	Trp	Val	Phe	Ser	Ala	Leu	Tyr	Gly	Leu	Ile	His	Ile
145					150					155				160	
Leu	Leu	Met	Thr	Arg	Val	Thr	Phe	Cys	Gly	Ser	Gln	Lys	Ile	His	Tyr
			165						170				175		
Leu	Phe	Cys	Glu	Met	Tyr	Phe	Leu	Leu	Arg	Leu	Ala	Cys	Ser	Asn	Ile
		180						185					190		
His	Val	Asn	His	Thr	Val	Leu	Val	Ala	Met	Gly	Cys	Phe	Ile	Phe	Leu
		195					200					205			
Ile	Pro	Leu	Gly	Phe	Met	Ile	Thr	Ser	Tyr	Ala	Arg	Ile	Val	Arg	Ala
		210				215					220				
Ile	Leu	Gln	Ile	Pro	Pro	Ala	Thr	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr
225					230					235				240	
Cys	Ala	Ser	His	Leu	Ala	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Leu	Gly
			245						250				255		
Ile	Val	Tyr	Leu	Gln	Pro	Pro	Gln	Thr	Tyr	Ser	Met	Lys	Asp	Ser	Val
		260						265					270		
Ala	Thr	Val	Met	Tyr	Val	Val	Val	Thr	Pro	Met	Ile	Asn	Pro	Phe	Ile
		275					280					285			
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	His	Gly	Asp	Leu	Gly	Arg	Leu	Arg
		290				295					300				
Gln	Gly	Lys	Ala	Phe	Gln	Lys	Leu	Thr							
305					310										

&lt;210&gt; 2426

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p136-dir-0-11 conceptual translation of range 1-939)

&lt;400&gt;2426

Met	Asp	Gly	Gly	Asn	Gln	Ser	Lys	Gly	Ser	Glu	Phe	Leu	Leu	Leu	Gly
1				5					10					15	
Met	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Arg	Ile	Leu	Phe	Trp	Met	Phe	Leu
		20						25					30		
Ser	Met	Tyr	Leu	Val	Thr	Val	Val	Gly	Asn	Ala	Leu	Ile	Ile	Leu	Ala
		35					40					45			
Ile	Thr	Ser	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Val
		50				55					60				
Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	Val	Thr	Asn	Thr	Ile	Pro	Lys
65					70				75					80	
Met	Leu	Val	Asn	Leu	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ala	Tyr	Ala	Gly
			85						90					95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Ala	Leu	Asp	Asn
		100						105					110		
Leu	Ile	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
		115					120					125			
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Ile	Leu	Leu
		130				135					140				
Leu	Ser	Leu	Cys	Trp	Val	Phe	Ser	Val	Leu	Tyr	Gly	Leu	Ile	His	Thr
145					150					155				160	
Leu	Leu	Met	Thr	Arg	Val	Thr	Phe	Cys	Gly	Ser	Arg	Lys	Ile	His	Tyr
			165						170				175		
Leu	Phe	Cys	Glu	Met	Tyr	Val	Leu	Leu	Gln	Leu	Ala	Cys	Ser	Asn	Ile

```

      180      185      190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
      195      200      205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala
      210      215      220
Ile Leu Arg Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly
      245      250      255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
      260      265      270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
      275      280      285
Tyr Ser Leu Lys Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
      290      295      300
Gln Gly Lys Ala Phe Trp Lys Leu Thr
      305      310

```

&lt;210&gt; 2427

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p163-dir-0-11 conceptual translation of range 1-939)

&lt;400&gt;2427

```

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
1      5      10      15
Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
      20      25      30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35      40      45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50      55      60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65      70      75      80
Met Leu Val Asn Leu Gln Ser Gln Asp Lys Ala Ile Ser Tyr Ala Gly
      85      90      95
Cys Leu Thr Gln Leu Tyr Phe Leu Leu Ser Leu Val Thr Leu Asp Asn
      100      105      110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
      115      120      125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Arg Leu Cys Ile Leu Leu
      130      135      140
Leu Ser Leu Cys Trp Val Phe Ser Val Leu Tyr Gly Leu Ile His Thr
      145      150      155      160
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
      165      170      175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
      180      185      190
Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
      195      200      205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala
      210      215      220
Ile Leu Arg Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly
      245      250      255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Thr Lys Asp Ser Val
      260      265      270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
      275      280      285
Tyr Ser Leu Arg Asn Lys Asp Ile His Gly Ala Leu Gly Arg Leu Leu

```

290                      295                      300  
 Gln Gly Lys Ala Phe Gln Lys Leu Thr  
 305                      310

<210> 2428

<211> 312

<212> PRT

<213> Unknown (p18-dir-0-11 conceptual translation of range 1-936)

<400>2428

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly  
 1                      5                      10                      15  
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu  
                     20                      25                      30  
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala  
 35                      40                      45  
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala  
 50                      55                      60  
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys  
 65                      70                      75                      80  
 Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly  
                     85                      90                      95  
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn  
                     100                      105                      110  
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys  
 115                      120                      125  
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu  
 130                      135                      140  
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr  
 145                      150                      155                      160  
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr  
                     165                      170                      175  
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile  
                     180                      185                      190  
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu  
 195                      200                      205  
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala  
 210                      215                      220  
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr  
 225                      230                      235                      240  
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys  
                     245                      250                      255  
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val  
                     260                      265                      270  
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile  
 275                      280                      285  
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu  
 290                      295                      300  
 Asp Lys His Phe Lys Arg Leu Thr  
 305                      310

<210> 2429

<211> 312

<212> PRT

<213> Unknown (p32-dir-0-11 conceptual translation of range 1-936)

<400>2429

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly  
 1                      5                      10                      15  
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu  
                     20                      25                      30

Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn  
 100 105 110  
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys  
 115 120 125  
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu  
 130 135 140  
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr  
 145 150 155 160  
 Ile Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr  
 165 170 175  
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile  
 180 185 190  
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu  
 195 200 205  
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys  
 245 250 255  
 Met Val Tyr Leu Lys Pro Leu His Thr Phe Ser Val Lys Asp Ser Val  
 260 265 270  
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu  
 290 295 300  
 Asp Thr His Phe Lys Arg Leu Thr  
 305 310

&lt;210&gt; 2430

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p130-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2430

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ser Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly  
 85 90 95  
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn  
 100 105 110  
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys  
 115 120 125  
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu  
 130 135 140



Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr  
 145 150 155 160  
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr  
 165 170 175  
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile  
 180 185 190  
 Gln Thr Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu  
 195 200 205  
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala  
 210 215 220  
 Ile Leu Arg Ile Pro Ser Leu Ser Lys Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys  
 245 250 255  
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val  
 260 265 270  
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu  
 290 295 300  
 Asp Lys His Phe Lys Arg Leu Thr  
 305 310

&lt;210&gt; 2431

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (p143-dir-0-8 conceptual translation of range 2-646)

&lt;400&gt;2431

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val  
 1 5 10 15  
 Ser Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Pro Gly Cys Leu Thr  
 20 25 30  
 Gln Leu Phe Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His  
 50 55 60  
 Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Ile Leu  
 65 70 75 80  
 Cys Trp Ala Leu Ser Ile Leu Tyr Gly Leu Ile His Thr Leu Leu Met  
 85 90 95  
 Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys  
 100 105 110  
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Asn  
 115 120 125  
 His Met Met Leu Ile Ala Thr Gly Cys Phe Val Phe Leu Val Pro Phe  
 130 135 140  
 Gly Phe Met Ile Met Ser Tyr Ile Cys Ile Val Arg Ala Ile Leu Lys  
 145 150 155 160  
 Ile Pro Ser Ala Ser Asn Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser  
 165 170 175  
 His Leu Ala Val Val Ala Leu Phe Tyr Gly Thr Leu Cys Met Val Tyr  
 180 185 190  
 Leu Lys Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val  
 195 200 205  
 Met Tyr Ala Val Val Thr Pro  
 210 215

&lt;210&gt; 2432

&lt;211&gt; 312

&lt;212&gt; PRT

<213> Unknown (p89-dir-0-11 conceptual translation of range 1-935)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2432

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1          5          10          15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
      20          25          30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
      35          40          45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
      50          55          60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
      65          70          75          80
Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
      85          90          95
Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
      100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
      115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
      130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
      145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Xaa Gly Asn Gln Glu Val Ala Asn
      165          170          175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
      180          185          190
Arg Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Pro Val
      195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
      210          215          220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
      225          230          235          240
Gly Ser His Leu Thr Val Val Cys Phe Val Tyr Gly Thr Val Met Gly
      245          250          255
Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
      260          265          270
Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
      275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
      290          295          300
Lys Arg Ile Ser Ser Xaa Pro Met
305          310

```

<210> 2433

<211> 312

<212> PRT

<213> Unknown (p88-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2433

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly

```

```

1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
85           90           95
Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
165          170          175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
180          185          190
His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
210          215          220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
245          250          255
Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
260          265          270
Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
290          295          300
Lys Arg Ile Ser Ser Xaa Pro Met
305          310

```

&lt;210&gt; 2434

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p33-dir-0-11 conceptual translation of range 1-936)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2434

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Ile Leu Ala
35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80

```

Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly  
                             85                            90                            95  
 Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser  
                             100                            105                            110  
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg  
                             115                            120                            125  
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu  
                             130                            135                            140  
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr  
                             145                            150                            155                            160  
 Leu Leu Thr Ala Ser Leu Ser Phe Xaa Gly Asn Gln Glu Val Ala Asn  
                             165                            170                            175  
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile  
                             180                            185                            190  
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val  
                             195                            200                            205  
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val  
                             210                            215                            220  
 Phe Gln Gly Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys  
                             225                            230                            235                            240  
 Gly Ser His Leu Thr Val Val Ser Leu Asp Tyr Gly Thr Val Lys Gly  
                             245                            250                            255  
 Lys Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile  
                             260                            265                            270  
 Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
                             275                            280                            285  
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn  
                             290                            295                            300  
 Lys Arg Ile Ser Ser Xaa Pro Met  
                             305                            310

&lt;210&gt; 2435

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p43-dir-0-11 conceptual translation of range 1-936)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(312)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2435

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly  
   1                            5                            10                            15  
 Val Thr Gly Gln Gln Glu Gln Asp Phe Phe Tyr Ile Leu Phe Leu  
                             20                            25                            30  
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala  
                             35                            40                            45  
 Ile Cys Ser Asp Val Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala  
                             50                            55                            60  
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys  
                             65                            70                            75                            80  
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly  
                             85                            90                            95  
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser  
                             100                            105                            110  
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser His  
                             115                            120                            125  
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu  
                             130                            135                            140  
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr

145                      150                      155                      160  
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn  
                                  165                      170                      175  
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile  
                                  180                      185                      190  
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val  
                                  195                      200                      205  
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val  
                                  210                      215                      220  
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys  
 225                      230                      235                      240  
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly  
                                  245                      250                      255  
 Thr Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile  
                                  260                      265                      270  
 Thr Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
                                  275                      280                      285  
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg Lys Leu Phe Asn  
                                  290                      295                      300  
 Lys Arg Ile Ser Ser Xaa Pro Met  
 305                      310  
  
 <210> 2436  
 <211> 309  
 <212> PRT  
 <213> Unknown (p180-dir-0-11 conceptual translation of range 1-927)

<400>2436  
 Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly  
 1                      5                      10                      15  
 Val Thr Gly Gln Gln Glu Gln Asp Phe Phe Tyr Ile Leu Phe Leu  
                                  20                      25                      30  
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala  
                                  35                      40                      45  
 Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala  
                                  50                      55                      60  
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys  
 65                      70                      75                      80  
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly  
                                  85                      90                      95  
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser  
                                  100                      105                      110  
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg  
                                  115                      120                      125  
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu  
                                  130                      135                      140  
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr  
 145                      150                      155                      160  
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn  
                                  165                      170                      175  
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile  
                                  180                      185                      190  
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val  
                                  195                      200                      205  
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val  
                                  210                      215                      220  
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys  
 225                      230                      235                      240  
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly  
                                  245                      250                      255  
 Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile

```
<210> 2437
<211> 309
<212> PRT
<213> Unknown (p204-dir-0-11 conceptual translation of range 1-927)
```

```
<210> 2438
<211> 214
<212> PRT
<213> Unknown (p179-dir-0-8 conceptual translation of range 2-643)
```

1480

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala  
 1 5 10 15  
 Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala  
 20 25 30  
 Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu  
 35 40 45  
 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His  
 50 55 60  
 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly  
 65 70 75 80  
 Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr  
 85 90 95  
 Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys  
 100 105 110  
 Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn  
 115 120 125  
 Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu  
 130 135 140  
 Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val  
 145 150 155 160  
 Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His  
 165 170 175  
 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe  
 180 185 190  
 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met  
 195 200 205  
 Tyr Thr Ala Val Thr Pro  
 210

&lt;210&gt; 2439

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Unknown (p191-dir-0-8 conceptual translation of range 2-643)

&lt;400&gt;2439

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala  
 1 5 10 15  
 Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala  
 20 25 30  
 Gln Met Tyr Phe Met Ile Gly Leu Ala Asn Thr Asp Ser Tyr Ile Leu  
 35 40 45  
 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His  
 50 55 60  
 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly  
 65 70 75 80  
 Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr  
 85 90 95  
 Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys  
 100 105 110  
 Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn  
 115 120 125  
 Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu  
 130 135 140  
 Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val  
 145 150 155 160  
 Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His  
 165 170 175  
 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe  
 180 185 190  
 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met  
 195 200 205

Tyr Thr Ala Val Thr Pro  
210

<210> 2440

<211> 222

<212> PRT

<213> Unknown (3983387-dir-0-8 conceptual translation of range 1-666)

<400>2440

Ala	Asn	Leu	Ser	Phe	Val	Asp	Val	Cys	Phe	Thr	Thr	Asn	Leu	Ile	Pro
1				5					10					15	
Arg	Leu	Leu	Ala	Gly	His	Val	Ala	Gly	Thr	Arg	Thr	Ile	Ser	Tyr	Val
			20					25					30		
His	Cys	Leu	Thr	Gln	Thr	Tyr	Phe	Leu	Ile	Ser	Phe	Ala	Asn	Val	Asp
		35					40					45			
Thr	Phe	Leu	Leu	Ala	Ala	Met	Ala	Leu	Asp	Arg	Phe	Val	Ala	Ile	Cys
	50					55					60				
Tyr	Pro	Leu	Gln	Tyr	His	Thr	Ile	Ile	Thr	Pro	Gln	Leu	Cys	Val	Gly
65					70					75					80
Leu	Ala	Ala	Val	Val	Trp	Met	Cys	Ser	Ala	Leu	Ile	Ser	Leu	Met	His
			85						90					95	
Thr	Leu	Leu	Met	Ser	Arg	Leu	Ser	Phe	Cys	Ser	Ser	Ile	Pro	Glu	Ile
			100					105					110		
Ser	His	Phe	Tyr	Cys	Asp	Ala	Tyr	Leu	Leu	Met	Lys	Leu	Ala	Cys	Ser
	115						120					125			
Asp	Thr	Arg	Val	Asn	Gln	Leu	Val	Phe	Leu	Gly	Ala	Val	Val	Leu	Phe
	130					135					140				
Val	Ala	Pro	Cys	Ile	Leu	Ile	Val	Val	Ser	Tyr	Val	Arg	Ile	Thr	Met
145					150					155					160
Val	Val	Leu	Gln	Ile	Pro	Ser	Ala	Lys	Gly	Arg	His	Lys	Thr	Phe	Ser
			165						170					175	
Thr	Cys	Ser	Ser	His	Leu	Ser	Val	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Val
		180						185					190		
Leu	Gly	Ile	Tyr	Ile	Arg	Pro	Pro	Asp	Ser	Phe	Ser	Thr	Gln	Asp	Thr
	195					200						205			
Val	Ala	Thr	Ile	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn		
	210					215					220				

<210> 2441

<211> 314

<212> PRT

<213> Unknown (205837-dir-0-11 conceptual translation of range 1-942)

<400>2441

Met	Thr	Arg	Arg	Asn	Gln	Thr	Ala	Ile	Ser	Gln	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Leu	Pro	Phe	Pro	Pro	Glu	Tyr	Gln	His	Leu	Phe	Tyr	Ala	Leu	Phe	Leu
		20						25					30		
Ala	Met	Tyr	Leu	Thr	Thr	Leu	Leu	Gly	Asn	Leu	Ile	Ile	Ile	Ile	Leu
		35					40					45			
Ile	Leu	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser
	50					55					60				
Asn	Leu	Ser	Phe	Ala	Asp	Leu	Cys	Phe	Ser	Ser	Val	Thr	Met	Pro	Lys
65					70					75					80
Leu	Leu	Gln	Asn	Met	Gln	Ser	Gln	Val	Pro	Ser	Ile	Pro	Tyr	Ala	Gly
			85						90					95	
Cys	Leu	Ala	Gln	Ile	Tyr	Phe	Phe	Leu	Phe	Phe	Gly	Asp	Leu	Gly	Asn
		100						105					110		
Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe
	115					120						125			
Pro	Leu	His	Tyr	Met	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys	Val	Ser	Leu



130	135	140
Val Val Leu Ser Trp	Val Leu Thr Thr Phe His Ala Met Leu His Thr	
145	150	155
Leu Leu Met Ala Arg	Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His	160
165	170	175
Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr		
180	185	190
His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val		
195	200	205
Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser		
210	215	220
Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile		
245	250	255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr		
260	265	270
Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe		
275	280	285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Asp Ala Leu Glu Lys Ile		
290	295	300
Met Cys Lys Lys Gln Ile Pro Ser Phe Leu		
305	310	

&lt;210&gt; 2442

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769630-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2442

Leu Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro	
1	5
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala	10
20	25
Gly Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly	30
35	40
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys	45
50	55
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser	60
65	70
Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His	75
85	90
Thr Leu Leu Met Ala Arg Leu Ser Phe Arg Glu Asp Ser Val Ile Pro	95
100	105
His Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Pro Asp	110
115	120
Thr His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val	125
130	135
Val Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser	140
145	150
Ser Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser	155
165	170
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Ile Tyr Gly Thr Val	175
180	185
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu	190
195	200
Thr Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met	205
210	215
	220

&lt;210&gt; 2443

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (1504111-dir-0-11 conceptual translation of range 1-942)

&lt;400&gt;2443

```

Met Thr Glu Arg Asn Gln Thr Val Il Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
          20          25          30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45
Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
          85          90          95
Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
          100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
          130          135          140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
          195          200          205
Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
          210          215          220
Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
          245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr
          260          265          270
Val Met Ser Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Arg Ile
          290          295          300
Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu
305          310

```

&lt;210&gt; 2444

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769633-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2444

```

Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
 1          5          10          15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
          20          25          30
Gly Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly
          35          40          45
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
65          70          75          80

```

Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His  
                   85                                  90                  95  
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro  
                   100                                  105                  110  
 His Ph Phe Cys Asp Thr Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp  
                   115                                  120                  125  
 Thr Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu  
                   130                                  135                  140  
 Val Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser  
                   145                                  150                  155                  160  
 Ser Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Glu Ala Phe Ser  
                   165                                  170                  175  
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val  
                   180                                  185                  190  
 Ile Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu  
                   195                                  200                  205  
 Thr Val Met Ser Leu Met Tyr Thr Val Val Thr Pro Met  
                   210                                  215                  220

&lt;210&gt; 2445

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769632-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2445

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro  
   1                                  5                                  10                  15  
 Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Val  
                   20                                  25                  30  
 Gly Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly  
                   35                                  40                  45  
 Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys  
                   50                                  55                  60  
 Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser  
                   65                                  70                  75                  80  
 Leu Val Val Leu Ser Trp Val Arg Thr Thr Phe His Ala Met Leu His  
                   85                                  90                  95  
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro  
                   100                                  105                  110  
 His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp  
                   115                                  120                  125  
 Thr Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu  
                   130                                  135                  140  
 Val Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser  
                   145                                  150                  155                  160  
 Ser Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser  
                   165                                  170                  175  
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val  
                   180                                  185                  190  
 Ile Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu  
                   195                                  200                  205  
 Thr Val Met Ser Leu Met Tyr Thr Ala Val Thr Pro Met  
                   210                                  215                  220

&lt;210&gt; 2446

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (902347-dir-0-6 conceptual translation of range 2-472)

&lt;400&gt;2446

Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys

```

1           5           10           15
Val Ser Leu Val Leu Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
20           25           30
Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
35           40           45
Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
50           55           60
Ser Asp Thr His Val Asn Glu Leu Val Ile Phe Val Thr Gly Gly Leu
65           70           75           80
Ile His Val Ile Pro Leu Val Leu Ile Leu Val Ser Tyr Ala Gln Ile
85           90           95
Val Ser Ser Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys Ala
100          105          110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
115          120          125
Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asp Asn Ser Thr Val
130          135          140
Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr
145          150          155

```

&lt;210&gt; 2447

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (902682-dir-0-6 conceptual translation of range 2-472)

&lt;400&gt;2447

```

Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys
1           5           10           15
Val Ser Leu Val Leu Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
20           25           30
Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
35           40           45
Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
50           55           60
Ser Asp Thr His Val Asn Glu Leu Val Ile Phe Val Thr Gly Gly Leu
65           70           75           80
Ile Leu Val Ile Pro Phe Val Leu Ile Leu Val Ser Tyr Ala Gln Ile
85           90           95
Val Ser Ser Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys Ala
100          105          110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
115          120          125
Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asp Asn Ser Thr Val
130          135          140
Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr
145          150          155

```

&lt;210&gt; 2448

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769627-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2448

```

Gly Asn Ile Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
1           5           10           15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
20           25           30
Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu
35           40           45
Ser Phe Leu Leu Glu Ala Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys
50           55           60

```

Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser  
 65 70 75 80  
 Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His  
 85 90 95  
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro  
 100 105 110  
 His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp  
 115 120 125  
 Thr His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile  
 130 135 140  
 Val Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala  
 145 150 155 160  
 Ser Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser  
 165 170 175  
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile  
 180 185 190  
 Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu  
 195 200 205  
 Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met  
 210 215 220

&lt;210&gt; 2449

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769629-dir-0-8 conceptual translation of range 1-663)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(221)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2449

Ser Asn Ile Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro  
 1 5 10 15  
 Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala  
 20 25 30  
 Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu  
 35 40 45  
 Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys  
 50 55 60  
 Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser  
 65 70 75 80  
 Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His  
 85 90 95  
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro  
 100 105 110  
 His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp  
 115 120 125  
 Arg His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile  
 130 135 140  
 Val Ile Pro Phe Val Leu Ile Ile Val Ser Xaa Ala Arg Val Val Ala  
 145 150 155 160  
 Ser Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser  
 165 170 175  
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile  
 180 185 190  
 Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu  
 195 200 205  
 Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met  
 210 215 220

&lt;210&gt; 2450

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (205845-dir-0-11 conceptual translation of range 1-942)

&lt;400&gt;2450

```

Met Thr Glu Glu Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Phe
 1          5          10          15
Leu Pro Ile Pro Ser Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
 20          25          30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
 35          40          45
Ile His Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Phe Ala Gly
 85          90          95
Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu Ser
 100         105         110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115         120         125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130         135         140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145         150         155         160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
 165         170         175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180         185         190
His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
 195         200         205
Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
 210         215         220
Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr
 225         230         235         240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245         250         255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
 260         265         270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275         280         285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Ile Arg Val
 290         295         300
Leu Cys Lys Lys Lys Ile Thr Phe Cys Leu
 305         310

```

&lt;210&gt; 2451

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921663-dir-1-7 conceptual translation of range 101-676)

&lt;400&gt;2451

```

Met Tyr Phe Phe Leu Tyr Phe Thr Asp Leu Glu Ser Phe Leu Leu Val
 1          5          10          15
Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Met His Tyr
 20          25          30
Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile Met Ser Pro Met
 35          40          45
Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 50          55          60

```

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp  
 65 70 75 80  
 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu  
 85 90 95  
 Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly  
 100 105 110  
 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala  
 115 120 125  
 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys  
 130 135 140  
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe  
 145 150 155 160  
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser  
 165 170 175  
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro  
 180 185 190

&lt;210&gt; 2452

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (p25-dir-0-11 conceptual translation of range 1-969)

&lt;400&gt;2452

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile  
 130 135 140  
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu  
 145 150 155 160  
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys  
 165 170 175  
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala  
 180 185 190  
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile  
 195 200 205  
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu  
 210 215 220  
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser  
 225 230 235 240  
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val  
 245 250 255  
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser  
 260 265 270  
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr  
 275 280 285  
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg  
 290 295 300

Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro  
 305 310 315 320  
 Phe Leu Leu

<210> 2453

<211> 314

<212> PRT

<213> Unknown (p181-dir-0-11 conceptual translation of range 1-942)

<400>2453

Met Met Glu Gln Asn Gln Thr Ser Thr Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val  
 130 135 140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr  
 260 265 270  
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val  
 290 295 300  
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Ile  
 305 310

<210> 2454

<211> 149

<212> PRT

<213> Unknown (p166-dir-0-6 conceptual translation of range 2-448)

<400>2454

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln  
 1 5 10 15  
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Val Asp Cys Leu Thr



20 25 30  
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu  
 35 40 45  
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
 50 55 60  
 Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu  
 65 70 75 80  
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met  
 85 90 95  
 Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Val Pro His Phe Phe Cys  
 100 105 110  
 Asp Met Pro Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn  
 115 120 125  
 Glu Ser Gly Ile Phe Ile Thr Gly Gly Leu Ile Leu Gly Ile Pro Phe  
 130 135 140  
 Leu Leu Ile Leu Gly  
 145

&lt;210&gt; 2455

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (p17-dir-0-11 conceptual translation of range 1-942)

&lt;400&gt;2455

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Phe Gly Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu  
 130 135 140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr  
 260 265 270  
 Val Met Ala Met Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val

290 295 300  
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu  
 305 310

<210> 2456

<211> 314

<212> PRT

<213> Unknown (p90-dir-0-11 conceptual translation of range 1-942)

<400>2456

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met His Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val  
 130 135 140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Phe Lys Gly Ile Cys Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr  
 260 265 270  
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val  
 290 295 300  
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Leu  
 305 310

<210> 2457

<211> 314

<212> PRT

<213> Unknown (p175-dir-0-11 conceptual translation of range 1-942)

<400>2457

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30

Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
           35                          40                          45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
           50                          55                          60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65                          70                          75                          80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
                           85                          90                          95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser  
                           100                          105                          110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
                           115                          120                          125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val  
                           130                          135                          140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145                          150                          155                          160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
                           165                          170                          175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
                           180                          185                          190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val  
                           195                          200                          205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser  
                           210                          215                          220  
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Leu Ser Thr  
 225                          230                          235                          240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
                           245                          250                          255  
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr  
                           260                          265                          270  
 Val Met Ala Met Ile Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
                           275                          280                          285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val  
                           290                          295                          300  
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu  
 305                          310

&lt;210&gt; 2458

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (p170-dir-0-11 conceptual translation of range 1-942)

&lt;400&gt;2458

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
   1                          5                          10                          15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
                           20                          25                          30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
                           35                          40                          45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
                           50                          55                          60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65                          70                          75                          80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
                           85                          90                          95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser  
                           100                          105                          110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
                           115                          120                          125  
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Leu  
                           130                          135                          140

Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Glu Thr  
 260 265 270  
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val  
 290 295 300  
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Leu  
 305 310

&lt;210&gt; 2459

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (p31-dir-0-11 conceptual translation of range 1-942)

&lt;400&gt;2459

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Ala Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Leu  
 130 135 140  
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
 245 250 255

Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Glu Thr  
 260 265 270  
 Val M t Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gly Asp Met Lys Gly Ala Leu Ser Arg Val  
 290 295 300  
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu  
 305 310

&lt;210&gt; 2460

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Unknown (890-dir-5-12 conceptual translation of range 642-1613)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(324)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2460

Arg Gln Ser Met Thr Glu Lys Asn Gln Thr Val Val Ser Glu Phe Val  
 1 5 10 15  
 Leu Leu Gly Leu Pro Ile Asp Pro Asp Gln Arg Asp Leu Phe Tyr Ala  
 20 25 30  
 Leu Phe Leu Ala Met Tyr Val Thr Thr Ile Leu Gly Asn Leu Leu Ile  
 35 40 45  
 Ile Val Leu Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Leu  
 50 55 60  
 Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr  
 65 70 75 80  
 Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro  
 85 90 95  
 Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp  
 100 105 110  
 Leu Glu Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys Phe Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Leu Cys  
 130 135 140  
 Phe Ser Leu Leu Val Leu Ser Trp Val Leu Thr Met Phe His Ala Val  
 145 150 155 160  
 Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asn Thr Ile  
 165 170 175  
 Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser  
 180 185 190  
 Asp Thr Gln Val Asn Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile  
 195 200 205  
 Leu Val Ile Pro Phe Leu Leu Ile Ile Thr Ser Tyr Ala Arg Ile Val  
 210 215 220  
 Ser Ser Ile Leu Lys Val Pro Ser Ala Ile Gly Ile Cys Lys Val Phe  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr  
 245 250 255  
 Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys  
 260 265 270  
 Glu Thr Ile Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn  
 275 280 285  
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg  
 290 295 300  
 Arg Val Ile Cys Arg Lys Lys Ile Thr Phe Ser Val Xaa Trp Xaa His  
 305 310 315 320  
 Leu Ile Leu Leu

&lt;210&gt; 2461

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Unknown (4877306-dir-0-6 conceptual translation of range 2-487)

&lt;400&gt;2461

Val	Ala	Ile	Cys	Phe	Pro	Leu	His	Tyr	Thr	Thr	Ile	Met	Ser	Pro	Arg
1				5					10					15	
Leu	Cys	Leu	Phe	Leu	Val	Leu	Leu	Pro	Trp	Ile	Leu	Thr	Thr	Phe	His
		20						25					30		
Ala	Met	Leu	His	Thr	Leu	Leu	Met	Ala	Arg	Leu	His	Phe	Cys	Glu	Asp
		35					40					45			
Asn	Val	Ile	Pro	His	Phe	Phe	Cys	Asp	Ser	Ser	Ala	Leu	Leu	Lys	Leu
	50					55					60				
Ser	Cys	Ser	Asp	Thr	Arg	Val	Asn	Glu	Leu	Val	Ile	Phe	Phe	Val	Gly
65					70					75					80
Gly	Leu	Ile	Ile	Ile	Ile	Pro	Phe	Leu	Leu	Ile	Ile	Met	Ser	Tyr	Ala
			85						90					95	
Arg	Ile	Val	Ser	Ser	Ile	Leu	Lys	Val	Pro	Ser	Ala	Lys	Gly	Ile	Cys
		100						105					110		
Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Leu	Phe
		115					120					125			
Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr	Leu	Cys	Pro	Ser	Ala	His	Asn	Ser
	130					135					140				
Thr	Val	Lys	Glu	Thr	Val	Met	Ser	Met	Met	Tyr	Thr	Val	Val	Ala	Pro
145					150					155					160
Met	Leu														

&lt;210&gt; 2462

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p194-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2462

Phe	Thr	Asp	Leu	Cys	Phe	Ser	Thr	Val	Thr	Met	Pro	Asn	Phe	Leu	Gln
1				5					10					15	
Asn	Met	Gln	Ser	Gln	Val	Ser	Ser	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ala
		20						25					30		
Gln	Met	Tyr	Phe	Phe	Leu	Phe	Phe	Gly	Asp	Val	Glu	Ser	Leu	Leu	Leu
		35					40					45			
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His
	50					55					60				
Tyr	Thr	Arg	Ile	Met	Ser	Pro	Asn	Leu	Cys	Val	Ser	Met	Val	Leu	Leu
65				70						75					80
Ser	Trp	Ala	Leu	Thr	Thr	Leu	Cys	Ala	Met	Leu	His	Thr	Leu	Leu	Leu
			85						90				95		
Thr	Arg	Leu	Ser	Phe	Cys	Lys	Asn	Asn	Val	Ile	Pro	His	Phe	Phe	Cys
		100						105					110		
Asp	Leu	Ser	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ile	His	Ile	Asn
		115					120					125			
Glu	Leu	Met	Ile	Met	Ile	Ile	Gly	Ala	Leu	Val	Val	Ile	Leu	Pro	Phe
	130					135					140				
Leu	Leu	Ile	Ile	Val	Ser	Tyr	Ala	His	Ile	Val	Ser	Ser	Ile	Leu	Lys
145					150					155					160
Val	Pro	Ser	Thr	Arg	Gly	Ile	His	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ser
				165					170					175	
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Ser	Val	Ile	Val	Leu	Tyr
			180					185					190		

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser  
           195                          200                  205  
 Met Met Tyr Thr Val Val Thr Pro  
           210                          215

<210> 2463

<211> 157

<212> PRT

<213> Unknown (902674-dir-0-6 conceptual translation of range 2-472)

<400>2463

Ile Cys Phe Pro Leu His Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys  
   1                  5                  10                  15  
 Val Ser Met Val Leu Leu Ser Trp Ala Leu Thr Thr Leu Cys Ala Met  
           20                  25                  30  
 Leu Arg Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Lys Asn Asn Val  
   35                  40                  45  
 Ile Pro His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys  
   50                  55                  60  
 Ser Asp Ile His Ile Asn Glu Leu Met Ile Met Ile Ile Gly Ala Leu  
   65                  70                  75                  80  
 Val Val Ile Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala His Ile  
           85                  90                  95  
 Val Ser Ser Ile Leu Lys Val Pro Ser Thr Arg Gly Ile His Lys Val  
           100                  105                  110  
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly  
           115                  120                  125  
 Ser Val Ile Val Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val  
           130                  135                  140  
 Lys Asp Thr Val Met Ser Met Met Tyr Thr Val Val Thr  
   145                  150                  155

<210> 2464

<211> 216

<212> PRT

<213> Unknown (p197-dir-0-8 conceptual translation of range 2-649)

<220>

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400>2464

Phe Thr Asp Leu Xaa Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln  
   1                  5                  10                  15  
 Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr  
           20                  25                  30  
 Gln Met Tyr Phe Leu Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu  
           35                  40                  45  
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
   50                  55                  60  
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu  
   65                  70                  75                  80  
 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu  
           85                  90                  95  
 Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys  
           100                  105                  110  
 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn  
           115                  120                  125  
 Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe  
   130                  135                  140

Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys  
 145 150 155 160  
 Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr  
 180 185 190  
 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser  
 195 200 205  
 Met Met Tyr Thr Val Val Thr Pro  
 210 215

&lt;210&gt; 2465

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p195-dir-0-8 conceptual translation of range 2-650)

&lt;400&gt;2465

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Leu  
 1 5 10 15  
 Asn Met Gln Ser Gln Ile Pro Ser Ile Ser Tyr Ala Ser Cys Leu Ala  
 20 25 30  
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Ala Leu Glu Asn Phe Leu Leu  
 35 40 45  
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His  
 50 55 60  
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Met Val Val Met  
 65 70 75 80  
 Cys Trp Val Leu Thr Thr Phe Asp Ala Met Leu His Thr Leu Leu Met  
 85 90 95  
 Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys  
 100 105 110  
 Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn  
 115 120 125  
 Glu Val Val Ile Phe Ile Ile Gly Gly Leu Gly Val Val Leu Pro Phe  
 130 135 140  
 Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys  
 145 150 155 160  
 Val Pro Ser Thr Gln Gly Ile Gln Lys Val Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr  
 180 185 190  
 Leu Gly Pro Ser Ala Tyr Tyr Ser Thr Leu Lys Asp Thr Val Met Ser  
 195 200 205  
 Met Met Tyr Thr Val Val Thr Pro  
 210 215

&lt;210&gt; 2466

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (902672-dir-0-6 conceptual translation of range 2-472)

&lt;400&gt;2466

Ile Cys Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys  
 1 5 10 15  
 Val Ser Met Val Val Met Cys Arg Val Leu Thr Thr Phe Asp Ala Met  
 20 25 30  
 Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val  
 35 40 45  
 Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys  
 50 55 60  
 Ser Asp Thr His Val Asn Glu Val Val Ile Phe Ile Ile Gly Gly Leu



```

65          70          75          80
Gly Val Val Leu Pro Phe Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile
      85          90          95
Ile Ser Ser Ile Leu Lys Val Pro Ser Thr Gln Gly Ile Gln Lys Val
      100         105         110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
      115         120         125
Thr Ile Ile Gly Leu Tyr Leu Gly Pro Ser Ala Tyr Tyr Ser Thr Leu
      130         135         140
Lys Asp Thr Val Met Ser Met Met Tyr Thr Val Val Thr
145          150          155

```

&lt;210&gt; 2467

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p196-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2467

```

Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
1      5      10      15
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
      20      25      30
Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu
      35      40      45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50      55      60
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu
65      70      75      80
Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met
      85      90      95
Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys
      100     105     110
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn
      115     120     125
Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe
      130     135     140
Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
145     150     155     160
Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
      165     170     175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
      180     185     190
Leu Cys Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala
      195     200     205
Val Met Tyr Thr Val Val Thr Pro
210          215

```

&lt;210&gt; 2468

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p91-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2468

```

Phe Ser Asp Met Cys Phe Ser Ser Val Ser Ile Pro Lys Leu Leu Val
1      5      10      15
Asn Met Gln Ser Lys Lys Pro Ala Ile Pro Tyr Ala Gly Cys Leu Ser
      20      25      30
Gln Met Tyr Phe Phe Leu Phe Phe Ala Asp Leu Glu Ser Phe Leu Leu
      35      40      45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50          55          60

```

Tyr Ile Val Ile Met Ser Pro Lys Leu Cys Ser Ser Leu Val Val Leu  
 65 70 75 80  
 Ser Trp Val Leu Thr Ala Phe His Ala Leu Leu His Thr Leu Leu Met  
 85 90 95  
 Ser Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys  
 100 105 110  
 Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Gln Pro Asn  
 115 120 125  
 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Val Pro Phe  
 130 135 140  
 Leu Leu Ile Ile Thr Ser Tyr Ala His Ile Ile Ser Ser Ile Leu Arg  
 145 150 155 160  
 Val Pro Ser Val Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr  
 180 185 190  
 Leu Cys Pro Ser Thr Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser  
 195 200 205  
 Ile Met Tyr Thr Val Val Thr Pro  
 210 215

&lt;210&gt; 2469

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (p29-dir-0-11 conceptual translation of range 1-942)

&lt;400&gt;2469

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp  
 85 90 95  
 Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu  
 130 135 140  
 Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr  
 180 185 190  
 Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val  
 195 200 205  
 Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr  
 210 215 220  
 Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Leu Thr Asn His Asn Thr Val Lys Asp Thr  
 260 265 270

Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Thr Leu Gly Arg Val  
 290 295 300  
 Phe Ser Thr Lys Lys Ile Phe Leu Ser Leu  
 305 310

<210> 2470

<211> 314

<212> PRT

<213> Unknown (p132-dir-0-11 conceptual translation of range 1-942)

<400>2470

Met Thr Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Phe Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu  
 35 40 45  
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Cys Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp  
 85 90 95  
 Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser  
 100 105 110  
 Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu Gln Tyr Thr Thr Ile Met Ser Ser Lys Gly Cys Leu Ala Leu  
 130 135 140  
 Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Arg Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Gln Val Asn Gly Trp Val Met Phe Phe Thr Gly Gly Leu Ile Leu Val  
 195 200 205  
 Ile Pro Phe Leu Leu Leu Ile Met Ser Tyr Ala Arg Ile Leu Ser Thr  
 210 215 220  
 Ile Leu Arg Val Pro Cys Ala Gly Gly Ile Gln Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Ser Thr Asn His Asn Thr Val Lys Asp Thr  
 260 265 270  
 Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Asn Pro Gly Gln Ser  
 290 295 300  
 Leu Gln His Lys Glu Asn Phe Phe Val Phe  
 305 310

<210> 2471

<211> 310

<212> PRT

<213> Unknown (205831-dir-0-11 conceptual translation of range 1-930)

<400>2471

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro

```

1           5           10           15
Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
20           25           30
Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
35           40           45
Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
50           55           60
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
65           70           75           80
Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
85           90           95
Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
100          105          110
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
115          120          125
His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
130          135          140
Leu Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu
145          150          155          160
Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
165          170          175
Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
180          185          190
Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
195          200          205
Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
210          215          220
Lys Val Pro Ser Thr Gln Gly Ile Cys Lys Val Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
245          250          255
Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
260          265          270
Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
290          295          300
Ser Met Lys Ile Thr Leu
305          310

```

&lt;210&gt; 2472

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769635-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2472

```

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu
1           5           10           15
Lys Leu Leu Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala
20           25           30
Gly Cys Leu Thr Gln Ile Phe Phe Leu Leu Phe Gly Tyr Leu Gly
35           40           45
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
50           55           60
Phe Pro Leu His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys
65           70           75           80
Leu Leu Leu Val Phe Trp Ile Met Thr Ser Ser His Ala Met Val His
85           90           95
Thr Leu Leu Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu
100          105          110
Asn Phe Phe Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp

```

115	120	125
Thr Tyr Val Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile		
130	135	140
Val Ile Pro Phe Val Leu Ile Val Ile S r Tyr Ala Lys Ile Ile Ser		
145	150	155
Ser Ile Leu Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser		160
165	170	175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile		
180	185	190
Ile Gly Leu Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly		
195	200	205
Ser Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met		
210	215	220

&lt;210&gt; 2473

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769637-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2473

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro		
1	5	10
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala		15
20	25	30
Gly Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Ala Asp Met Glu		
35	40	45
Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys		
50	55	60
Phe Pro Leu His Tyr Thr Thr Ile Met Ser Thr Lys Val Cys Ala Ser		
65	70	75
Leu Leu Ile Leu Leu Trp Met Leu Thr Thr Ser His Ala Leu Leu His		80
85	90	95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu		
100	105	110
His Phe Phe Cys Asp Ile Thr Ala Leu Leu Lys Leu Ser Cys Ser Asp		
115	120	125
Thr Tyr Val Asn Glu Met Met Met His Ile Leu Gly Gly Leu Ile Ser		
130	135	140
Val Ile Pro Phe Leu Phe Ile Val Met Ser Tyr Val Arg Ile Phe Phe		
145	150	155
Ser Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile His Lys Val Phe Ser		160
165	170	175
Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile		
180	185	190
Phe Gly Leu Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu		
195	200	205
Ile Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met		
210	215	220

&lt;210&gt; 2474

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769639-dir-0-8 conceptual translation of range 1-663)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(221)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2474

Gly Asn Phe Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro

1	5	10	15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala			
	20	25	30
Gly Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Ala Asp Met Glu			
	35	40	45
Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys			
	50	55	60
Phe Pro Leu His Tyr Thr Thr Ile Met Ser Thr Lys Val Cys Ala Ser			
	65	70	75
Leu Leu Ile Leu Leu Xaa Met Leu Thr Thr Ser His Ala Pro Leu His			
	85	90	95
Thr Leu Leu Met Ala Arg Leu Pro Phe Tyr Glu Lys Asn Val Ile Leu			
	100	105	110
His Phe Phe Cys Asp Val Thr Ala Leu Leu Lys Leu Ser Cys Ser Asp			
	115	120	125
Thr Tyr Val Asn Glu Met Met Met Tyr Ile Leu Gly Gly Leu Ile Ser			
	130	135	140
Val Ile Pro Phe Leu Phe Ile Val Met Ser Tyr Val Arg Ile Phe Phe			
	145	150	155
Ser Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile His Lys Val Phe Ser			
	165	170	175
Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile			
	180	185	190
Phe Gly Leu Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu			
	195	200	205
Ile Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met			
	210	215	220

&lt;210&gt; 2475

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (205843-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2475

Met Thr Gly Asn Asn Gln Thr Leu Ile Leu Glu Phe Leu Leu Leu Gly			
1	5	10	15
Leu Pro Ile Pro Ser Glu Tyr His Leu Leu Phe Tyr Ala Leu Phe Leu			
	20	25	30
Ala Met Tyr Leu Thr Ile Ile Leu Gly Asn Leu Leu Ile Ile Val Leu			
	35	40	45
Val Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Phe Leu Ser			
	50	55	60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys			
	65	70	75
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Thr Gly			
	85	90	95
Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser			
	100	105	110
Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe			
	115	120	125
Pro Leu Arg Tyr Thr Thr Ile Met Ser Thr Lys Phe Cys Ala Ser Leu			
	130	135	140
Val Leu Leu Leu Trp Met Leu Thr Met Thr His Ala Leu Leu His Thr			
	145	150	155
Leu Leu Ile Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His			
	165	170	175
Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile			
	180	185	190
Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu Ile Ile Ile			
	195	200	205
Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser			

210	215	220
Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Phe		240
	245	250
Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu Ile		255
	260	265
Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val		285
	290	295
Ile Cys Thr Lys Lys Ile Ser Leu		300
305	310	

&lt;210&gt; 2476

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p198-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2476

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln		
1	5	10
Asn Met Gln Ser Gln Val Pro Thr Ile Ser Tyr Ala Asp Cys Leu Thr		15
	20	25
Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu		30
	35	40
Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His		45
	50	55
Tyr Thr Ser Ile Met Ser Thr Lys Phe Cys Ala Leu Leu Val Leu Leu		60
	65	70
Leu Trp Met Leu Thr Ile Ser His Ala Leu Leu His Thr Leu Leu Met		75
	85	90
Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His Phe Phe Cys		95
	100	105
Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Tyr Val Asn		110
	115	120
Glu Leu Met Ile Phe Ile Met Gly Gly Ile Ile Ser Ile Ile Pro Phe		125
	130	135
Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys		140
	145	150
Val Pro Ser Ser Gln Asp Ile His Lys Val Phe Ser Thr Cys Gly Ser		155
	165	170
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr		175
	180	185
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Asn Glu Ile Ser Met Ala		190
	195	200
Met Met Tyr Thr Val Val Thr Pro		205
210	215	

&lt;210&gt; 2477

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Unknown (3810822-dir-0-8 conceptual translation of range 1-708)

&lt;400&gt;2477

Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Ser Asp Leu Cys Phe		
1	5	10
Ser Ser Val Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp		15
	20	25
Thr Ser Ile Thr Tyr Val Gly Cys Leu Thr Gln Ser Val Leu Phe Leu		30
	35	40
		45

```

Ile Phe Phe Gly Gly Leu Glu Ile Phe Leu Leu Val Val Met Ala Tyr
  50          55          60
Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His Tyr Ser Ser Ile Met
65          70          75          80
Ser Leu Lys Phe Cys Val Cys Ala Val Leu Ile Ser Trp Ile Asn Ser
          85          90          95
Pro Trp Tyr Ser Lys Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe
          100          105          110
Cys Glu Asp Asn Ile Ile Cys His Phe Phe Cys Asp Met Ser Ala Leu
          115          120          125
Leu Lys Leu Ala Cys Ser Asp Ile Tyr Ile Asn Glu Leu Val Ile Phe
          130          135          140
Ile Leu Gly Gly Pro Leu Val Val Ile Pro Phe Leu Leu Ile Val Val
145          150          155          160
Ser Tyr Val Gln Ile Ile Phe Ser Ile Leu Lys Ala Ser Ser Thr Arg
          165          170          175
Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Thr Tyr Leu Thr Val Val
          180          185          190
Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Glu
          195          200          205
Lys Leu Tyr Ser Lys Glu Ala Ser Ile Thr Met Met Tyr Thr Val Val
          210          215          220
Thr Pro Met His Pro Phe Ile Tyr Thr Leu Arg Asn
225          230          235

```

&lt;210&gt; 2478

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (OST044-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2478

```

Leu Ala Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
  1          5          10          15
Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys Ile Ser
          20          25          30
Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe Leu Ile
          35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val Ala Val
65          70          75          80
Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu Leu Leu
          85          90          95
Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val Phe Cys
          100          105          110
Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe Leu Asn
          115          120          125
Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu Pro Phe
          130          135          140
Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg
145          150          155          160
Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys Gly Ser
          165          170          175
His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly Gln Tyr
          180          185          190
Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile Val Ala
          195          200          205
Leu Met Tyr Thr Val Val Thr Pro
          210          215

```

&lt;210&gt; 2479



&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg152-dir-0-8 conceptual translation of range 1-648)

&lt;400&gt;2479

```

Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
 1          5          10          15
Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys Ile Ser
          20          25          30
Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe Leu Ile
          35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Val Val Met Arg Glu Glu Leu Cys Val Phe Leu Val Ala Val
          65          70          75          80
Ser Trp Ile Leu Ser Cys Asp Ser Ser Leu Ser His Thr Leu Leu Leu
          85          90          95
Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val Phe Cys
          100          105          110
Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe Leu Asn
          115          120          125
Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu Pro Phe
          130          135          140
Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg
          145          150          155          160
Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys Gly Ser
          165          170          175
His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly Gln Tyr
          180          185          190
Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile Val Ala
          195          200          205
Leu Met Tyr Thr Val Val Thr Pro
          210          215

```

&lt;210&gt; 2480

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Unknown (1142973-dir-0-5 conceptual translation of range 1-336)

&lt;400&gt;2480

```

His Pro Leu His Tyr Ile Thr Ile Met Ser Gln Ser Arg Cys Ala Met
 1          5          10          15
Leu Val Ala Val Ser Trp Val Ile Ala Ser Ala Cys Ala Leu Leu His
          20          25          30
Ser Leu Leu Leu Asp Gln Leu Ser Phe Cys Ala Asp His Thr Val Pro
          35          40          45
His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp
          50          55          60
Thr Ser Leu Asn Gln Leu Val Ile Phe Thr Ala Gly Leu Ala Ala Ile
          65          70          75          80
Met Leu Pro Phe Leu Cys Ile Leu Ile Ser Tyr Gly Arg Ile Gly Phe
          85          90          95
Thr Ile Leu Gln Val Pro Thr Thr Lys Gly Ile Cys Lys Ala Leu Ser
          100          105          110

```

&lt;210&gt; 2481

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg32-dir-0-8 conceptual translation of range 1-648)

&lt;400&gt;2481

```

Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
 1          5          10          15
Asn Met Gln Thr Gln His Leu Ala Val Phe Tyr Lys Gly Cys Ile Ser
      20          25          30
Gln Thr Tyr Phe Phe Ile Phe Phe Ala Asp Leu Asp Ser Phe Leu Ile
      35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50          55          60
Tyr Ala Thr Ile Met Thr Gln Ser Gln Cys Val Met Leu Val Ala Gly
      65          70          75          80
Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu Asp Thr Leu Leu Leu
      85          90          95
Ala Gln Leu Ser Phe Cys Ala Asp His Ile Ile Pro His Tyr Phe Cys
      100          105          110
Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn
      115          120          125
Gln Leu Ala Ile Phe Thr Ala Ala Leu Thr Ala Ile Met Leu Pro Phe
      130          135          140
Leu Cys Ile Leu Val Ser Tyr Gly His Ile Gly Val Thr Ile Leu Gln
      145          150          155          160
Ile Pro Ser Thr Lys Gly Ile Cys Lys Ala Leu Ser Thr Cys Gly Ser
      165          170          175
His Leu Ser Val Val Thr Ile Tyr Tyr Arg Thr Ile Ile Gly Leu Tyr
      180          185          190
Phe Leu Pro Pro Ser Ser Asn Thr Asn Asp Lys Asn Ile Ile Ala Ser
      195          200          205
Val Ile Tyr Thr Ala Val Thr Pro
      210          215

```

&lt;210&gt; 2482

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Unknown (3983375-dir-0-8 conceptual translation of range 1-669)

&lt;400&gt;2482

```

Ser His Leu Ala Phe Thr Asp Ile Ser Phe Ser Ser Val Thr Ala Pro
 1          5          10          15
Lys Met Leu Met Asn Met Leu Thr His Ser Gln Ser Ile Ser His Ala
      20          25          30
Gly Cys Val Ser Gln Ile Tyr Phe Phe Leu Leu Phe Gly Cys Ile Asp
      35          40          45
Asn Phe Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      50          55          60
His Pro Leu His Tyr Thr Thr Ile Met Ser Gln Ser Leu Cys Val Leu
      65          70          75          80
Leu Val Met Val Ser Trp Ala Phe Ser Ser Ser Asn Gly Leu Val His
      85          90          95
Thr Leu Leu Phe Ala Arg Leu Ser Leu Phe Arg Asp Asn Thr Val His
      100          105          110
His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ser Ser Ser Asp
      115          120          125
Thr Thr Ile Asn Glu Leu Val Ile Leu Thr Leu Ala Val Val Val Ile
      130          135          140
Thr Val Pro Phe Ile Cys Ile Leu Val Ser Tyr Gly His Met Gly Ala
      145          150          155          160
Thr Ile Leu Arg Thr Pro Ser Ile Lys Gly Ile Cys Lys Ala Leu Ser
      165          170          175
Thr Cys Gly Ser His Leu Cys Val Val Ser Leu Tyr Tyr Gly Ala Ile
      180          185          190
Ile Gly Leu Tyr Phe Phe Pro Ser Ser Asn Asn Thr Asn Asp Lys Asp
      195          200          205

```

Val Ile Val Ala Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn  
 210 215 220

<210> 2483

<211> 176

<212> PRT

<213> Unknown (3273636-dir-0-7 conceptual translation of range 4-531)

<400>2483

Gln Ala Leu Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro Leu His  
 1 5 10 15  
 Tyr Arg Thr Ile Met Arg Asp Gly Phe Cys Val Leu Leu Val Val Gly  
 20 25 30  
 Ser Trp Phe Phe Ser Cys Val His Ala Leu Leu His Thr Leu Leu Leu  
 35 40 45  
 Ser Arg Leu Ser Phe Cys Ala Asp Asn Ala Ile Pro His Phe Phe Cys  
 50 55 60  
 Asp Phe Thr Ala Val Leu Lys Met Thr Cys Ser Asp Thr Ser Ile Asn  
 65 70 75 80  
 Glu Leu Val Ile Phe Ile Glu Gly Gly Leu Leu Thr Ser Leu Pro Leu  
 85 90 95  
 Ser Ala Ile Leu Gly Ser Tyr Val Arg Ile Gly Ala Ser Ile Leu Arg  
 100 105 110  
 Val Pro Ser Met Lys Arg Ile Cys Lys Ala Leu Ser Thr Cys Gly Ser  
 115 120 125  
 His Leu Phe Val Val Phe Leu Tyr Tyr Gly Thr Ile Ala Met Thr Tyr  
 130 135 140  
 Phe Phe Pro Ser Ser Tyr Asn Ser Lys Val Lys Gly Ile Ile Ala Ser  
 145 150 155 160  
 Val Ile Tyr Thr Val Val Ala Pro Met Leu Asn Pro Phe Ile Cys Ser  
 165 170 175

<210> 2484

<211> 222

<212> PRT

<213> Unknown (4877296-dir-0-8 conceptual translation of range 2-667)

<400>2484

Ser His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Leu Pro  
 1 5 10 15  
 Lys Met Leu Met Asn Met Gln Thr Arg Cys Gln Ala Ile Thr Tyr Ala  
 20 25 30  
 Gly Cys Ile Ser Gln Val Tyr Cys Phe Ile Phe Phe Gly Cys Leu Asp  
 35 40 45  
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys  
 50 55 60  
 His Pro Leu His Tyr Thr Ala Ile Met Arg Asp Glu Leu Cys Val Ile  
 65 70 75 80  
 Leu Val Ala Gly Arg Trp Leu Ala Ala Cys Ala Gln Ala Leu Leu His  
 85 90 95  
 Thr Leu Leu Val Asp Gln Leu Thr Leu Cys Ala Gly Thr Val Ile Pro  
 100 105 110  
 His Phe Phe Cys Asp Leu Ala Val Val Leu Lys Ser Ser Cys Ser Asp  
 115 120 125  
 Thr Ser Leu Asn Glu Leu Leu Ile Leu Thr Glu Gly Gly Leu Ile Phe  
 130 135 140  
 Thr Leu Pro Leu Gly Gly Ile Leu Gly Ser Tyr Ile Arg Met Ala Ala  
 145 150 155 160  
 Ile Ile Leu Lys Val Pro Ser Phe Thr Arg Ile Phe Lys Ala Leu Ser  
 165 170 175  
 Thr Cys Gly Ser His Leu Phe Val Val Phe Leu Tyr Tyr Gly Thr Ile

```
<210> 2485
<211> 173
<212> PRT
<213> Unknown (3273660-dir-0-7 conceptual translation of range 1-519)
```

```
<210> 2486
<211> 135
<212> PRT
<213> Unknown (3273658-dir-0-6 conceptual translation of range 1-405)
```

**<210> 2487**

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Unknown (3273646-dir-0-7 conceptual translation of range 1-528)

&lt;400&gt;2487

Gln Ala Leu Ala Tyr Asp Arg Phe Leu Ala Val Cys His Pro Leu His  
 1 5 10 15  
 Tyr Ala Ile Phe Met Arg Glu Arg Leu Cys Ile Phe Leu Leu Ala Gly  
 20 25 30  
 Ser Trp Leu Leu Ser Gly Ala Ser Ala Leu Thr His Thr Leu Leu Val  
 35 40 45  
 Val Gln Leu Ser Phe Cys Ala Asp Asn Ile Ile Leu His Phe Phe Cys  
 50 55 60  
 Asp Leu Val Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn  
 65 70 75 80  
 Glu Leu Val Ile Phe Thr Val Gly Ser Val Gly Leu Val Phe Pro Leu  
 85 90 95  
 Ser Gly Ile Leu Val Ser Tyr Gly Arg Ile Gly Leu Ser Ile Leu Arg  
 100 105 110  
 Val Pro Ser Thr Lys Gly Val Cys Lys Ala Leu Ser Thr Cys Gly Ser  
 115 120 125  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Met Ala Val Tyr  
 130 135 140  
 Phe Ser Ser Ser Ser Gly Gln Ser His Glu Lys Asp Ile Ile Ala Ser  
 145 150 155 160  
 Met Met Tyr Thr Val Val Thr Pro Met Val Asn Pro Val Ile Cys Ser  
 165 170 175

&lt;210&gt; 2488

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (205815-dir-0-11 conceptual translation of range 1-939)

&lt;400&gt;2488

Met Ser Ser Thr Asn Gln Ser Ser Val Thr Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Ser Arg Gln Pro Gln Gln Gln Gln Leu Leu Phe Leu Leu Phe Leu  
 20 25 30  
 Ile Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Leu Ala  
 35 40 45  
 Ile Gly Thr Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Val Leu Ala Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly  
 85 90 95  
 Cys Leu Thr Gln Leu Tyr Phe Leu Ala Val Phe Gly Asn Met Asp Asn  
 100 105 110  
 Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu  
 130 135 140  
 Val Val Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr  
 180 185 190  
 His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val  
 195 200 205  
 Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala

210	215	220
Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile		240
	245	250
Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met		255
	260	265
Ala Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu Arg Lys Val		285
	290	300
Leu Ala Met Arg Phe Pro Ser Lys Gln		
305	310	

&lt;210&gt; 2489

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg91-dir-0-8 conceptual translation of range 1-648)

&lt;400&gt;2489

Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala		
1	5	10
Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr		15
	20	25
Gln Leu Tyr Phe Leu Ala Val Cys Gly Asn Met Asp Asn Phe Leu Leu		30
	35	40
Gly Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His		45
	50	55
Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu Val Val Gly		60
	65	70
Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile Leu Leu Met		75
	85	90
Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His Phe Phe Cys		95
	100	105
Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn		110
	115	120
Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val Thr Pro Phe		125
	130	135
Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val Leu Arg		140
	145	150
Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr Cys Gly Ser		155
	165	170
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr		175
	180	185
Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met Ala Ala Ala		190
	195	200
Val Met Tyr Pro Val Val Thr Pro		205
210	215	

&lt;210&gt; 2490

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (902718-dir-0-6 conceptual translation of range 2-472)

&lt;400&gt;2490

Ile Cys His Pro Leu Gln Tyr Thr Thr Lys Met Thr His Gln Leu Cys		
1	5	10
Ala Leu Leu Val Val Gly Ser Trp Val Val Ala Asn Leu Asn Cys Leu		15
	20	25
Leu His Ile Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ile		30
	35	40
		45

Ile Pro His Phe Phe Cys Asp Ala Thr Pro Leu Leu Lys Leu Ser Cys  
 50 55 60  
 Ser Asp Thr His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val  
 65 70 75 80  
 Ile Ile Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Val  
 85 90 95  
 Thr Cys Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ala  
 100 105 110  
 Phe Ser Thr Arg Gly Ser His Pro Ala Val Val Cys Leu Phe Tyr Gly  
 115 120 125  
 Thr Ile Ile Ala Glu Tyr Phe Ser Ser Ser Ser Pro His Ser Ala Gly  
 130 135 140  
 Arg Asp Met Ala Gly Ala Met Met Tyr Thr Val Val Thr  
 145 150 155

&lt;210&gt; 2491

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769625-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2491

Ser Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Ala Pro  
 1 5 10 15  
 Ser Val Leu Ala Asn His Ile Leu Gly Ser Gln Lys Ile Ser Phe Ser  
 20 25 30  
 Gly Cys Leu Thr Gln Leu Tyr Phe Leu Cys Ile Phe Gly Asp Met Asp  
 35 40 45  
 Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
 50 55 60  
 His Pro Leu Arg Tyr Thr Thr Lys Met Thr His Gln Val Cys Ala Leu  
 65 70 75 80  
 Leu Val Met Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His  
 85 90 95  
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Ser Ile Ile Pro  
 100 105 110  
 His Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp  
 115 120 125  
 Thr His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met  
 130 135 140  
 Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Trp  
 145 150 155 160  
 Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ala Phe Ser  
 165 170 175  
 Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Leu Tyr Gly Thr Val  
 180 185 190  
 Ile Thr Val Tyr Phe Asn Pro Ser Thr Ser Tyr Ser Ala Gly Arg Asp  
 195 200 205  
 Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Met  
 210 215 220

&lt;210&gt; 2492

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Unknown (3769644-dir-0-8 conceptual translation of range 1-663)

&lt;400&gt;2492

Thr Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Ser Thr Val Pro  
 1 5 10 15  
 Lys Val Leu Ala Asn His Ile Leu Gly Ser Gln Glu Ile Ser Phe Ser  
 20 25 30  
 Gly Cys Leu Thr Gln Met Tyr Phe Leu Ser Val Phe Ala Asp Met Asp

35	40	45
Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys		
50	55	60
His Pro Leu His Tyr Thr Glu Lys Met Thr Arg Gln Leu Cys Ala Leu		
65	70	75
Leu Val Val Glu Ser Trp Val Ala Ala Asn Leu Asn Ala Leu Leu His		
85	90	95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Gly Asp Asn Ile Ile Pro		
100	105	110
His Phe Phe Cys Asp Ala Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp		
115	120	125
Thr His Leu Asn Glu Leu Met Ile Leu Thr Val Ala Gly Leu Ile Leu		
130	135	140
Leu Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Ile Leu Ile Ala Cys		
145	150	155
Ala Val Val Arg Val Ser Ser Thr Gly Gly Arg Trp Lys Ala Phe Ser		
165	170	175
Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile		
180	185	190
Ile Ala Val Tyr Phe Asn Pro Ala Ser Ser His Ser Ala Gly Arg Asp		
195	200	205
Met Ala Ser Ala Met Met Tyr Thr Val Val Thr Pro Met		
210	215	220

&lt;210&gt; 2493

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown (2808536-dir-0-11 conceptual translation of range 16-996)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(327)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2493

Val Cys Phe Xaa Ile His Cys Leu Leu Cys Ser Trp Val Gln Thr Tyr	
1	5
Glu Arg Asp Lys Pro Val Ser Val Ser Glu Phe Leu Leu Gly Leu	10
20	25
Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu Ser	30
35	40
Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile	45
50	55
Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn	60
65	70
Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu	75
85	90
Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu	95
100	105
Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu	110
115	120
Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu	125
130	135
His Tyr Thr Ala Lys Met Ile His Gln Leu Cys Ala Leu Leu Val Thr	140
145	150
Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu His Thr Leu Leu	155
165	170
Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe	175
180	185
Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu	190
195	200
	205



Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro  
 210 215 220  
 Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu  
 225 230 235 240  
 Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly  
 245 250 255  
 Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro  
 260 265 270  
 Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala  
 275 280 285  
 Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr  
 290 295 300  
 Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala  
 305 310 315 320  
 Val Lys Phe Phe Ser Val Gln  
 325

&lt;210&gt; 2494

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (2370144-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2494

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser  
 35 40 45  
 Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His  
 115 120 125  
 Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu  
 130 135 140  
 Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His  
 165 170 175  
 Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asn Thr  
 180 185 190  
 His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile  
 195 200 205  
 Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr  
 210 215 220  
 Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile  
 245 250 255  
 Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr  
 260 265 270  
 Met Ala Thr Val Leu Tyr Thr Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val  
 290 295 300

Ile Gly Arg Val Val Phe Ser Val  
305 310

<210> 2495

<211> 216

<212> PRT

<213> Unknown (2921659-dir-0-8 conceptual translation of range 2-649)

<400>2495

Phe	Val	Asp	Ile	Cys	Phe	Ser	Phe	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1			5					10						15	
Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Asn	Phe	Leu	Leu
	35					40					45				
Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His
	50				55						60				
Tyr	Thr	Ala	Lys	Val	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly
65					70				75					80	
Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	Leu	Leu	Met
			85					90					95		
Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	Phe	Phe	Cys
		100					105					110			
Asp	Val	Thr	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Leu	Asn
	115					120					125				
Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	Thr	Pro	Phe
	130					135					140				
Leu	Cys	Ile	Leu	Ala	Ser	Tyr	Met	His	Ile	Thr	Cys	Thr	Val	Leu	Lys
145					150				155					160	
Val	Pro	Ser	Thr	Lys	Gly	Arg	Trp	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser
			165					170					175		
His	Leu	Ala	Val	Val	Leu	Leu	Phe	Tyr	Ser	Thr	Ile	Ile	Ala	Val	Tyr
		180					185					190			
Phe	Asn	Pro	Leu	Ser	Ser	His	Ser	Ala	Glu	Lys	Asp	Thr	Met	Ala	Thr
	195					200						205			
Val	Leu	Tyr	Thr	Val	Val	Thr	Pro								
	210					215									

<210> 2496

<211> 216

<212> PRT

<213> Unknown (2921657-dir-0-8 conceptual translation of range 2-649)

<400>2496

Phe	Val	Asp	Ile	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1			5					10						15	
Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Tyr	Phe	Leu	Leu
	35					40					45				
Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His
	50				55						60				
Tyr	Thr	Ala	Lys	Met	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly
65					70				75					80	
Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	Leu	Leu	Met
			85					90					95		
Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	Phe	Phe	Cys
		100					105					110			
Asp	Val	Thr	Pro	Leu	Leu	Glu	Leu	Ser	Cys	Ser	Asp	Thr	His	Leu	Asn
	115					120					125				
Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	Thr	Pro	Phe

130	135	140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys		
145	150	155
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser		160
	165	170
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr		175
	180	185
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr		190
	195	200
Val Leu Tyr Thr Val Val Thr Pro		205
210	215	

&lt;210&gt; 2497

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921653-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2497

Phe Val Asp Ile Cys Phe Ser Ser Thr Thr Val Pro Lys Met Leu Ala		
1	5	10
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Leu Cys Gly Cys Leu Thr		15
	20	25
Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn Phe Leu Leu		30
	35	40
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His		45
	50	55
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly		60
65	70	75
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met		80
	85	90
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys		95
	100	105
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn		110
	115	120
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe		125
	130	135
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys		140
145	150	155
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser		160
	165	170
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr		175
	180	185
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Pro Thr		190
	195	200
Val Leu Tyr Thr Val Val Thr Pro		205
210	215	

&lt;210&gt; 2498

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921655-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2498

Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys Met Leu Ala		
1	5	10
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr		15
	20	25
Gln Met Tyr Phe Val Phe Thr Phe Val Asp Met Asp Asn Phe Leu Leu		30
	35	40
Ala Val Met Ala Tyr Asp His Phe Val Ala Glu Cys His Pro Leu His		45
	50	55
		60

```

Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65          70          75          80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
          85          90          95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
          100        105        110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115        120        125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
          130        135        140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
          145        150        155        160
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
          165        170        175
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
          180        185        190
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr
          195        200        205
Val Leu Tyr Thr Val Val Thr Pro
          210        215

```

&lt;210&gt; 2499

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921651-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2499

```

Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys Met Leu Ala
1          5          10          15
Asp His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
          20          25          30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn Phe Leu Leu
          35          40          45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
          50          55          60
Tyr Thr Ala Arg Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65          70          75          80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
          85          90          95
Ala Pro Leu Ser Phe Tyr Ala Asp Asn Ala Ile Thr His Phe Phe Cys
          100        105        110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115        120        125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
          130        135        140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
          145        150        155        160
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
          165        170        175
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
          180        185        190
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Ile Ala Thr
          195        200        205
Val Leu Tyr Thr Val Val Thr Pro
          210        215

```

&lt;210&gt; 2500

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921692-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2500

```

Phe Val Asp Ile Cys Phe Ser Cys Thr Thr Val Pro Lys Met Leu Ala
 1           5           10           15
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
           20           25           30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Thr Asp Asn Phe Leu Leu
           35           40           45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
           50           55           60
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
           65           70           75           80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
           85           90           95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
           100           105           110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
           115           120           125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
           130           135           140
Leu Cys Asn Leu Ala Ser Tyr Met His Ile Thr Cys Thr Gly Leu Lys
           145           150           155           160
Gly Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
           165           170           175
His Leu Ala Val Gly Leu Leu Phe Tyr Ser Thr Ile Thr Ala Val Tyr
           180           185           190
Phe Asn Pro Leu Ser Ser His Ser Ala Ala Lys Asp Thr Met Ala Thr
           195           200           205
Val Leu Tyr Thr Val Val Thr Pro
           210           215

```

&lt;210&gt; 2501

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Unknown (4877342-dir-0-8 conceptual translation of range 2-673)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(224)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2501

```

Cys Asn Leu Ser Phe Gly Asp Ile Cys Phe Ser Ser Thr Thr Val Pro
 1           5           10           15
Lys Met Leu Ala Asn His Ile Leu Arg Lys Gln Thr Ile Pro Phe Ser
           20           25           30
Arg Cys Leu Ala Gln Met Tyr Phe Val Phe Thr Phe Met Asp Met Asp
           35           40           45
Asn Phe Leu Leu Ala Met Met Ala Tyr Asp His Phe Val Ala Val Cys
           50           55           60
His Pro Leu His Tyr Tyr Ala Lys Met Thr His Gln Leu Cys Ala Leu
           65           70           75           80
Leu Val Thr Gly Ser Trp Val Ile Ala Asn Leu Asp Met Leu Leu His
           85           90           95
Thr Leu Leu Met Ala Xaa Leu Ser Phe Cys Ala Asp Asn Ala Ile Pro
           100           105           110
His Phe Phe Cys Asp Val Thr Thr Leu Leu Lys Leu Ser Cys Ser Asp
           115           120           125
Thr His Leu Ser Glu Val Met Ile Leu Thr Glu Ala Arg Pro Val Met
           130           135           140
Ser Thr Pro Phe Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Asn Cys
           145           150           155           160

```

Ala Val Leu Arg Val Gln Ser Thr Lys Gly Arg Trp Lys Thr Phe Ser  
                                   165                                  170                                  175  
 Thr Cys Gly Ser His Leu Ala Met Val Phe Leu Phe Tyr Gly Thr Met  
                                   180                                  185                                  190  
 Ile Phe Leu Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Ile Asp  
                                   195                                  200                                  205  
 Ile Ala Ala Ala Ala Met Arg Cys Leu Tyr Met Val Thr Pro Met Leu  
                                   210                                  215                                  220

&lt;210&gt; 2502

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p105-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2502

Leu Val Asp Phe Cys Phe Thr Ser Ala Thr Val Pro Lys Met Leu Leu  
   1                                  5                                  10                                  15  
 Asn Ile His Arg Gln Ile Gln Ser Ile Ser His Glu Gly Cys Leu Thr  
                                   20                                  25                                  30  
 Gln Ile Tyr Phe Cys Ile Leu Leu Ala Asn Met Asp Asn Phe Leu Leu  
                                   35                                  40                                  45  
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Gln  
                                   50                                  55                                  60  
 Tyr Thr Thr Ile Met Ser Leu Gln Leu Cys Cys Leu Met Leu Ala Gly  
   65                                  70                                  75                                  80  
 Ser Trp Leu Ile Ala Asn Phe His Ser Leu Leu His Thr Leu Leu Met  
                                   85                                  90                                  95  
 Ala Arg Leu Asp Phe Cys Ala Lys Asn Val Met Pro Tyr Phe Phe Cys  
                                   100                                  105                                  110  
 Asp Leu Val Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Asn  
                                   115                                  120                                  125  
 Gln Leu Met Ile Leu Leu Val Gly Gly Leu Ile Val Leu Ile Pro Phe  
                                   130                                  135                                  140  
 Leu Cys Ile Leu Ile Ser Tyr Thr His Ile Val Ser Val Val Leu Lys  
   145                                  150                                  155                                  160  
 Val Pro Ser Ala Leu Gly Lys Gln Lys Ala Phe Ser Thr Cys Gly Ser  
                                   165                                  170                                  175  
 His Leu Thr Val Val Ile Leu Phe Tyr Gly Thr Ile Thr Gly Val Tyr  
                                   180                                  185                                  190  
 Leu Asn Pro Ser Ser Ser His Ser Ala Glu Lys Asp Ser Val Ala Ser  
                                   195                                  200                                  205  
 Val Met Tyr Met Val Val Thr Pro  
                                   210                                  215

&lt;210&gt; 2503

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p110-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2503

Phe Val Asp Leu Cys Gln Ala Ser Thr Thr Met Pro Lys Met Leu Ile  
   1                                  5                                  10                                  15  
 Asn Ile Leu Thr His Ser Lys Ala Ile Pro Tyr Ala Gly Cys Leu Ile  
                                   20                                  25                                  30  
 Gln Met Tyr Ser Phe His Leu Phe Gly Thr Met Asp Ser Phe Leu Leu  
                                   35                                  40                                  45  
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg  
                                   50                                  55                                  60  
 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Ile Leu Leu Val Gly Gly  
   65                                  70                                  75                                  80  
 Pro Trp Gly Thr Thr Asn Leu Gln Ser Val Val His Thr Ser Leu Met

85								90					95			
Ala	Lys	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Lys	Ile	Pro	His	Phe	Phe	Cys	
100								105					110			
Asp	Leu	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Ile	Asn	
115								120					125			
Glu	Leu	Val	Val	Leu	Val	Phe	Gly	Ile	Phe	Met	Gly	Ile	Ser	Pro	Leu	
130								135					140			
Val	Cys	Ile	Leu	Leu	Ser	Tyr	Ile	Cys	Ile	Phe	Cys	Ala	Val	Leu	Gln	
145								150					155			
Val	Pro	Ser	Ala	Glu	Gly	Lys	Arg	Lys	Ala	Phe	Ser	Thr	Arg	Gly	Ser	
165								170					175			
His	Leu	Thr	Val	Val	Leu	Leu	Phe	Tyr	Gly	Thr	Ile	Phe	Ala	Val	Tyr	
180								185					190			
Leu	Gln	Pro	Ser	Gly	Pro	Thr	Ser	Pro	Glu	Lys	Asp	Lys	Ala	Ala	Ala	
195								200					205			
Val	Met	Cys	Ala	Val	Val	Ile	Pro									
210								215								

<210> 2504

**<211> 216**

<212> PRT

<213> Unknown (p94-dir-0-8 conceptual translation of range 2-649)

<400>2504

Phe 1	Val	Asp	Leu	Cys 5	Gln	Ala	Ser	Thr	Thr 10	Met	Pro	Lys	Met	Leu 15	Ile
Asn	Ile	Leu	Thr	His	Ser	Lys	Ala	Ile 25	Pro	Tyr	Ala	Gly	Cys 30	Leu	Ile
Gln	Met	Tyr 35	Ser	Phe	His	Leu	Phe 40	Gly	Thr	Met	Asp	Ser	Phe 45	Leu	Leu
Ala	Val 50	Met	Ala	Tyr	Asp	Arg 55	Phe	Val	Ala	Ile	Phe 60	His	Pro	Leu	Arg
Tyr 65	Ala	Thr	Ile	Met	Ser	Pro 70	Arg	Leu	Cys	Ile 75	Leu	Leu	Val	Gly 80	Gly
Pro	Trp	Gly	Thr	Thr 85	Asn	Leu	Gln	Ser	Val 90	Val	His	Thr	Ser	Leu 95	Met
Ala	Lys	Leu	Thr 100	Phe	Cys	Ala	Asp	Asn 105	Lys	Ile	Pro	His	Phe 110	Phe	Cys
Asp	Leu	Met 115	Pro	Leu	Leu	Lys 120	Leu	Ser	Cys	Ser	Asp	Thr 125	His	Ile	Asn
Glu 130	Leu	Val	Val	Leu	Val	Phe 135	Gly	Ile	Phe	Met	Gly 140	Ile	Ser	Pro	Leu
Val 145	Cys	Ile	Leu	Leu	Ser 150	Tyr	Ile	Cys	Ile	Phe 155	Cys	Ala	Val	Leu	Gln 160
Val	Pro	Ser	Ala	Glu 165	Gly	Lys	Arg	Lys	Ala 170	Phe	Ser	Thr	Cys 175	Gly	Ser
His	Leu	Thr 180	Val	Val	Leu	Val	Phe 185	Tyr	Gly	Thr	Ile 190	Phe	Ala 195	Val	Tyr
Val	Gln 195	Pro	Ser	Gly	Pro	Thr 200	Ser	Pro	Glu	Lys	Asp 205	Lys	Ala	Ala	Ala
Val	Met 210	Cys	Ala	Val	Val	Ile 215	Pro								

**<210> 2505**

**<211> 169**

<212> PRT

<213> Unknown (4877330-dir-0-7 conceptual translation of range 3-509)

**<400>2505**

Asn Leu Ser Leu Val Asp Val Phe Leu Ser Ser Thr Thr Val Pro Lys  
1 5 10 15

Met Leu Val Asn Leu Trp Thr Gln Pro Ser His Pro Ser Val Cys Leu  
                   20                  25                  30  
 Ala Gln Met His Ala Phe His Leu Phe Gly Thr Ile Asp Ser Phe Leu  
                   35                  40                  45  
 Leu Ala Val Met Ala Ile Asp Arg Phe Met Ala Ile Val His Arg Leu  
                   50                  55                  60  
 Cys Tyr Leu Ala Ile Met Ser Pro Arg Val Trp Gly Leu Leu Val Gly  
 65                  70                  75                  80  
 Glu Pro Trp Gln Ile Thr Asn Leu Gln Ser Leu Val His Thr Cys Leu  
                   85                  90                  95  
 Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Pro His Phe Phe  
                   100                  105                  110  
 Cys Asp Leu Ile Pro Leu Pro Lys Leu Ser Ser Ser Asp Thr His Thr  
                   115                  120                  125  
 Asn Glu Pro Val Ile Phe Pro Phe Gly Ile Ile Leu Gly Ile Ser Ser  
                   130                  135                  140  
 Leu Ala Cys Ile Leu Phe Ser Tyr Thr Ser Ile Phe Gln Ala Val Phe  
 145                  150                  155                  160  
 Lys Ile Leu Ser Ala Gln Val Lys Trp  
                   165

&lt;210&gt; 2506

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (3184261-dir-59-13 conceptual translation of range 6034-6978)

&lt;400&gt;2506

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly  
 1                  5                  10                  15  
 Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu  
                   20                  25                  30  
 Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala  
                   35                  40                  45  
 Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe  
                   50                  55                  60  
 Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys  
 65                  70                  75                  80  
 Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly  
                   85                  90                  95  
 Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser  
                   100                  105                  110  
 Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His  
                   115                  120                  125  
 Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu  
                   130                  135                  140  
 Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr  
 145                  150                  155                  160  
 Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His  
                   165                  170                  175  
 Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr  
                   180                  185                  190  
 His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr  
                   195                  200                  205  
 Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr  
                   210                  215                  220  
 Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr  
 225                  230                  235                  240  
 Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe  
                   245                  250                  255  
 Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys  
                   260                  265                  270



Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe  
           275                          280                          285  
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu  
           290                          295                          300  
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro  
 305                          310                          315

<210> 2507

<211> 216

<212> PRT

<213> Unknown (p97-dir-0-8 conceptual translation of range 2-649)

<400>2507

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Ala  
   1                          5                          10                          15  
 Asn His Val Ser Gly Asn Lys Ala Ile Pro Tyr Ala Gly Cys Arg Thr  
           20                          25                          30  
 Gln Val Phe Phe Phe Ile Trp Phe Pro Gly Val Asp Ser Ile Leu Leu  
           35                          40                          45  
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His  
           50                          55                          60  
 Tyr Ser Met Ile Met Thr Pro Lys Val Cys Ala Phe Leu Ile Val Val  
   65                          70                          75                          80  
 Ser Trp Phe Gly Ala Tyr Ala Ile Ala Leu Ile His Thr Val Leu Leu  
           85                          90                          95  
 Thr His Leu Ser Phe Cys Gly His Ser Glu Ile Pro His Phe Phe Cys  
           100                          105                          110  
 Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn  
           115                          120                          125  
 Asn Leu Met Val Asn Thr Val Gly Ala Leu Thr Ile Ile Ile Pro Phe  
   130                          135                          140  
 Ile Gly Ile Leu Ile Ser Tyr Thr Gln Ile Phe Met Thr Val Leu Arg  
   145                          150                          155                          160  
 Ile Pro Ser Thr Val Gly Lys Trp Lys Ala Phe Ser Thr Cys Ser Ser  
           165                          170                          175  
 His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Leu Ile Gly Val Tyr  
           180                          185                          190  
 Phe Ser Pro Thr Thr Thr His Thr Ala Gln Gln Asp Thr Ala Ala Ala  
           195                          200                          205  
 Ala Met Tyr Thr Val Val Thr Pro  
           210                          215

<210> 2508

<211> 216

<212> PRT

<213> Unknown (p99-dir-0-8 conceptual translation of range 2-649)

<400>2508

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Ala  
   1                          5                          10                          15  
 Asn His Val Ser Gly Asn Lys Met Ile Pro Tyr Pro Gly Cys Leu Thr  
           20                          25                          30  
 Gln Val Phe Phe Phe Ile Trp Phe Ala Gly Ile Asp Ser Phe Leu Leu  
           35                          40                          45  
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His  
           50                          55                          60  
 Tyr Ser Thr Val Met Thr Leu Arg Val Cys Val Leu Leu Leu Met Val  
   65                          70                          75                          80  
 Ser Trp Phe Ser Ala Phe Ile Asn Ala Leu Thr His Ala Ala Leu Leu  
           85                          90                          95  
 Thr Pro Leu Ser Phe Cys Gly His Asn Glu Ile Pro His Phe Phe Cys

```

      100      105      110
Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
      115      120      125
Asp Leu Met Val Tyr Thr Val Gly Ala Leu Pro Ile Ile Thr Pro Phe
      130      135      140
Ile Gly Ile Leu Ile Ser Tyr Thr Arg Ile Phe Met Ala Val Leu Arg
      145      150      155      160
Val Pro Ser Ala Gly Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Ile Gly Val Tyr
      180      185      190
Phe Ser Pro Thr Ser Thr Arg Thr Ala Gln Glu Asp Thr Val Ala Ala
      195      200      205
Val Met Tyr Thr Val Val Thr Pro
      210      215

```

&lt;210&gt; 2509

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p96-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2509

```

Leu Val Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Asn
 1      5      10      15
Asn Tyr Ile Ser Gln Asn Arg Thr Ile Ser Tyr Ala Gly Cys Leu Thr
      20      25      30
Gln Val Phe Phe Phe Leu Trp Phe Ala Gly Met Asp Ser Val Leu Leu
      35      40      45
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Ser Leu His
      50      55      60
Tyr Ser Thr Val Met Thr Pro Lys Ile Cys Ala Leu Leu Val Gly Val
      65      70      75      80
Ser Trp Phe Trp Ala Tyr Asn Asn Ala Leu Ile His Thr Val Leu Leu
      85      90      95
Thr Arg Leu Ser Phe Cys Gly His Asn Glu Ile Pro His Phe Phe Cys
      100      105      110
Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
      115      120      125
Asp Leu Met Ile Tyr Thr Val Gly Ala Leu Thr Ile Ile Leu Pro Phe
      130      135      140
Ile Gly Ile Met Ile Ser Tyr Val His Ile Phe Met Ala Val Leu Lys
      145      150      155      160
Ile Ser Ser Val Ser Gly Lys Gln Lys Val Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
      180      185      190
Phe Ser Pro Thr Ser Thr His Thr Ala Gln Gln Asp Thr Ala Ala Thr
      195      200      205
Val Met Tyr Thr Val Val Thr Pro
      210      215

```

&lt;210&gt; 2510

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p92-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2510

```

Leu Phe Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
 1      5      10      15
Asn His Ile Ser Lys Asn Lys Val Ile Pro Tyr Ser Met Cys Leu Thr
      20      25      30

```

Gln Thr Phe Phe Phe Ser Trp Phe Ile Gly Thr Asp Gly Val Leu Leu  
           35                                  40                  45  
 Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His  
           50                                  55                  60  
 Cys Thr Met Ile Ile Thr Pro Arg Val Cys Val Phe Leu Val Ala Val  
 65                                  70                  75                  80  
 Ser Trp Ile Trp Thr Cys Val Asn Ser Leu Ile His Thr Thr Ser Leu  
                                   85                  90                  95  
 Asn Arg Leu Ser Phe Cys Gly His Asn Glu Ile His His Phe Phe Cys  
                                   100                  105                  110  
 Asp Leu Ser Ala Leu Ile Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn  
                                   115                  120                  125  
 Asp Leu Leu Ile Tyr Thr Val Gly Gly Leu Lys Ala Ile Val Pro Phe  
 130                                  135                  140  
 Ile Gly Ile Leu Leu Ser Tyr Ile His Ile Phe Val Ala Val Leu Arg  
 145                                  150                  155                  160  
 Ile Pro Ser Ala Gly Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser  
                                   165                  170                  175  
 His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr  
                                   180                  185                  190  
 Phe Ser Pro Thr Ser Thr His Thr Ala Gln Lys Asp Thr Ala Val Ala  
                                   195                  200                  205  
 Val Met Tyr Thr Val Val Thr Pro  
           210                                  215

&lt;210&gt; 2511

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (p95-dir-0-8 conceptual translation of range 2-649)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(216)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2511

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Thr Leu Val  
   1                  5                                  10                  15  
 Asn Tyr Val Ser Gly Asn Lys Ala Ile Leu Tyr Ile Ser Cys Leu Ala  
           20                                  25                  30  
 Gln Val Phe Phe Phe Ser Trp Phe Ala Gly Leu Asp Ser Ile Leu Leu  
           35                                  40                  45  
 Ala Ser Met Ala Tyr Asp Arg Xaa Ile Ala Ile Cys Asp Pro Leu His  
           50                                  55                  60  
 Tyr Thr Thr Val Met Thr Pro Arg Val Cys Val Leu Leu Val Ala Met  
 65                                  70                  75                  80  
 Cys Leu Phe Gly Gly Cys Ala Asn Ser Leu Thr His Asn Ile Leu Leu  
                                   85                  90                  95  
 Thr Gln Leu Ser Phe Cys Gly His Thr Glu Ile Pro Leu Phe Phe Cys  
                                   100                  105                  110  
 Asp Leu Asn Val Val Ile Arg Leu Ala Cys Ser Asp Thr Phe Ile Asn  
                                   115                  120                  125  
 Asp Trp Met Ile Tyr Thr Met Gly Gly Leu Thr Ala Ile Ile Pro Phe  
 130                                  135                  140  
 Ser Gly Ile Leu Ile Ser Tyr Ile His Ile Phe Val Ala Met Leu Arg  
 145                                  150                  155                  160  
 Ile Leu Ser Ala Gln Gly Lys Trp Lys Val Phe Ser Thr Cys Gly Ser  
                                   165                  170                  175  
 His Leu Ile Ala Val Tyr Leu Leu Asn Gly Thr Ile Ile Gly Val Tyr  
                                   180                  185                  190  
 Leu Asn Pro Thr Ser Ser His Thr Ala Gln Gln Asp Thr Ala Ser Ala

195 200 205  
 Val Met Tyr Thr Met Val Thr Pro  
 210 215  
 <210> 2512  
 <211> 216  
 <212> PRT  
 <213> Unknown (p125-dir-0-8 conceptual translation of range 2-649)

<400>2512  
 Phe Val Asp Leu Cys Phe Thr Thr Thr Thr Val Pro Lys Met Leu Val  
 1 5 10 15  
 Asn His Ile Ser Gly Asn Lys Thr Ile Pro Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Phe Phe Phe Ile Trp Phe Ala Ser Ile Asp Ser Phe Leu Leu  
 35 40 45  
 Val Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg  
 50 55 60  
 Tyr Ala Ser Leu Met Ile Pro Arg Leu Cys Ala Leu Leu Val Ala Thr  
 65 70 75 80  
 Ser Trp Ser Phe Ala Cys Ile Asn Ala Leu Thr His Thr Val Leu Leu  
 85 90 95  
 Thr Gln Leu Ser Phe Cys Ser His Asn Glu Ile Pro His Phe Phe Cys  
 100 105 110  
 Asp Leu Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ile Asn  
 115 120 125  
 Asp Val Leu Val Tyr Thr Val Gly Ala Leu Pro Ile Leu Met Pro Phe  
 130 135 140  
 Val Gly Ile Leu Val Ser Tyr Thr Arg Ile Phe Ala Ala Val Leu Arg  
 145 150 155 160  
 Ile Pro Ser Ala Arg Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Val Ile Gly Val Tyr  
 180 185 190  
 Leu Ser Pro Met Ser Tyr His Thr Val Glu Lys Asp Thr Ala Ala Ala  
 195 200 205  
 Val Met Tyr Thr Val Val Thr Pro  
 210 215

<210> 2513  
 <211> 216  
 <212> PRT  
 <213> Unknown (p123-dir-0-8 conceptual translation of range 2-649)

<400>2513  
 Phe Val Asp Leu Cys Leu Thr Thr Thr Thr Val Pro Lys Met Leu Leu  
 1 5 10 15  
 Asn Ile Gln Thr Gln Lys Lys Thr Ile Ser Tyr Ala Gly Cys Leu Thr  
 20 25 30  
 Gln Met Tyr Phe Phe Leu Leu Leu Leu Asp Leu Asp Asn Met Ile Leu  
 35 40 45  
 Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys His Pro Leu His  
 50 55 60  
 Tyr Thr Ser Val Met Leu Pro Ser Leu Cys Gly Leu Leu Met Ala Val  
 65 70 75 80  
 Leu Trp Val Val Ala Asn Leu Phe Ser Leu Leu Phe Thr Leu Leu Met  
 85 90 95  
 Ala Gln Leu Ser Phe Cys Gly Asn Asn Thr Ile Pro His Phe Phe Cys  
 100 105 110  
 Asp Leu Ser Val Leu Leu Lys Leu Ser Cys Ser Asp Thr His Ile Val  
 115 120 125

Glu Asn Leu Leu Leu Ile Val Ser Gly Leu Leu Gly Val Thr Pro Leu  
 130 135 140  
 Ile Cys Ile Leu Val Ser Tyr Ser Arg Ile Val Ala Thr Val Met Arg  
 145 150 155 160  
 Ile Pro Ser Ala Lys Gly Lys Arg Lys Thr Phe Ser Thr Cys Gly Ser  
 165 170 175  
 His Leu Thr Val Val Ala Leu Phe Tyr Cys Ala Gly Phe Gly Val Phe  
 180 185 190  
 Phe Thr Pro Pro Ser Ser His Ser Gly Gly Lys Asp Thr Ala Ala Ser  
 195 200 205  
 Val Met Tyr Thr Val Val Thr Pro  
 210 215

&lt;210&gt; 2514

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (3983377-dir-0-8 conceptual translation of range 1-666)

&lt;400&gt;2514

Ala Asn Leu Ser Ser Val Asp Ile Ser Ala Pro Ser Val Ile Val Pro  
 1 5 10 15  
 Lys Ala Leu Val Asn His Met Leu Gly Ser Lys Ser Ile Ser Tyr Thr  
 20 25 30  
 Gly Cys Met Thr Gln Ile Tyr Phe Phe Ile Thr Phe Asn Asn Met Asp  
 35 40 45  
 Gly Phe Leu Leu Ser Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 50 55 60  
 His Pro Leu His Tyr Thr Met Met Met Arg Pro Arg Leu Cys Val Leu  
 65 70 75 80  
 Leu Val Ala Ile Ser Trp Ala Ile Thr Asn Leu His Ala Leu Leu His  
 85 90 95  
 Thr Leu Leu Met Val Arg Leu Thr Phe Cys Ser His Asn Ala Val His  
 100 105 110  
 His Phe Phe Cys Asp Pro Tyr Pro Ile Leu Lys Leu Ser Cys Ser Asp  
 115 120 125  
 Thr Phe Ile Asn Asp Leu Met Val Phe Thr Ile Gly Gly Leu Val Phe  
 130 135 140  
 Met Thr Pro Phe Thr Cys Ile Ile Val Ser Tyr Ala Tyr Ile Phe Ser  
 145 150 155 160  
 Lys Val Leu Lys Leu Lys Ser Ala His Gly Ile Arg Lys Ala Leu Ser  
 165 170 175  
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ala Ile  
 180 185 190  
 Leu Gly Ile Tyr Met His Pro Ser Ser Thr Tyr Thr Val Gln Asp Thr  
 195 200 205  
 Val Ala Thr Val Ile Phe Thr Val Val Thr Pro Met Val Asn  
 210 215 220

&lt;210&gt; 2515

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Unknown (902714-dir-0-6 conceptual translation of range 2-469)

&lt;400&gt;2515

Ile Cys His Pro Leu His Tyr Thr Val Met Met Arg Pro Arg Leu Cys  
 1 5 10 15  
 Val Leu Leu Val Ala Val Ser Trp Val Ile Thr Asn Leu His Ala Leu  
 20 25 30  
 Leu His Thr Leu Leu Met Val Gln Leu Thr Phe Cys Ser His Asn Ala  
 35 40 45  
 Val His His Phe Phe Cys Asp Pro Tyr Pro Ile Leu Lys Leu Ser Cys

50	55	60
Ser Asp Thr Phe Ile Asn Asp Ile Thr Ala Phe Thr Val Gly Gly Leu		
65	70	75
Thr Ser Ile Thr Pro Phe Thr Cys Ile Thr Val Ser Tyr Ala Tyr Ile		80
	85	90
Leu Ser Ser Val Leu Lys Phe Pro Ser Ile Gln Gly Ile Arg Lys Ala		95
	100	105
Leu Ser Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly		110
	115	120
Ala Ile Leu Gly Val Tyr Met His Pro Ser Ser Thr Tyr Ser Leu Gln		125
	130	135
Asp Thr Val Ala Thr Ala Phe Phe Thr Val Val Thr		140
145	150	155

&lt;210&gt; 2516

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (OST034-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2516

Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val		
1	5	10
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr		15
	20	25
Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu		30
	35	40
Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn		45
	50	55
Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile		60
	65	70
Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu		75
	85	90
Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys		95
	100	105
Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn		110
	115	120
Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe		125
	130	135
Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg		140
	145	150
Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser		155
	165	170
His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr		175
	180	185
Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala		190
	195	200
Val Leu Phe Thr Val Val Thr Pro		205
210	215	

&lt;210&gt; 2517

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (p156-dir-0-12 conceptual translation of range 34-1003)

&lt;400&gt;2517

Ser Glu Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu		
1	5	10
Leu Trp Gly Leu Ser Asp Gln Pro Gln Gln His Ile Phe Phe Leu		15
	20	25
Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile		30
	35	40
		45

Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Phe Thr Ser Thr Thr  
 65 70 75 80  
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser  
 85 90 95  
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Gly Thr Ala Leu Leu  
 100 105 110  
 Leu Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala Thr Met Ala  
 115 120 125  
 Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Met Met Ile  
 130 135 140  
 Met Ser Leu His Arg Cys Ala Leu Leu Val Thr Ala Cys Trp Thr Leu  
 145 150 155 160  
 Thr Ser Leu Val Ala Met Thr His Thr Phe Leu Ile Phe Arg Leu Ser  
 165 170 175  
 Phe Cys Ser Lys Ile Leu Pro Asp Phe Phe Cys Asp Leu Gly Pro Leu  
 180 185 190  
 Met Lys Val Ser Cys Ser Asp Ala Gln Val Asn Glu Leu Val Leu Leu  
 195 200 205  
 Phe Leu Gly Gly Ala Val Ile Leu Ile Pro Phe Met Leu Ile Leu Val  
 210 215 220  
 Ser Tyr Ile Arg Ile Val Ser Ala Ile Leu Arg Ala Pro Ser Ala Gln  
 225 230 235 240  
 Gly Arg Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Val Val  
 245 250 255  
 Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu Cys Pro Ser Ser  
 260 265 270  
 Ser Ser Ser Asn Ser Val Lys Glu Asp Thr Val Ala Ala Val Met Tyr  
 275 280 285  
 Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn  
 290 295 300  
 Lys Asp Met Lys Ala Val Val Arg Leu Leu Lys Gly Arg Val Ser  
 305 310 315 320  
 Leu Ser Gln

&lt;210&gt; 2518

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Unknown (p38-dir-0-11 conceptual translation of range 34-993)

&lt;400&gt;2518

Ser Asp Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu  
 1 5 10 15  
 Leu Ser Gly Leu Ser Asp Gln Pro Gln Gln His Ile Leu Phe Leu  
 20 25 30  
 Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile  
 35 40 45  
 Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Phe Thr Ser Thr Thr  
 65 70 75 80  
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser  
 85 90 95  
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp  
 100 105 110  
 Met Asp Ile Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Met Ala  
 115 120 125  
 Ile Cys His Pro Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys  
 130 135 140

Ala Leu Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Val Ala Met  
 145 150 155 160  
 Thr His Thr Phe Leu Ile Phe Arg Leu Ser Phe Cys Ser Lys Ile Ile  
 165 170 175  
 Pro Asp Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Val Ser Cys Ser  
 180 185 190  
 Asp Thr Gln Val Ser Glu Leu Val Leu Phe Leu Gly Gly Ala Val  
 195 200 205  
 Ile Leu Ile Pro Phe Met Leu Ile Leu Val Ser Tyr Ile Arg Ile Val  
 210 215 220  
 Ser Ala Ile Leu Arg Ala Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Val Val Val Ala Leu Phe Phe Gly Thr  
 245 250 255  
 Val Ile Arg Ala Tyr Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val  
 260 265 270  
 Asp Glu Asp Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Leu  
 275 280 285  
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Ala Ala  
 290 295 300  
 Val Val Arg Leu Leu Lys Gly Arg Val Ser Phe Ser Gln Gly Gln Gly  
 305 310 315 320

&lt;210&gt; 2519

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (p27-dir-0-11 conceptual translation of range 34-984)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(317)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2519

Ser Glu Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu  
 1 5 10 15  
 Leu Trp Gly Leu Ser Asp Gln Pro Gln Gln Gln His Ile Phe Phe Leu  
 20 25 30  
 Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile  
 35 40 45  
 Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Ser Thr Ser Thr Thr  
 65 70 75 80  
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser  
 85 90 95  
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp  
 100 105 110  
 Met Asp Ile Phe Leu Pro Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Leu Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys  
 130 135 140  
 Ala Phe Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Leu Ala Met  
 145 150 155 160  
 Thr Arg Thr Phe Leu Ile Phe Arg Leu Ser Leu Cys Ser Xaa Ile Leu  
 165 170 175  
 Pro Gly Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Val Ser Cys Ser  
 180 185 190  
 Asp Ala Gln Val Asn Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val  
 195 200 205  
 Ile Leu Ile Pro Phe Met Leu Ile Leu Val Ser Tyr Ile Arg Ile Val



210	215	220
Ser Ala Ile Leu Arg Ala	Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe	
225	230	235
Ser Thr Cys Asp Ser His	Leu Val Val Val Ala Leu Phe Phe Gly Thr	240
	245	250
Val Ile Arg Ala Tyr Leu Cys	Pro Ser Ser Ser Ser Ser Asn Ser Val	255
	260	265
Lys Glu Asp Thr Ala Ala Ala	Val Met Tyr Thr Val Val Thr Pro Leu	270
	275	280
Leu Asn Pro Phe Ile Tyr Ser	Met Arg Asn Lys Asp Met Lys Ala Ala	285
	290	295
Val Val Arg Leu Leu Lys	Gly Arg Val Ser Phe Ser Gln	300
305	310	315

&lt;210&gt; 2520

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Unknown (p80-dir-0-9 conceptual translation of range 5-731)

&lt;400&gt;2520

Thr Asp Ile Phe Phe Thr	Ser Thr Thr Val Pro Lys Ala Leu Val Asn
1	5 10 15
Ile Gln Thr Gln Ser Thr	Ser Ile Ser Tyr Ala Gly Cys Leu Ala Gln
	20 25 30
Leu Tyr Phe Phe Leu Thr	Phe Gly Asp Met Asp Ile Phe Leu Leu Ala
	35 40 45
Val Met Ala Tyr Asp Arg	Tyr Val Ala Ile Cys His Pro Leu His Tyr
	50 55 60
Met Met Ile Met Ser Leu	Arg Arg Cys Ala Val Leu Val Ala Ala Cys
65	70 75 80
Trp Thr Leu Thr Ser Leu	Val Ala Met Thr His Thr Phe Leu Ile Ser
	85 90 95
Gln Leu Ser Phe Cys Ser	Lys Ile Ile Pro Asp Phe Phe Cys Asp Leu
	100 105 110
Gly Pro Leu Met Lys Val	Ser Cys Phe Asp Thr Gln Val Asn Glu Leu
	115 120 125
Val Leu Leu Phe Leu Gly	Gly Thr Val Ile Leu Ile Pro Phe Met Leu
	130 135 140
Val Leu Val Ser Tyr Ile	Gln Ile Val Ser Ala Ile Leu Arg Ala Pro
145	150 155 160
Ser Ala Gln Gly Arg Arg	Lys Ala Phe Ser Thr Cys Gly Ser His Leu
	165 170 175
Val Val Val Ala Leu Phe	Phe Gly Thr Val Ile Arg Ala Tyr Leu Cys
	180 185 190
Pro Ser Ser Ser Ser Ser	Ser Val Glu Glu Asp Thr Ala Ala Ala
	195 200 205
Val Met Tyr Thr Val Val	Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser
	210 215 220
Leu Arg Asn Lys Asp Met	Lys Ala Ala Val Val Arg Leu Leu Lys Gly
225	230 235 240
Arg Val	

&lt;210&gt; 2521

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Unknown (3983403-dir-0-8 conceptual translation of range 1-675)

&lt;400&gt;2521

Ala Thr Leu Ser Cys Val	Asp Ile Leu Phe Thr Ser Thr Thr Val Pro
1	5 10 15

Lys Ala Leu Val Asn Ile His Thr Gln Ser Arg Thr Ile Ser Tyr Ala  
                   20                  25                  30  
 Gly Cys Leu Val Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp  
                   35                  40                  45  
 Ile Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Phe Val Ala Ile Cys  
                   50                  55                  60  
 His Pro Leu His Tyr Arg Met Ile Met Ser Phe Gln Arg Cys Ser Leu  
   65                  70                  75                  80  
 Leu Val Thr Val Cys Trp Thr Leu Thr Thr Val Val Ala Met Thr His  
                   85                  90                  95  
 Thr Phe Leu Ile Phe Arg Leu Ser Phe Cys Ser Gln Lys Val Ile Pro  
                   100                  105                  110  
 Asp Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Ile Ala Cys Ser Glu  
                   115                  120                  125  
 Thr Arg Ile Asn Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val Ile  
                   130                  135                  140  
 Leu Ile Pro Phe Leu Leu Ile Leu Met Ser Tyr Ile Arg Ile Val Ser  
   145                  150                  155                  160  
 Ala Ile Leu Arg Val Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser  
                   165                  170                  175  
 Thr Cys Gly Ser His Leu Ser Val Val Ala Leu Phe Phe Gly Thr Val  
                   180                  185                  190  
 Ile Arg Ala Tyr Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val Val  
                   195                  200                  205  
 Glu Asp Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Val Leu  
                   210                  215                  220  
 Asn  
 225

&lt;210&gt; 2522

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (p144-dir-0-8 conceptual translation of range 5-654)

&lt;400&gt;2522

Asp Asp Ile Leu Leu Val Ser Thr Ile Val Pro Lys Ala Leu Val Asn  
   1                  5                  10                  15  
 Ile His Thr Gln Ser Arg Thr Ile Ser Tyr Ala Gly Cys Leu Val Gln  
                   20                  25                  30  
 Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala  
                   35                  40                  45  
 Thr Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His Tyr  
                   50                  55                  60  
 Arg Met Ile Met Ser Phe Gln Arg Cys Ser Leu Val Thr Val Cys  
   65                  70                  75                  80  
 Trp Ile Leu Thr Thr Val Val Ala Met Thr His Thr Phe Leu Ile Phe  
                   85                  90                  95  
 Trp Phe Ser Phe Tyr Ser Lys Lys Val Ile Pro Gly Phe Phe Cys Asp  
                   100                  105                  110  
 Leu Glu Pro Leu Ile Lys Ile Pro Cys Ser Glu Thr Arg Ile Asn Glu  
                   115                  120                  125  
 Leu Val Leu Leu Phe Leu Gly Ser Ala Val Val Phe Ile Leu Leu Leu  
                   130                  135                  140  
 Leu Ile Leu Val Ser Tyr Ile Gln Ile Val Ser Ala Ile Phe Arg Val  
   145                  150                  155                  160  
 Pro Ser Ala Gln Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His  
                   165                  170                  175  
 Leu Ser Val Val Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu  
                   180                  185                  190  
 Cys Pro Ser Ser Ser Ser Ser Asn Ser Val Val Glu Asp Thr Ala Ala  
                   195                  200                  205

Ala Val Met Tyr Thr Val Val Thr Pro  
210 215

<210> 2523

<211> 215

<212> PRT

<213> Unknown (p111-dir-0-8 conceptual translation of range 2-646)

<220>

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400>2523

Val	Val	Asp	Val	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1				5					10					15	
Asp	Met	Gln	Thr	Gly	Ser	His	Thr	Ile	Ser	Gln	Ala	Asp	Cys	Leu	Ser
		20						25					30		
Gln	Val	Tyr	Phe	Ser	Ile	Leu	Phe	Gly	Asp	Leu	Asp	Asp	Phe	Leu	Leu
		35					40					45			
Ala	Val	Met	Ser	Phe	Asp	Xaa	Tyr	Met	Ala	Ile	Cys	Arg	Pro	Leu	Cys
		50				55					60				
Tyr	Ala	Thr	Ala	Met	Ser	Ser	Gln	Cys	Cys	Val	Leu	Leu	Val	Ala	Thr
		65			70				75					80	
Cys	Trp	Val	Ile	Ala	Gln	Leu	Asn	Ser	Leu	Leu	His	Thr	Val	Leu	Leu
			85						90					95	
Ala	Gln	Leu	Thr	Phe	Cys	Ala	Asp	His	Thr	Ile	Pro	His	Phe	Phe	Cys
		100						105					110		
Asp	Leu	Ala	Leu	Leu	Leu	Pro	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Ile	Asn
		115					120					125			
Glu	Leu	Val	Leu	Met	Ser	Met	Gly	Gly	Ala	Gly	Ile	Leu	Ile	Pro	Leu
		130				135					140				
Met	Cys	Ile	Leu	Gly	Ser	Tyr	Ala	Gln	Ile	Ile	Ser	Ala	Ile	Leu	Arg
		145			150					155				160	
Met	Pro	Ser	Ala	Gly	Ser	Lys	Arg	Ile	Ala	Phe	Ser	Thr	Ser	Ser	Ser
			165					170						175	
His	Leu	Ala	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Val	Ile	Ser	Glu	Tyr
		180						185					190		
Leu	Cys	Pro	Ser	Pro	Ser	Gly	Ser	Ser	Asp	Glu	Ser	Ser	Leu	Ala	Ala
		195					200					205			
Val	Leu	Tyr	Ala	Val	Val	Thr									
		210				215									

<210> 2524

<211> 216

<212> PRT

<213> Unknown (2921629-dir-0-8 conceptual translation of range 2-649)

<400>2524

Phe	Val	Asp	Met	Gly	Leu	Thr	Ser	Ser	Thr	Val	Thr	Lys	Met	Leu	Val
1				5					10					15	
Asn	Ile	Gln	Thr	Arg	His	His	Thr	Ile	Thr	Tyr	Thr	Gly	Cys	Leu	Thr
		20						25					30		
Gln	Met	Tyr	Phe	Phe	Leu	Met	Phe	Gly	Asp	Leu	Asp	Ser	Phe	Phe	Leu
		35					40					45			
Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Cys
		50				55					60				
Tyr	Ser	Thr	Val	Met	Arg	Pro	Gln	Val	Cys	Ala	Leu	Met	Leu	Ala	Leu
		65			70				75					80	
Cys	Trp	Val	Leu	Thr	Asn	Ile	Val	Ala	Leu	Thr	His	Thr	Phe	Leu	Met
			85					90						95	

Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys  
 100 105 110  
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn  
 115 120 125  
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe  
 130 135 140  
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg  
 145 150 155 160  
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser  
 165 170 175  
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr  
 180 185 190  
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala  
 195 200 205  
 Ala Met Tyr Thr Ile Val Thr Pro  
 210 215

&lt;210&gt; 2525

&lt;211&gt; 342

&lt;212&gt; PRT

&lt;213&gt; Unknown (1256388-dir-2-13 conceptual translation of range 379-1402)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(342)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2525

Phe Xaa Leu Ser Phe Leu Asn Tyr Arg Cys Ser Ile Arg Met Glu Asn  
 1 5 10 15  
 Gln Ser Ser Val Ser Glu Phe Phe Leu Arg Gly Ile Ser Gly Phe Pro  
 20 25 30  
 Glu Gln Gln Gln Leu Leu Tyr Gly Leu Phe Leu Cys Met Tyr Leu Val  
 35 40 45  
 Thr Leu Thr Gly Asn Val Leu Ile Ile Leu Ala Ile Gly Ser Asp Pro  
 50 55 60  
 His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Ala  
 65 70 75 80  
 Asp Met Gly Leu Ile Ser Ser Thr Val Thr Lys Met Leu Phe Asn Val  
 85 90 95  
 Gln Thr Gln Cys His Thr Ile Ser Tyr Thr Gly Cys Leu Thr Gln Met  
 100 105 110  
 Tyr Leu Phe Met Met Phe Gly Asp Leu Asp Ser Phe Phe Leu Ala Val  
 115 120 125  
 Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Ser  
 130 135 140  
 Thr Ile Met Asn Ala Arg Ile Cys Val Leu Met Leu Ile Leu Cys Trp  
 145 150 155 160  
 Ile Leu Thr Asn Val Val Ala Leu Thr His Thr Leu Leu Met Ala Arg  
 165 170 175  
 Leu Ser Phe Cys Val Val Gly Glu Ile Ala His Phe Phe Cys Asp Val  
 180 185 190  
 Thr Ser Val Met Lys Leu Ser Cys Ser Asp Thr His Val Asn Glu Leu  
 195 200 205  
 Val Leu Ser Gly Phe Gly Gly Thr Val Leu Met Val Pro Phe Val Ser  
 210 215 220  
 Ile Val Ile Ser Tyr Val His Ile Val Phe Ala Val Leu Arg Ile Gln  
 225 230 235 240  
 Ser Ser Gly Gly Ser Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu  
 245 250 255  
 Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Val Tyr Leu Phe

```
<210> 2526
<211> 216
<212> PRT
<213> Unknown (p101-dir-0-8 conceptual translation of range 2-649)
```

```
<210> 2527
<211> 176
<212> PRT
<213> Unknown (3273640-dir-0-7 conceptual translation of range 4-531)
```

1535

```

Asp Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
65          70          75          80
Lys Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe
      85          90          95
Ile Cys Ile Leu Ala Ser Tyr Val Arg Ile Ile Val Ala Ile Met Lys
      100        105        110
Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
      115        120        125
His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
      130        135        140
Leu Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala
145          150        155        160
Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Cys Ser
      165        170        175

```

&lt;210&gt; 2528

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Unknown (3273644-dir-0-7 conceptual translation of range 4-528)

&lt;400&gt;2528

```

Ala Leu Glu Tyr Asp Arg Phe Leu Ala Ile Cys His Pro Leu His Tyr
1          5          10          15
Thr Thr Ile Met Ser Pro Gln Leu Cys Gly Leu Leu Ala Gly Gly Leu
      20          25          30
Trp Met Leu Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met Ala
      35          40          45
Arg Leu Val Phe Cys Gly Asn Asn Lys Ile Pro His Tyr Phe Cys Asp
      50          55          60
Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn Lys
65          70          75          80
Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe Ile
      85          90          95
Cys Ile Leu Ala Ser Tyr Val Arg Ile Ile Val Ala Ile Met Lys Val
      100        105        110
Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His
      115        120        125
Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr Leu
      130        135        140
Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala Val
145          150        155        160
Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Cys Ser
      165        170        175

```

&lt;210&gt; 2529

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (3273656-dir-0-6 conceptual translation of range 4-477)

&lt;400&gt;2529

```

Ala Leu Glu Tyr Asp Arg Phe Leu Ala Ile Cys His Pro Leu His Tyr
1          5          10          15
Thr Thr Thr Met Ser Pro Gln Leu Cys Gly Leu Leu Ala Gly Gly Leu
      20          25          30
Trp Met Leu Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met Ala
      35          40          45
Arg Leu Val Phe Cys Gly Asn Asn Lys Ile Pro His Tyr Phe Cys Asp
      50          55          60
Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn Lys
65          70          75          80
Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe Ile

```



Thr Thr Ile Gly Val Tyr Leu Cys Pro Ser Ser Val Arg Thr Ala Val  
 130 135 140  
 Lys Glu Lys Ala Ser Ala Val Met Tyr Thr Ala Val Thr  
 145 150 155

<210> 2532

<211> 313

<212> PRT

<213> Unknown (p82-dir-0-11 conceptual translation of range 1-939)

<400>2532

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe  
 20 25 30  
 Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys  
 65 70 75 80  
 Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys  
 85 90 95  
 Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser  
 100 105 110  
 Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu  
 130 135 140  
 Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His  
 165 170 175  
 Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr  
 180 185 190  
 Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala  
 195 200 205  
 Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala  
 210 215 220  
 Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile  
 245 250 255  
 Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys  
 260 265 270  
 Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu  
 290 295 300  
 Val Asn Arg Lys Ile Thr Ser Ser Ser  
 305 310

<210> 2533

<211> 157

<212> PRT

<213> Unknown (902331-dir-0-6 conceptual translation of range 2-472)

<400>2533

Ile Cys His Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys  
 1 5 10 15  
 Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu



```

      20      25      30
Leu His Thr Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile
      35      40      45
Ile His His Phe Leu Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys
      50      55      60
Ser Asp Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Asp Leu
      65      70      75      80
Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Ser Tyr Gly Leu Ile
      85      90      95
Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala
      100      105      110
Val Ser Thr Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly
      115      120      125
Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu
      130      135      140
Ser Asp Thr Leu Ser Thr Ile Met Tyr Ser Met Val Ala
      145      150      155

```

&lt;210&gt; 2534

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (p152-rev-0-8 conceptual translation of range 2-652)

&lt;400&gt;2534

```

Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys Met Leu Asp
 1      5      10      15
His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu Cys Leu Thr
      20      25      30
Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn Asn Phe Leu
      35      40      45
Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser His Pro Leu
      50      55      60
His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu Leu Val Ala
      65      70      75      80
Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His Thr Leu Leu
      85      90      95
Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro His Phe Phe
      100      105      110
Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser Thr Cys Val
      115      120      125
Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu Ile Ala Pro
      130      135      140
Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu Ala Ile Leu
      145      150      155      160
Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser Ser Cys Thr
      165      170      175
Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala Ile Gly Val
      180      185      190
Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp Arg Val Phe
      195      200      205
Ser Val Met Tyr Thr Val Val Thr Pro
      210      215

```

&lt;210&gt; 2535

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Unknown (902317-dir-0-6 conceptual translation of range 5-472)

&lt;400&gt;2535

```

Cys His Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val
 1      5      10      15

```

Lys Met Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu  
                   20                  25                  30  
 His Thr Phe Leu Met Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile  
                   35                  40                  45  
 Pro His Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr  
                   50                  55                  60  
 Ser Thr Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val  
 65                  70                  75                  80  
 Ile Ser Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile  
                   85                  90                  95  
 Leu Val Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe  
                   100                  105                  110  
 Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr  
                   115                  120                  125  
 Leu Ser Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys  
 130                  135                  140  
 Gly Arg Ile Ile Thr Val Val Tyr Thr Val Val Thr  
 145                  150                  155

&lt;210&gt; 2536

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (OST226-dir-0-8 conceptual translation of range 2-646)

&lt;400&gt;2536

Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Gln  
   1                  5                  10                  15  
 Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly Cys Leu Ala  
                   20                  25                  30  
 Gln Thr Tyr Ser Ser Leu Leu Arg Arg His Glu Asn Phe Ile Leu Ala  
                   35                  40                  45  
 Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Phe His Tyr  
                   50                  55                  60  
 Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met Val Val Met Cys  
 65                  70                  75                  80  
 His Ala Leu Ser His Leu His Ala Met Leu His Thr Phe Leu Met Gly  
                   85                  90                  95  
 Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His Phe Phe Cys Asp  
                   100                  105                  110  
 Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr Tyr Leu Asn Thr  
                   115                  120                  125  
 Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser Gly Ala Leu Ala  
                   130                  135                  140  
 Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val Val Leu Arg Ile  
 145                  150                  155                  160  
 Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr Arg Gly Ser His  
                   165                  170                  175  
 Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser Trp Val Tyr Phe  
                   180                  185                  190  
 Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg Ile Ile Thr Val  
                   195                  200                  205  
 Val Tyr Thr Val Val Thr Pro  
                   210                  215

&lt;210&gt; 2537

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (4190944-dir-20-13 conceptual translation of range 2175-3131)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(319)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2537

Gln Gln Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu  
 1 5 10 15  
 Leu Gly Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val  
 20 25 30  
 Phe Ser Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile  
 35 40 45  
 Thr Leu Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe  
 50 55 60  
 Leu Ser Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val  
 65 70 75 80  
 Pro Lys Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr  
 85 90 95  
 Thr Gly Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met  
 100 105 110  
 Glu Asn Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile  
 115 120 125  
 Cys His Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val  
 130 135 140  
 Lys Met Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu  
 145 150 155 160  
 His Thr Phe Leu Ile Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile  
 165 170 175  
 Pro His Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr  
 180 185 190  
 Ser Thr Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val  
 195 200 205  
 Ile Ser Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile  
 210 215 220  
 Leu Val Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr  
 245 250 255  
 Leu Ser Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys  
 260 265 270  
 Gly Arg Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn  
 275 280 285  
 Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met  
 290 295 300  
 Lys Trp Met Ser Arg Met Gln Thr Phe Phe Phe Arg Xaa Asn Pro  
 305 310 315

&lt;210&gt; 2538

&lt;211&gt; 326

&lt;212&gt; PRT

&lt;213&gt; Unknown (4190944-dir-490-12 conceptual translation of range 49118-50095)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(326)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2538

Ile Cys Tyr Ser Val Ser Leu Ser Leu Gly Glu Pro Thr Thr Met Gly  
 1 5 10 15  
 Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly Leu Ser  
 20 25 30

Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu Pro Ile  
 35 40 45  
 Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala Ile Arg  
 50 55 60  
 Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Ile Leu  
 65 70 75 80  
 Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys Met Leu  
 85 90 95  
 Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu Cys Leu  
 100 105 110  
 Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser Tyr Leu  
 115 120 125  
 Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Phe  
 130 135 140  
 His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu Leu Val  
 145 150 155 160  
 Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile Leu Leu  
 165 170 175  
 Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His Phe Phe  
 180 185 190  
 Cys Asp Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His Phe Val  
 195 200 205  
 Lys Glu Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met Thr Pro  
 210 215 220  
 Phe Ser Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr Val Leu  
 225 230 235 240  
 Lys Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly  
 245 250 255  
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser Tyr Val  
 260 265 270  
 Tyr Phe Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile Ala Thr  
 275 280 285  
 Ile Ile Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser  
 290 295 300  
 Leu Arg Asn Lys Asp Met Lys Gln Gly Leu Ala Lys Leu Met His Arg  
 305 310 315 320  
 Met Lys Cys Gln Xaa Lys  
 325

&lt;210&gt; 2539

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg23-dir-0-8 conceptual translation of range 4-645)

&lt;400&gt;2539

Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys Met Leu Val Asn  
 1 5 10 15  
 Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Ser Glu Cys Leu Thr Gln  
 20 25 30  
 Met Tyr Phe Phe Leu Ala Cys Gly Asn Thr Asp Ser Tyr Leu Leu Ala  
 35 40 45  
 Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Phe His Tyr  
 50 55 60  
 Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu Leu Val Leu Ser  
 65 70 75 80  
 Phe Cys Ile Pro His Leu His Ser Leu Leu His Ile Leu Leu Thr Asn  
 85 90 95  
 Gln Val Ile Phe Cys Ala Ser Asn Val Ile His His Phe Phe Cys Asp  
 100 105 110  
 Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His Phe Val Lys Glu  
 115 120 125

Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met Thr Pro Phe Ser  
 130 135 140  
 Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr Val Leu Lys Ile  
 145 150 155 160  
 Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser His  
 165 170 175  
 Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser Tyr Leu Tyr Phe  
 180 185 190  
 Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile Ala Thr Ile Ile  
 195 200 205  
 Tyr Pro Val Leu Thr Pro  
 210

<210> 2540

<211> 316

<212> PRT

<213> Unknown (4190944-dir-624-13 conceptual translation of range 62576-63523)

<400>2540

Met Gly Met Ser Asn Leu Thr Arg Leu Ser Glu Phe Ile Leu Leu Gly  
 1 5 10 15  
 Leu Ser Ser Arg Ser Glu Asp Gln Arg Pro Leu Phe Ala Leu Phe Leu  
 20 25 30  
 Ile Ile Tyr Leu Val Thr Leu Met Gly Asn Leu Leu Ile Ile Leu Ala  
 35 40 45  
 Ile His Ser Asp Pro Arg Leu Gln Asn Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Ile Leu Ser Phe Ala Asp Ile Cys Tyr Thr Thr Val Ile Val Pro Lys  
 65 70 75 80  
 Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala Glu  
 85 90 95  
 Cys Leu Ala Gln Met Tyr Phe Phe Leu Val Phe Gly Asn Ile Asp Ser  
 100 105 110  
 Tyr Leu Leu Ala Ala Met Ala Ile Asn Arg Cys Val Ala Ile Cys Asn  
 115 120 125  
 Pro Phe His Tyr Val Thr Val Met Asn Arg Arg Cys Cys Val Leu Leu  
 130 135 140  
 Leu Ala Phe Pro Ile Thr Phe Ser Tyr Phe His Ser Leu Leu His Val  
 145 150 155 160  
 Leu Leu Val Asn Arg Leu Thr Phe Cys Thr Ser Asn Val Ile His His  
 165 170 175  
 Phe Phe Cys Asp Val Asn Pro Val Leu Lys Leu Ser Cys Ser Ser Thr  
 180 185 190  
 Phe Val Asn Glu Ile Val Ala Met Thr Glu Gly Leu Ala Ser Val Met  
 195 200 205  
 Ala Pro Phe Val Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Ala  
 210 215 220  
 Val Leu Lys Ile Pro Ser Ala Ala Gly Lys His Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Ile Ser  
 245 250 255  
 Tyr Val Tyr Leu Gln Pro Leu Ser Ser Tyr Thr Val Lys Asp Arg Ile  
 260 265 270  
 Ala Thr Ile Asn Tyr Thr Val Leu Thr Ser Val Leu Asn Pro Phe Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Gln Lys Leu Ile  
 290 295 300  
 Asn Lys Ile Lys Ser Gln Met Ser Arg Phe Ser Thr  
 305 310 315

<210> 2541  
 <211> 327  
 <212> PRT  
 <213> Unknown (4190944-dir-1371-13 conceptual translation of range 137254-138234)

<220>  
 <221> VARIANT  
 <222> (1)...(327)  
 <223> Xaa = Any Amino Acid

<400>2541

```

Arg Lys Ser Arg Asp Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser
 1           5           10           15
Gly Phe Ile Leu Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro
      20           25           30
Leu Phe Ala Ile Phe Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn
      35           40           45
Val Leu Ile Ile Pro Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro
      50           55           60
Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr
      65           70           75           80
Thr Val Ile Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys
      85           90           95
Val Ile Ser Tyr Val Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala
      100          105          110
Phe Gly Asn Thr Asp Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg
      115          120          125
Leu Val Ala Ile Cys Asn Pro Leu His Tyr Asp Val Val Met Lys Pro
      130          135          140
Arg His Cys Leu Leu Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu
      145          150          155          160
His Ser Leu Phe Arg Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala
      165          170          175
Ser His Ile Ile Lys His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys
      180          185          190
Leu Ser Cys Ser Asp Thr Ser Ser Ser Gln Met Val Val Met Thr Glu
      195          200          205
Thr Leu Ala Val Ile Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr
      210          215          220
Leu Arg Ile Met Val Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys
      225          230          235          240
Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu
      245          250          255
Phe Tyr Gly Ser Ile Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr
      260          265          270
Ser Val Val Arg Asp Arg Val Ala Thr Val Met Tyr Thr Val Val Thr
      275          280          285
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys
      290          295          300
Arg Gly Leu Lys Lys Leu Gln Asp Arg Ile Tyr Arg Xaa Lys Glu Gln
      305          310          315          320
Asn Val Gly Val Ser Xaa Leu
      325

```

<210> 2542  
 <211> 216  
 <212> PRT  
 <213> Unknown (hgl6-dir-0-8 conceptual translation of range 1-648)

<400>2542

```

Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val
 1          5          10          15
Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val Gly Cys Leu Ala
      20          25          30
Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
      35          40          45
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
      50          55          60
Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu Met Leu Leu Gly
65          70          75          80
Ser Tyr Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
      85          90          95
Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
      100          105          110
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
      115          120          125
Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
      130          135          140
Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val Thr Val Leu Arg
145          150          155          160
Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165          170          175
His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
      180          185          190
Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp Arg Val Ala Thr
      195          200          205
Val Met Tyr Thr Val Val Thr Pro
      210          215

```

&lt;210&gt; 2543

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Unknown (4190944-dir-1112-13 conceptual translation of range 111405-112373)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(323)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2543

```

Arg Asp Met Glu Thr Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile
 1          5          10          15
Leu Leu Gly Leu Ser Ser Asn Pro Lys Leu Gln Lys Pro Leu Phe Ala
      20          25          30
Ile Phe Leu Ile Met Tyr Leu Leu Thr Ala Val Gly Asn Val Leu Ile
      35          40          45
Ile Leu Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe
      50          55          60
Phe Leu Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile
65          70          75          80
Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser
      85          90          95
Tyr Val Gly Cys Leu Ile Gln Met Tyr Phe Phe Met Ala Phe Gly Asn
      100          105          110
Thr Asp Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala
      115          120          125
Ile Cys Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Trp His Cys
      130          135          140
Leu Leu Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu
145          150          155          160

```

```

Phe Arg Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile
      165      170      175
Ile Lys His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys
      180      185      190
Ser Asp Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala
      195      200      205
Val Ile Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile
      210      215      220
Ile Val Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly
      245      250      255
Ser Val Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met
      260      265      270
Lys Gly Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu
      275      280      285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu
      290      295      300
Lys Lys Leu Arg His Arg Ile Tyr Ser Xaa Lys Glu Gln Asn Val Gly
      305      310      315      320
Met Ser Lys

```

&lt;210&gt; 2544

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (OST046-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2544

```

Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val
  1      5      10      15
Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser Tyr Val Gly Cys Leu Val
      20      25      30
Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
      35      40      45
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
      50      55      60
Tyr Asp Val Val Met Lys Pro Trp His Cys Leu Leu Met Leu Leu Gly
      65      70      75      80
Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
      85      90      95
Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
      100      105      110
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
      115      120      125
Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
      130      135      140
Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val Thr Val Leu Arg
      145      150      155      160
Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr
      180      185      190
Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly Arg Val Ala Thr
      195      200      205
Val Met Tyr Thr Val Val Thr Pro
      210      215

```

&lt;210&gt; 2545

&lt;211&gt; 216

&lt;212&gt; PRT



<213> Unknown (p100-dir-0-8 conceptual translation of range 2-649)

<400>2545

```

Leu Val Asp Leu Cys Phe Thr Thr Val Ile Val Pro Gln Met Leu Val
 1           5           10           15
Ser Met Leu Met Gln Asn Lys Ala Ile Ser Phe Ala Gln Cys Ile Ala
      20           25           30
Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu
      35           40           45
Ala Ala Met Pro Ile Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu His
      50           55           60
Tyr Thr Thr Thr Met Ser Pro Arg Arg Cys Val Leu Leu Val Ala Met
65           70           75           80
Ser Trp Val Val Ser His Phe His Ser Leu Val His Thr Leu Leu Met
      85           90           95
Ala Arg Leu Ser Phe Cys Gly Pro Asn Ala Ile His His Phe Phe Cys
      100          105          110
Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn
      115          120          125
Glu Val Leu Ala Phe Thr Glu Gly Ser Leu Val Ile Met Ser Pro Phe
      130          135          140
Leu Phe Ile Val Ile Ser Tyr Val Trp Ile Thr Arg Ala Val Leu Arg
145          150          155          160
Val Pro Ser Gly Arg Gly Arg Tyr Lys Ala Phe Ser Thr Cys Ser Ser
      165          170          175
His Ile Thr Val Val Val Leu Phe Tyr Gly Thr Ile Val Ser Val Tyr
      180          185          190
Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr
      195          200          205
Val Ile Tyr Thr Val Val Thr Pro
      210          215

```

<210> 2546

<211> 328

<212> PRT

<213> Unknown (4190944-rev-159-13 conceptual translation of range 16099-17082)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400>2546

```

Phe Gln Ala Gly Xaa Leu Ser Leu Met Met Ser Phe Ala Pro Asn Ala
 1           5           10           15
Ser His Ser Pro Val Phe Leu Leu Leu Gly Phe Ser Arg Ala Asn Ile
      20           25           30
Ser Tyr Thr Leu Leu Phe Phe Leu Phe Leu Ala Ile Tyr Leu Thr Thr
      35           40           45
Ile Leu Gly Asn Val Thr Leu Val Leu Leu Ile Ser Trp Asp Ser Arg
      50           55           60
Leu His Ser Pro Met Tyr Tyr Leu Leu Arg Gly Leu Ser Val Ile Asp
65           70           75           80
Met Gly Leu Ser Thr Val Thr Leu Pro Gln Leu Leu Ala His Leu Val
      85           90           95
Ser His Tyr Pro Thr Ile Pro Ala Ala Arg Cys Leu Ala Gln Phe Phe
      100          105          110
Phe Phe Tyr Ala Phe Gly Val Thr Asp Thr Leu Val Ile Ala Val Met
      115          120          125
Ala Leu Asp Arg Tyr Val Ala Ile Cys Asp Pro Leu His Tyr Ala Leu

```

130	135	140
Val Met Asn His Gln Arg Cys Ala Cys Leu Leu Ala Leu Ser Trp Val		
145	150	155
Val Ser Ile Leu His Thr Met Leu Arg Val Gly Leu Val Leu Pro Leu		160
	165	170
Cys Trp Thr Gly Asp Ala Gly Gly Asn Val Asn Leu Pro His Phe Phe		175
	180	185
Cys Asp His Arg Pro Leu Leu Arg Ala Ser Cys Ser Asp Ile His Ser		190
	195	200
Asn Glu Leu Ala Ile Phe Phe Glu Gly Gly Phe Leu Met Leu Gly Pro		205
	210	215
Cys Ala Leu Ile Val Leu Ser Tyr Val Arg Ile Gly Ala Ala Ile Leu		220
225	230	235
Arg Leu Pro Ser Ala Gly Arg Arg Arg Ala Val Ser Thr Cys Gly		240
	245	250
Ser His Leu Thr Met Val Gly Phe Leu Tyr Gly Thr Ile Ile Cys Val		255
	260	265
Tyr Phe Gln Pro Pro Phe Gln Asn Ser Gln Tyr Gln Asp Met Val Ala		270
	275	280
Ser Val Met Tyr Thr Ala Ile Thr Pro Leu Ala Asn Pro Phe Val Tyr		285
	290	295
Ser Leu His Asn Lys Asp Val Lys Gly Ala Leu Cys Arg Leu Leu Glu		300
305	310	315
Trp Val Lys Val Asp Pro Xaa Leu		320
	325	

&lt;210&gt; 2547

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg99-dir-0-8 conceptual translation of range 1-648)

&lt;400&gt;2547

Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro Lys Met Leu Asp		
1	5	10
Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala Gly Cys Leu Thr		15
	20	25
Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp Ser Cys Leu Leu		30
	35	40
Ala Asp Met Ala Tyr Asp Cys Tyr Val Asp Ile Arg His Pro Leu Pro		45
	50	55
Tyr Asp Thr Arg Met Ser Arg Ala Met Cys Ala Ala Leu Val Gly Met		60
65	70	75
Ala Trp Val Val Ser His Val His Ser Leu Leu Tyr Ile Leu Leu Met		80
	85	90
Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro His Phe Phe Cys		95
	100	105
Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp Asn His His Ile		110
	115	120
Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val Val Thr Pro Phe		125
	130	135
Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala Ala Val Leu Gln		140
145	150	155
Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser Thr Cys Gly Ser		160
	165	170
His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr		175
	180	185
Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly Arg Val Ala Thr		190
	195	200
Val Met Tyr Thr Val Val Thr Pro		205
	210	215

&lt;210&gt; 2548

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Unknown (p16-dir-0-11 conceptual translation of range 1-960)

&lt;400&gt;2548

```

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1           5           10           15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
          20           25           30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
          35           40           45
Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
          50           55           60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
65           70           75           80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
          85           90           95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
          100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
          115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
          130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
          165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
          180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
          195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
          210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
          245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
          260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
          275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
          290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
305          310          315

```

&lt;210&gt; 2549

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (2564509-dir-0-6 conceptual translation of range 1-474)

&lt;400&gt;2549

```

Ile Cys Ser Pro Leu His Tyr Gly Met Val Met Ser Arg Arg Met Cys
 1           5           10           15
Phe Cys Leu Val Ala Ile Ser Trp Leu Val Ile Ala Val His Ser Val
          20           25           30
Leu His Ser Val Leu Thr Ser Arg Leu Ser Phe Cys Gly Ser Asn Gln
          35           40           45
Ile His His Phe Phe Cys Asp Met Thr Pro Leu Leu Lys Leu Ser Cys
          50           55           60

```

Ser Asp Thr Ser Val Asn Glu Leu Val Ile Phe Ile Glu Gly Pro Phe  
 65 70 75 80  
 Ser Val Ala Val Pro Leu Gly Ile Val Leu Val Ser Tyr Val Arg Ile  
 85 90 95  
 Ile Ser Ala Ile Leu Lys Ile Arg Ser Pro Glu Gly Arg His Arg Ala  
 100 105 110  
 Phe Ser Thr Cys Ser Ser His Leu Met Val Val Ile Leu Tyr Phe Gly  
 115 120 125  
 Thr Ile Ile Phe Met Tyr Phe Arg Pro Thr Ser Ser Tyr Ser Leu Asp  
 130 135 140  
 Tyr Asp Arg Val Val Ser Val Met Tyr Thr Val Val Ala Pro  
 145 150 155

&lt;210&gt; 2550

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Unknown (2564511-dir-0-6 conceptual translation of range 1-468)

&lt;400&gt;2550

Asn Pro Leu His Tyr Thr Thr Val Met Ser Lys Lys Val Cys Leu Leu  
 1 5 10 15  
 Leu Val Gly Met Leu Trp Leu Trp Ala Val Leu Tyr Ser Leu Met His  
 20 25 30  
 Ile Val Leu Ile Ser Arg Leu Ser Phe Cys Gly Ser Asn Gln Ile Asn  
 35 40 45  
 His Phe Val Cys Asp Thr Val Pro Leu Phe Lys Leu Ser Cys Ser Asp  
 50 55 60  
 Thr Ser Thr Asn Gln Leu Val Ile Phe Thr Val Gly Ser Leu Ile Val  
 65 70 75 80  
 Met Val Pro Phe Leu Ile Val Leu Ile Ser Tyr Ala Arg Ile Val Phe  
 85 90 95  
 Ala Ile Leu Lys Ile Ser Ser Thr Asp Gly Arg Arg Lys Thr Phe Ser  
 100 105 110  
 Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr Phe Gly Thr Ile  
 115 120 125  
 Met Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Leu Thr Lys Asp  
 130 135 140  
 Arg Val Ala Ser Val Met Tyr Thr Val Leu Ala Pro  
 145 150 155

&lt;210&gt; 2551

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (2564513-dir-0-6 conceptual translation of range 1-474)

&lt;400&gt;2551

Ile Cys Asp Pro Leu Arg Tyr Thr Val Val Met Ser Lys Arg Ile Cys  
 1 5 10 15  
 Leu Gln Met Val Ala Gly Ser Trp Val Leu Val Ser Leu His Ser Leu  
 20 25 30  
 Leu His Thr Val Leu Thr Ala Arg Leu Ser Phe Cys Gly Arg Asn Leu  
 35 40 45  
 Ile Arg His Phe Phe Cys Glu Met Ser Pro Leu Phe Ala Leu Ser Cys  
 50 55 60  
 Ser Asp Thr Thr Thr Asn Glu Leu Val Ile Phe Thr Glu Gly Ser Phe  
 65 70 75 80  
 Ser Leu Ala Leu Pro Phe Leu Leu Ile Leu Phe Ser Tyr Leu Arg Ile  
 85 90 95  
 Leu Ser Thr Val Leu Arg Ile Arg Ser Val Asp Gly Lys Cys Arg Ala  
 100 105 110  
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ala Leu Phe Tyr Gly

115	120	125
Thr Leu Phe Ser Val Tyr	Phe Arg Pro Ser Ser Ser	His Ser Leu Asp
130	135	140
Asn Asp Arg Val Val Ser	Ile Met Tyr Thr Ala Il	Thr Pro
145	150	155

&lt;210&gt; 2552

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (4808260-rev-1059-13 conceptual translation of range 106061-107005)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2552

Cys Leu Leu Ser Glu Val Met Leu Asn Thr Thr Ser Val Thr Glu Phe	
1 5 10 15	
Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe	
20 25 30	
Val Val Phe Leu Thr Ile Tyr Phe Ile Ser Val Thr Gly Asn Gly Ala	
35 40 45	
Val Leu Met Ile Val Ile Ser Asp Pro Arg Leu His Ser Leu Met Tyr	
50 55 60	
Phe Phe Leu Gly Asn Leu Ser Tyr Leu Asp Ile Cys Tyr Ser Thr Val	
65 70 75 80	
Thr Leu Pro Lys Met Leu Gln Asn Phe Leu Ser Thr His Lys Ala Ile	
85 90 95	
Ser Phe Leu Gly Cys Ile Ser Gln Leu His Phe Phe His Phe Leu Gly	
100 105 110	
Ser Thr Glu Ser Met Leu Phe Ala Val Met Ala Phe Asp Leu Ser Val	
115 120 125	
Ala Ile Cys Lys Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Gln Leu	
130 135 140	
Cys Thr Gln Met Ala Ile Thr Ile Trp Val Ile Gly Phe Phe His Ala	
145 150 155 160	
Leu Leu His Ser Val Met Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn	
165 170 175	
Arg Ile His His Phe Leu Cys Asp Ile Lys Pro Leu Leu Lys Leu Ala	
180 185 190	
Cys Gly Asn Thr Glu Leu Asn Gln Trp Leu Leu Ser Thr Val Thr Gly	
195 200 205	
Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu Leu Ser Tyr Phe Tyr	
210 215 220	
Ile Ile Thr Tyr Leu Phe Phe Lys Thr Arg Ser Cys Ser Met Leu Cys	
225 230 235 240	
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Ile Leu Phe	
245 250 255	
Tyr Ala Pro Val Leu Phe Thr Tyr Ile His Pro Ala Leu Glu Ser Phe	
260 265 270	
Met Asp Gln Asp Arg Ile Val Ala Ile Met Tyr Thr Val Val Thr Pro	
275 280 285	
Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly	
290 295 300	
Ala Leu Gly Arg Val Ile Arg Arg Leu Xaa Phe	
305 310 315	

&lt;210&gt; 2553

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Unknown (1617234-dir-0-6 conceptual translation of range 1-486)

&lt;400&gt;2553

```

Asn Ala Ile Cys Asn Pro Leu Leu Tyr Asn Thr Ile Met Asn Lys Arg
 1              5              10              15
Thr Cys Val Ile Leu Ile Val Gly Ser Trp Leu Ile Ala Ser Ile Asn
      20              25              30
Ser Leu Ile His Thr Ile Leu Thr Phe Met Leu Pro Phe Cys Gly Ser
      35              40              45
Asn Ala Ile Asp Ser Phe Phe Cys Asp Met Pro Pro Leu Leu Lys Leu
      50              55              60
Ala Cys Thr Asp Thr Leu Val Asn Gln Ile Val Ile Phe Val Thr Gly
65              70              75              80
Ser Cys Ile Ile Ala Gly Pro Phe Met Leu Thr Val Phe Ser Tyr Val
      85              90              95
Gln Ile Ile Ser Thr Ile Val Ser Ile Arg Ser Ser Ser Arg Lys Lys
      100             105             110
Lys Ala Phe Ser Thr Cys Thr Ser His Ile Thr Ala Val Val Ile Phe
      115             120             125
Tyr Val Pro Ser Ile Cys Ile Tyr Phe Arg Pro Lys Ser Asn Gln Ala
      130             135             140
Met Ile Gln Asp Lys Met Ala Thr Val Ile Cys Ala Val Ile Thr Pro
145              150              155              160
Leu Leu

```

&lt;210&gt; 2554

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Unknown (4877310-dir-0-6 conceptual translation of range 2-481)

&lt;400&gt;2554

```

Ala Ala Ile Cys Lys Pro Leu His Tyr Asn Thr Ile Met Asn Lys Arg
 1              5              10              15
Leu Cys Val Cys Leu Ala Leu Gly Cys Trp Gly Val Gly Val Ile Asn
      20              25              30
Ser Thr Ile His Val Phe Phe Thr Phe Gln Leu Pro Phe Cys Arg Ser
      35              40              45
Arg His Ile Asn His Phe Phe Cys Glu Val Pro Pro Phe Phe Arg Leu
      50              55              60
Ser Cys Gln Asp Thr Trp Phe Asn Glu Leu Ala Met Tyr Ile Ser Ala
65              70              75              80
Cys Ile Ile Ala Ile Cys Ala Phe Phe Leu Thr Leu Ile Ser Tyr Ile
      85              90              95
Tyr Ile Ile Ser Ser Ile Ala Lys Ile Arg Ala Pro Gln Gly Arg Tyr
      100             105             110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ala Val Tyr
      115             120             125
Tyr Gly Thr Ile Met Phe Ile Tyr Leu His Pro His Ser Ala Tyr Ser
      130             135             140
Pro Glu Met Gly Lys Ile Val Ser Ile Ile Tyr Thr Ser Val Thr Pro
145              150              155              160

```

&lt;210&gt; 2555

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Unknown (4877337-dir-0-6 conceptual translation of range 2-481)

&lt;400&gt;2555

```

Ile Cys Ser Pro Leu Leu Tyr Phe Thr Lys Met Ser Thr Arg Val Tyr

```

```

1           5           10           15
Val Gln Leu Leu Thr Val Ala Tyr Val Gly Gly Phe Leu Asn Ala Cys
      20           25           30
Ser Phe Thr Ile Cys Phe Tyr Tyr Leu Leu Leu Cys Gly Pro Asn Arg
      35           40           45
Val Asn His Phe Phe Cys Asp Phe Ala Pro Leu Val Glu Phe Ser Cys
      50           55           60
Ser Asp Ile Ser Ile Pro Ala Val Val Pro Ser Phe Thr Ala Gly Ser
      65           70           75           80
Ile Ile Val Val Thr Val Ile Val Ile Ala Ile Ser Tyr Ile Tyr Ile
      85           90           95
Leu Ile Thr Ile Leu Lys Met Arg Ser Thr Glu Gly His His Lys Ala
      100          105          110
Phe Ser Thr Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly
      115          120          125
Thr Ile Thr Leu Ile Tyr Val Met Pro Lys Ser Ser Phe Ser Thr Asp
      130          135          140
Gln Asn Lys Val Val Cys Val Phe Tyr Thr Val Val Ile Pro Met Leu
      145          150          155          160

```

&lt;210&gt; 2556

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (4680263-dir-1-12 conceptual translation of range 259-1203)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2556

```

Glu Met Glu Pro Gly Asn Tyr Thr Val Val Thr Glu Phe Ile Leu Leu
1           5           10           15
Gly Leu Thr Asp Asp Ile Thr Val Ser Val Ile Leu Phe Val Met Phe
      20           25           30
Leu Ile Val Tyr Ser Val Thr Leu Met Gly Asn Leu Asn Ile Ile Val
      35           40           45
Leu Ile Arg Thr Ser Pro Gln Leu His Thr Pro Met Tyr Leu Phe Leu
      50           55           60
Ser His Leu Ala Phe Leu Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro
      65           70           75           80
Ile Met Leu Arg Gly Phe Leu Arg Lys Gly Thr Phe Ile Pro Val Ala
      85           90           95
Gly Cys Val Ala Gln Leu Cys Ile Val Val Ala Phe Gly Thr Ser Glu
      100          105          110
Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115          120          125
Ser Pro Leu Leu Tyr Ser Thr Gln Met Ser Ser Thr Val Cys Ile Leu
      130          135          140
Leu Val Gly Thr Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Ile Phe
      145          150          155          160
Thr Gly Cys Ser Leu Asn Leu Ser Phe Cys Gly Pro Asn Lys Ile Asn
      165          170          175
His Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ser Cys Ser His
      180          185          190
Asp Phe Ser Phe Glu Val Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile
      195          200          205
Val Val Thr Val Phe Ile Ile Ala Leu Ser Tyr Val Tyr Ile Leu Val
      210          215          220
Ser Ile Leu Lys Met Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser
      225          230          235          240

```

```
<210> 2557
<211> 312
<212> PRT
<213> Unknown (1246533-dir-0-11 conceptual translation of range 1-936)
```

```
<210> 2558
<211> 313
<212> PRT
```



<213> Unknown (p28-dir-0-11 conceptual translation of range 1-939)

<400>2558

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
      20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
      35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
      65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
      85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
      100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
      130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
      145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
      165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
      180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
      195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
      210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
      225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
      245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
      260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
      290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
      305          310

```

<210> 2559

<211> 117

<212> PRT

<213> Unknown (2695895-dir-0-5 conceptual translation of range 2-351)

<220>

<221> VARIANT

<222> (1)...(117)

<223> Xaa = Any Amino Acid

<400>2559

```

Asp Leu Cys Tyr Ser Thr Val Ile Ala Pro Lys Ala Leu Ala Ile Phe
 1           5           10           15
Leu Ser Lys Asp Lys Lys Ile Ser Tyr Asn Gly His Ala Ala Xaa Phe
      20           25           30
Tyr Phe Leu Cys Cys Val Gly Thr Glu Gly Leu Leu Leu Ala Val Met
      35           40           45

```

Ala Tyr Asp His Phe Ser Ala Phe Cys Ser Pro Phe Leu Tyr Pro Val  
 50 55 60  
 Arg Met Ser Gln Gln Val Cys Val His Leu Val Ile Gly Ser Tyr Ile  
 65 70 75 80  
 Cys Gly Gly Ile Asn Ser Met Val Gln Thr Gly Phe Thr Phe Ser Leu  
 85 90 95  
 Asn Phe Cys Gly Glu Asn Xaa Leu Asp His Phe Phe Cys Asp Val Pro  
 100 105 110  
 Ala Leu Ile Lys Ile  
 115

&lt;210&gt; 2560

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921661-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2560

Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Ala  
 1 5 10 15  
 Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly Cys Leu Leu  
 20 25 30  
 Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala Phe Leu Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His Pro Leu His  
 50 55 60  
 Tyr Ile Leu Ile Met Ser Pro Gly Leu Arg Ile Phe Leu Val Ser Ala  
 65 70 75 80  
 Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr Leu Leu Met  
 85 90 95  
 Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His Phe Leu Cys  
 100 105 110  
 Asp Ile Asn Pro Leu Leu Gly Leu Ser Cys Thr Asp Pro Phe Thr Asn  
 115 120 125  
 Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu Ile Cys Val  
 130 135 140  
 Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr Ile Leu Lys  
 145 150 155 160  
 Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser  
 165 170 175  
 His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe Cys Val Asp  
 180 185 190  
 Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr Val Ala Ser  
 195 200 205  
 Val Met Tyr Thr Val Val Thr Pro  
 210 215

&lt;210&gt; 2561

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p19-dir-0-11 conceptual translation of range 1-939)

&lt;400&gt;2561

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly  
 1 5 10 15  
 Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu  
 20 25 30  
 Phe Met Tyr Leu Val Met Val Ala Gly Asn Leu Leu Ile Ile Leu Val  
 35 40 45  
 Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys

65					70					75				80
Met	Leu	Ala	Asn	Ile	Gln	Ile	Gln	Ser	Gln	Ala	Ile	Ser	Tyr	Ser Gly
				85					90					95
Cys	Leu	Leu	Gln	Leu	Tyr	Phe	Phe	Met	Leu	Phe	Val	Met	Leu	Glu Ala
			100					105					110	
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Ile	Cys His
			115				120					125		
Pro	Leu	His	Tyr	Ile	Leu	Ile	Met	Ser	Pro	Gly	Leu	Cys	Val	Phe Leu
			130				135					140		
Val	Ser	Ala	Ser	Trp	Ile	Met	Asn	Ala	Leu	Tyr	Ser	Leu	Leu	His Thr
					150					155				160
Leu	Leu	Met	Asn	Ser	Leu	Ser	Phe	Cys	Ala	Asn	His	Glu	Ile	Pro His
			165					170						175
Phe	Phe	Cys	Asp	Ile	Asp	Pro	Leu	Leu	Ser	Leu	Ser	Cys	Ala	Asp Pro
			180					185					190	
Phe	Thr	Asn	Glu	Leu	Val	Ile	Phe	Ile	Thr	Gly	Gly	Leu	Thr	Gly Leu
			195				200					205		
Ile	Cys	Val	Leu	Cys	Leu	Ile	Ile	Ser	Tyr	Thr	Asn	Val	Phe	Ser Thr
			210				215				220			
Ile	Leu	Lys	Ile	Pro	Ser	Ala	Gln	Gly	Lys	Arg	Lys	Ala	Phe	Ser Thr
					230					235				240
Cys	Ser	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Cys	Gly	Thr	Ser Phe
			245					250						255
Cys	Val	Tyr	Phe	Ser	Pro	Pro	Ser	Thr	Arg	Ser	Ala	Gln	Lys	Asp Thr
			260					265					270	
Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro Phe
			275				280					285		
Ile	Tyr	Ser	Leu	Arg	Asn	Gln	Glu	Ile	Lys	Ser	Ser	Leu	Arg	Lys Leu
			290			295					300			
Ile	Trp	Val	Arg	Lys	Ile	His	Ser	Pro						
305					310									

&lt;210&gt; 2562

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p40-dir-0-11 conceptual translation of range 1-938)

&lt;400&gt;2562

Met	Glu	Gly	Lys	Asn	Leu	Thr	Ser	Ile	Ser	Glu	Phe	Phe	Leu	Leu Gly
1				5					10					15
Phe	Ser	Glu	Gln	Leu	Glu	Glu	Gln	Lys	Ala	Leu	Leu	Val	Ser	Phe Leu
			20					25					30	
Phe	Met	Tyr	Leu	Val	Thr	Val	Ala	Gly	Asn	Leu	Leu	Ile	Ile	Leu Val
			35				40					45		
Ile	Ile	Thr	Asp	Thr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu Ala
			50			55					60			
Asn	Leu	Ser	Leu	Ala	Asp	Ala	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro Lys
					70				75					80
Met	Leu	Ala	Asn	Ile	Gln	Ile	Gln	Ser	Gln	Ala	Ile	Ser	Tyr	Ser Gly
			85					90					95	
Cys	Leu	Leu	Gln	Leu	Tyr	Phe	Phe	Met	Leu	Phe	Val	Met	Leu	Glu Ala
			100					105					110	
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Ile	Cys His
			115				120					125		
Pro	Leu	His	Tyr	Ile	Leu	Ile	Met	Ser	Pro	Gly	Leu	Cys	Val	Phe Leu
			130				135					140		
Val	Ser	Ala	Ser	Trp	Ile	Met	Asp	Ala	Leu	His	Ser	Leu	Leu	His Thr
					150				155					160
Leu	Leu	Met	Asn	Ser	Leu	Ser	Phe	Tyr	Ala	Asn	His	Glu	Thr	Pro His
			165					170						175
Phe	Phe	Cys	Asp	Ile	Asp	Pro	Leu	Leu	Ser	Leu	Ser	Cys	Thr	Asp Pro

```
<210> 2563
<211> 161
<212> PRT
<213> Unknown (293757-dir-0-6 conceptual translation of range 2-484)
```

```
<210> 2564
<211> 313
<212> PRT
<213> Unknown (p39-dir-0-11 conceptual translation of range 1-939)
```

1558

Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly  
 85 90 95  
 Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Val Phe Leu  
 130 135 140  
 Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr  
 145 150 155 160  
 Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Ile Asp Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro  
 180 185 190  
 Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu  
 195 200 205  
 Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Ile Phe Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe  
 245 250 255  
 Cys Val Tyr Phe Ile Pro Pro Ser Thr Arg Ser Ala Gln Lys Asp Thr  
 260 265 270  
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu  
 290 295 300  
 Ile Trp Val Arg Glu Ile His Ser Pro  
 305 310

&lt;210&gt; 2565

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (3738097-rev-723-12 conceptual translation of range 72448-73392)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(315)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2565

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly  
 1 5 10 15  
 Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe Phe Phe Leu Phe Leu  
 20 25 30  
 Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu  
 35 40 45  
 Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe  
 50 55 60  
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys  
 65 70 75 80  
 Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly  
 85 90 95  
 Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys  
 100 105 110  
 Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu  
 130 135 140  
 Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr  
 145 150 155 160  
 Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His  
 165 170 175  
 Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr  
 180 185 190  
 Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr  
 195 200 205  
 Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser  
 210 215 220  
 Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala  
 245 250 255  
 Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val  
 260 265 270  
 Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile  
 275 280 285  
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu  
 290 295 300  
 Ile Lys Ile Gln Arg Arg Asn Ile Phe Xaa Leu  
 305 310 315

&lt;210&gt; 2566

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (p41-dir-0-11 conceptual translation of range 1-938)

&lt;400&gt;2566

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly  
 1 5 10 15  
 Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu  
 20 25 30  
 Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val  
 35 40 45  
 Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala  
 50 55 60  
 Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys  
 65 70 75 80  
 Met Leu Ala Asn Ile Arg Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly  
 85 90 95  
 Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala  
 100 105 110  
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Val Phe Leu  
 130 135 140  
 Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr  
 145 150 155 160  
 Leu Leu Met Asn Ser Leu Ser Phe Cys Thr Asn Arg Glu Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro  
 180 185 190  
 Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Val Ala Gly Leu  
 195 200 205  
 Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Met Asn Val Phe Ser Thr  
 210 215 220  
 Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Ser Ser Phe Ser Thr  
 225 230 235 240

Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe  
                                   245                                  250                                  255  
 Cys Val Tyr Val Ser Pro Pro Ser Thr Leu Ser Ala Gln Lys Asp Thr  
                                   260                                  265                                  270  
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Phe  
                                   275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Ile  
                                   290                                  295                                  300  
 Ile Trp Val Arg Lys Ile His Ser Pro  
 305                                  310

<210> 2567

<211> 315

<212> PRT

<213> Unknown (2317703-dir-0-13 conceptual translation of range 211-1155)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2567

Met Ala Thr Gly Asn Tyr Cys Val Phe Pro Glu Phe Ile Leu Thr Gly  
   1                                  5                                  10                                  15  
 Leu Ser Lys Lys Ser Glu Leu Gln Met Pro Leu Phe Val Leu Phe Leu  
                                   20                                  25                                  30  
 Gly Ile Tyr Ile Val Thr Val Val Gly Asn Leu Gly Met Ile Thr Leu  
                                   35                                  40                                  45  
 Ile Arg Leu Ser Ser Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser  
                                   50                                  55                                  60  
 Ser Leu Ser Phe Ile Asp Leu Cys His Ser Thr Val Ile Thr Pro Lys  
   65                                  70                                  75                                  80  
 Met Leu Val Asn Phe Val Ala Glu Lys Asn Ile Ile Ser Tyr Thr Gly  
                                   85                                  90                                  95  
 Cys Met Thr Gln Leu Phe Phe Phe Leu Ile Phe Ala Ile Ala Glu Cys  
                                   100                                  105                                  110  
 His Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
                                   115                                  120                                  125  
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Tyr Gln Ser Tyr Ile Ser Met  
                                   130                                  135                                  140  
 Ile Ser Gly Val Tyr Ile Ile Gly Val Val Cys Ala Ser Ala His Thr  
   145                                  150                                  155                                  160  
 Gly Phe Met Ile Arg Ser Gln Phe Cys Asn Leu Asp Val Ile Asn His  
                                   165                                  170                                  175  
 Tyr Phe Cys Asp Leu Leu Pro Leu Leu Glu Leu Ala His Ser Ser Thr  
                                   180                                  185                                  190  
 Tyr Val Asn Glu Leu Val Ile Leu Ile Cys Gly Thr Cys Asn Ile Val  
                                   195                                  200                                  205  
 Val Pro Thr Leu Thr Ile Leu Thr Ser Tyr Ile Phe Ile Ile Ala Thr  
                                   210                                  215                                  220  
 Ile Leu His Ile Arg Ser Thr Glu Gly Arg Tyr Lys Ala Phe Ser Thr  
   225                                  230                                  235                                  240  
 Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Ala Ala  
                                   245                                  250                                  255  
 Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys  
                                   260                                  265                                  270  
 Val Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Leu Asn Pro Leu  
                                   275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Ser Thr Ala Leu Lys Lys Ile  
                                   290                                  295                                  300  
 Leu Glu Arg Lys Ser Phe Val Xaa Thr Glu Val

305

310

315

&lt;210&gt; 2568

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Unknown (888-dir-0-5 conceptual translation of range 2-343)

&lt;400&gt;2568

```

Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Ser Asn Thr Leu Cys
 1           5           10           15
Ile Arg Leu Leu Val Leu Ser Leu Leu Gly Gly Leu Leu His Ala Ile
          20           25           30
Ile His Ser Ser Phe Leu Phe Arg Leu Thr Phe Cys Asp Ser Ile Ile
          35           40           45
Val His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Thr Cys
          50           55           60
Thr Asp Pro Ser Ile Asn Tyr Leu Ile Val Phe Ile Phe Ala Gly Ser
65           70           75           80
Ile Gln Met Phe Thr Ile Leu Ile Val Leu Val Ser Tyr Thr Leu Val
          85           90           95
Leu Phe Thr Ile Leu Arg Lys Lys Ser Leu Gln Gly Ile Lys Lys Ala
          100          105          110
Phe Ser

```

&lt;210&gt; 2569

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Unknown (1514485-dir-0-6 conceptual translation of range 2-478)

&lt;400&gt;2569

```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Thr Ile Ser Met Pro Lys Ser
 1           5           10           15
Leu Cys Met Lys Leu Val Ala Gly Ser Tyr Leu Gly Gly Val Leu Asn
          20           25           30
Ser Leu Thr Gln Thr Cys Cys Leu Leu Pro Leu Pro Phe Cys Gly Pro
          35           40           45
Asn Val Ile Asn His Tyr Phe Cys Asp Thr Asn Pro Leu Leu Lys Leu
          50           55           60
Thr Cys Ser Asp Gly Arg Leu Asn Glu Leu Leu Val Thr Phe Asn
65           70           75           80
Gly Thr Ile Ser Met Thr Val Leu Leu Ile Val Ile Ser Tyr Val
          85           90           95
Tyr Ile Leu Val Ser Ile Leu Ser Ile Arg Ser Ala Arg Gly Arg His
          100          105          110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Leu Thr Val Thr Leu Phe
          115          120          125
Tyr Val Pro Ala Gly Leu Ser His Met Gln Pro Gly Ser Lys Tyr Ser
          130          135          140
Leu Asp Met Glu Lys Val Thr Ala Val Phe Tyr Thr Leu Leu Val
145          150          155

```

&lt;210&gt; 2570

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Unknown (1514487-dir-0-5 conceptual translation of range 2-394)

&lt;400&gt;2570

```

Val Ala Ile Cys Ser Pro Leu Leu Tyr Ser Thr Val Met Thr Lys Arg
 1           5           10           15
Val Cys Met Gln Leu Val Val Gly Ser Tyr Met Gly Gly Leu Leu Asn

```



```

                20                25                30
Ser Leu Thr His Thr Cys Gly Leu Leu Gly Leu Pro Phe Cys Gly Pro
   35                40                45
Asn Val Ile Asn His Tyr Phe Cys Asp Ile Pro Pro Leu Leu Gln Leu
   50                55                60
Ala Cys Ser Asp Thr His Arg Asn Glu Thr Leu Leu Leu Ala Phe Ser
65                70                75                80
Ala Val Ile Ala Leu Phe Thr Leu Phe Val Ile Thr Ala Ser Tyr Met
   85                90                95
Leu Ile Leu Ser Val Ile Leu Lys Ile Gln Ser Asp Asp Gly Arg Lys
   100                105                110
Lys Thr Phe His Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
   115                120                125
Phe Gly Ser
   130

```

&lt;210&gt; 2571

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Unknown (32508-dir-0-5 conceptual translation of range 2-343)

&lt;400&gt;2571

```

Ile Val Ser Pro Leu Leu Tyr Thr Val Ala Met Ser Asp Arg Lys Cys
1                5                10                15
Val Glu Leu Val Thr Gly Ser Trp Ile Gly Gly Ile Val Asn Thr Leu
   20                25                30
Ile His Thr Ile Ser Leu Arg Arg Leu Ser Phe Cys Arg Leu Asn Ala
   35                40                45
Val Ser His Phe Phe Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys
   50                55                60
Ser Asp Thr Ser Met Asn Glu Leu Leu Leu Leu Thr Phe Ser Gly Val
65                70                75                80
Ile Ala Met Ala Thr Phe Leu Thr Val Ile Ile Ser Tyr Ile Phe Ile
   85                90                95
Ala Phe Ala Ser Leu Arg Ile His Ser Ala Ser Gly Arg Gln Gln Ala
   100                105                110
Phe Ser

```

&lt;210&gt; 2572

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (p42-dir-0-11 conceptual translation of range 1-945)

&lt;400&gt;2572

```

Met Glu Ser Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
1                5                10                15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Ser Val Val Phe Val
   20                25                30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Thr Gly Gly Asn Pro Ser Ile
   35                40                45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Thr Pro Met Tyr Phe
   50                55                60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
65                70                75                80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Cys Ile Ile Ser
   85                90                95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
   100                105                110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Phe Leu Ala
   115                120                125

```

```

Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
 130                      135                      140
Gly Met Leu Val Ala Val Ser Trp Thr Cys Ala Phe Thr Asn Ala Leu
145                      150                      155                      160
Thr His Thr Ile Ala Leu Thr Thr Leu Asn Phe Cys Gly Pro Ser Val
                      165                      170                      175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
                      180                      185                      190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
                      195                      200                      205
Met Ala Val Val Pro Leu Val Leu Ile Ser Val Ser Tyr Ala His Val
                      210                      215                      220
Val Ala Ala Val Leu Gln Ile His Ser Ala Glu Gly Arg Lys Lys Ala
225                      230                      235                      240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
                      245                      250                      255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
                      260                      265                      270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
                      275                      280                      285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
                      290                      295                      300
Trp Gln Leu Leu Val Gly Lys Arg Ser Leu Thr
305                      310                      315

```

&lt;210&gt; 2573

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (p176-dir-0-11 conceptual translation of range 1-945)

&lt;400&gt;2573

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
 1                      5                      10                      15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val
                      20                      25                      30
Leu Phe Leu Phe Ala Tyr Leu Val Thr Val Gly Gly Asn Leu Ser Ile
                      35                      40                      45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ser Pro Met Tyr Phe
                      50                      55                      60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Ser Val Thr
65                      70                      75                      80
Val Pro Ser Met Leu Ser Arg Leu Leu Ser Arg Lys Arg Ala Val Pro
                      85                      90                      95
Cys Gly Ala Cys Leu Thr Gln Leu Phe Phe Phe His Leu Phe Val Gly
                      100                      105                      110
Val Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Phe Leu Ala
                      115                      120                      125
Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
                      130                      135                      140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145                      150                      155                      160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
                      165                      170                      175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
                      180                      185                      190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile
                      195                      200                      205
Met Ala Gly Thr Pro Met Ala Leu Ile Val Ile Ser Tyr Ile His Val
                      210                      215                      220
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
225                      230                      235                      240

```

Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Met Phe Tyr Gly  
                           245                          250                          255  
 Ser Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Thr Lys Leu Ser Asp  
                           260                          265                          270  
 Lys Asp Lys Ala Val Gly Ile Phe Asn Thr Val Ile Asn Pro Met Val  
                           275                          280                          285  
 Asn Pro Ile Ile Tyr Arg Phe Arg Asn Pro Glu Val Gln Ser Ala Ile  
                           290                          295                          300  
 Trp Arg Met Leu Thr Gly Arg Arg Ser Leu Ala  
 305                          310                          315

&lt;210&gt; 2574

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Unknown (1552397-dir-0-6 conceptual translation of range 1-486)

&lt;400&gt;2574

Val Ala Val Cys His Pro Leu Leu Tyr Val Phe His Met Ser Gln Lys  
 1                          5                          10                          15  
 His Cys Thr Phe Phe Val Ser Ala Ala Trp Ile Ile Gly Phe Leu Asp  
                           20                          25                          30  
 Pro Thr Ser Tyr Val Val Leu Ile Ser Lys Phe Ser Phe Cys Thr Ser  
                           35                          40                          45  
 Asn Ile Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Lys Leu  
                           50                          55                          60  
 Ser Cys Ser Asp Thr Phe Gln Ile Glu Val Leu Asn Tyr Val Glu Ser  
 65                          70                          75                          80  
 Ala Leu Val Thr Leu Asn Ser Phe Val Leu Thr Val Ile Ser Tyr Ile  
                           85                          90                          95  
 Phe Thr Ile Ser Ala Ile Leu Asn Ile Lys Ser Ala Glu Gly Arg His  
                           100                          105                          110  
 Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe  
                           115                          120                          125  
 Tyr Ser Thr Ile Ile Ser Leu Tyr Ile Arg Pro Ile Ser Thr Tyr Ala  
                           130                          135                          140  
 Pro Lys Gln Asp Gln Phe Phe Ala Leu Leu Tyr Ile Val Leu Ile Pro  
 145                          150                          155                          160  
 Leu Leu

&lt;210&gt; 2575

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Unknown (1552399-dir-0-6 conceptual translation of range 1-483)

&lt;400&gt;2575

Val Ala Ile Cys Tyr Pro Leu His Tyr Ala Leu Arg Met Ser Leu Lys  
 1                          5                          10                          15  
 His Cys Ala Lys Ile Ile Val Gly Val Trp Val Ala Gly Phe Leu Ala  
                           20                          25                          30  
 Pro Val Ile His Thr Val Leu Met Thr Asn Leu Ser Phe Cys Ser Ser  
                           35                          40                          45  
 Asn His Ile Asn His Phe Leu Cys Asp Leu Thr Pro Val Leu Lys Ile  
                           50                          55                          60  
 Ser Cys Ser Asp Thr Ser Leu Ile Glu Met Ile Thr Tyr Ile Asp Gly  
 65                          70                          75                          80  
 Val Ile Val Ala Phe Ser Thr Phe Thr Ile Thr Ser Val Ser Tyr Val  
                           85                          90                          95  
 Phe Ile Leu Phe Lys Ile Leu Lys Ile His Ser Ser Gln Gly Lys Lys  
                           100                          105                          110  
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe

```
<210> 2576
<211> 160
<212> PRT
<213> Unknown (4877302-dir-0-6 conceptual translation of range 2-481)
```

```
<210> 2577
<211> 153
<212> PRT
<213> Unknown (2564501-dir-0-6 conceptual translation of range 1-459)
```

1566

&lt;210&gt; 2578

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Unknown (2564499-dir-0-6 conceptual translation of range 1-456)

&lt;400&gt;2578

```

Asn Pro Leu Arg Tyr Thr Thr Ile Met Ser Arg Lys Val Cys Ser Leu
 1          5          10          15
Leu Val Leu Ala Cys Trp Val Gly Gly Ala Val His Ser Thr Ala Gln
      20          25          30
Val Leu Leu Val Met Thr Leu Pro Phe Cys Gly Pro Asn Glu Val Gly
      35          40          45
His Phe Phe Cys Asp Ile Pro Pro Leu Phe Pro Leu Val Cys Thr Asp
      50          55          60
Thr Phe Leu Ser Gly Val Leu Ile Met Ser Asn Ser Gly Leu Ile Ser
      65          70          75          80
Leu Ala Cys Phe Leu Thr Leu Ile Ile Ser Tyr Thr Leu Ile Leu Leu
      85          90          95
Ala Val Arg Arg Cys Ser Ala Glu Gly Lys Ser Lys Ala Leu Ser Thr
      100          105          110
Cys Gly Thr His Leu Thr Val Val Thr Ile Ala Phe Gly Pro Ser Ile
      115          120          125
Phe Ile Tyr Met Lys Pro Met Asn Leu Gln Val Asp Lys Ile Val Ala
      130          135          140
Leu Phe Phe Val Ile Ile Thr Pro
145          150

```

&lt;210&gt; 2579

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg449-dir-0-7 conceptual translation of range 1-616)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(205)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2579

```

Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr Asp
 1          5          10          15
Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala Gln
      20          25          30
Ile Phe Leu His Phe Cys Gly Ile Pro Trp Ile Phe Leu Leu Pro Leu
      35          40          45
Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr Thr
      50          55          60
Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe Trp
      65          70          75          80
Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val Gln
      85          90          95
Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp Leu
      100          105          110
Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly Val
      115          120          125
Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile Leu
      130          135          140
Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser Ala
      145          150          155          160
Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val Phe
      165          170          175

```

Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr Lys  
                   180                  185                  190  
 Asp Lys Leu Val Ala Val Phe Tyr Val Ile Ile Thr Pro  
                   195                  200                  205

<210> 2580

<211> 154

<212> PRT

<213> Unknown (902708-dir-0-6 conceptual translation of range 2-463)

<400>2580

Ile Cys Lys Pro Leu His Tyr Met Thr Ile Met Ser Arg Pro Val Cys  
   1                  5                  10                  15  
 Ile Phe Leu Val Gly Ala Ala Val Ile Leu Gly Phe Ile His Gly Ala  
                   20                  25                  30  
 Ile Gln Thr Leu Phe Met Ala Gln Leu Pro Phe Cys Gly Pro Asn Ile  
                   35                  40                  45  
 Ile Asn His Phe Met Cys Asp Leu Ile Pro Leu Leu Glu Leu Ala Cys  
                   50                  55                  60  
 Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser Gly Ser  
   65                  70                  75                  80  
 Leu Cys Leu Leu Thr Phe Ser Met Leu Val Val Ser Tyr Val Val Ile  
                   85                  90                  95  
 Pro Arg Ser Leu Arg Asn His Ser Ser Glu Gly Arg Arg Lys Ala Leu  
                   100                  105                  110  
 Ser Thr Cys Ala Ser His Val Thr Val Val Val Leu Phe Leu Val Pro  
                   115                  120                  125  
 Cys Ser Tyr Leu Tyr Leu Arg Pro Met Thr Ser Phe Pro Thr Asn Lys  
                   130                  135                  140  
 Ala Val Thr Val Phe Cys Thr Leu Val Thr  
   145                  150

<210> 2581

<211> 114

<212> PRT

<213> Unknown (32513-dir-0-5 conceptual translation of range 2-343)

<400>2581

Ile Cys Tyr Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Arg Ile Cys  
   1                  5                  10                  15  
 Val Ala Leu Ala Val Gly Thr Trp Leu Leu Gly Cys Ile His Ser Ser  
                   20                  25                  30  
 Ile Leu Thr Ser Leu Thr Phe Thr Leu Pro Tyr Cys Gly Pro Asn Glu  
                   35                  40                  45  
 Val Asp His Phe Phe Cys Asp Ile Pro Ala Leu Leu Pro Leu Ala Cys  
                   50                  55                  60  
 Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Thr Ser Val Gly Leu  
   65                  70                  75                  80  
 Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr Thr Arg Ile  
                   85                  90                  95  
 Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg Arg Arg Ala  
                   100                  105                  110  
 Phe Ser

<210> 2582

<211> 114

<212> PRT

<213> Unknown (32516-dir-0-5 conceptual translation of range 2-343)

<400>2582

```

Ile Cys His Pro Leu Asn Tyr Pro Val Ile Met Asn Arg Gly Val Phe
 1          5          10          15
Met Lys Leu Val Ile Phe Ser Trp Ile Ser Gly Ile Met Val Ala Thr
          20          25          30
Val Gln Thr Thr Trp Val Phe Ser Phe Pro Phe Cys Gly Pro Asn Glu
          35          40          45
Ile Asn His Leu Phe Cys Glu Thr Pro Pro Val Leu Glu Leu Val Cys
          50          55          60
Ala Asp Thr Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Ile Leu
65          70          75          80
Ile Val Met Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val
          85          90          95
Leu Phe Ala Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala
          100          105          110
Phe Ser

```

&lt;210&gt; 2583

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Unknown (2252615-dir-0-7 conceptual translation of range 1-586)

&lt;400&gt;2583

```

Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr
 1          5          10          15
Ser Cys Val Arg Pro Gln Met Leu Val His Leu Trp Gly Pro His Lys
          20          25          30
Thr Ile Ser Phe Leu Gly Cys Ala Val Gln Leu Phe Ile Phe Leu Leu
          35          40          45
Leu Gly Thr Thr Glu Cys Val Leu Leu Thr Val Met Ala Phe Asp Arg
          50          55          60
Tyr Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Met His Pro
65          70          75          80
Arg Leu Cys Arg Gln Leu Ala Ala Val Ala Trp Val Met Gly Leu Val
          85          90          95
Gln Ser Ile Val Gln Thr Pro Pro Thr Leu Arg Leu Pro Phe Cys Pro
          100          105          110
His Arg Gln Ile Asp Asp Phe Val Cys Gln Val Pro Ser Leu Ile Arg
          115          120          125
Leu Ser Cys Gly Asp Thr Thr Phe Asn Gly Ile Gln Leu Ala Val Ser
          130          135          140
Ser Val Val Phe Leu Val Val Pro Leu Ala Leu Ile Leu Ile Ser Tyr
145          150          155          160
Gly Ala Ile Ala Arg Ala Val Leu Arg Ile Ser Ser Ala Thr Ala Trp
          165          170          175
Arg Lys Ala Leu Gly Thr Cys Ser Ser His Leu Ala Val Val Thr Leu
          180          185          190
Phe Tyr Ser
          195

```

&lt;210&gt; 2584

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Unknown (3328023-dir-0-5 conceptual translation of range 1-318)

&lt;400&gt;2584

```

Thr Thr Glu Cys Val Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val
 1          5          10          15
Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Met His Pro Arg Leu
          20          25          30
Cys Arg Gln Leu Ala Ala Val Ala Trp Val Met Gly Leu Val Gln Ser

```

```

      35              40              45
Ile Val Gln Thr Pro Pro Thr Leu Arg Leu Pro Phe Cys Pro His Arg
  50              55              60
Arg Val Asp Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu Ser
  65              70              75              80
Cys Gly Asp Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Val
      85              90              95
Phe Ile Leu Val Val Pro Leu Ser Leu Ile
      100              105

```

&lt;210&gt; 2585

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Unknown (2828696-dir-0-7 conceptual translation of range 1-582)

&lt;400&gt;2585

```

Tyr Phe Phe Leu Ser Asp Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr
  1              5              10              15
Ser Cys Val Pro Gln Met Leu Val Asn Leu Trp Gly Pro Lys Lys Thr
      20              25              30
Ile Ser Phe Leu Gly Cys Ser Val Gln Leu Phe Ile Phe Leu Ser Leu
      35              40              45
Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr
      50              55              60
Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg
      65              70              75              80
Leu Cys Trp Gln Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Gln
      85              90              95
Ser Ile Val Gln Lys Pro Ser Thr Leu His Leu Pro Phe Cys Pro His
      100              105              110
Gln Gln Ile Asp Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Gly Leu
      115              120              125
Ser Cys Gly Asp Thr Ser Tyr Asn Glu Ile Gln Leu Ala Val Ser Ser
      130              135              140
Val Ile Phe Val Val Val Pro Leu Ser Leu Ile Leu Ala Tyr Tyr Gly
      145              150              155              160
Ala Thr Ala Gln Ala Val Leu Arg Ile Asn Ser Ala Thr Ala Trp Arg
      165              170              175
Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe
      180              185              190
Tyr Ser

```

&lt;210&gt; 2586

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (4160199-rev-489-12 conceptual translation of range 49035-49987)

&lt;400&gt;2586

```

Gln Glu Gln Ala Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu
  1              5              10              15
Leu Gly Phe Ser Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val
      20              25              30
Val Phe Thr Ser Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile
      35              40              45
Leu Leu Ser Ala Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe
      50              55              60
Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val
      65              70              75              80
Pro Gln Met Leu Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe

```



```
<210> 2587
<211> 320
<212> PRT
<213> Unknown (1041044-dir-3-13 conceptual translation of range 488-1447)
```

Gln 1	Glu	Gln	Ala	Met 5	Asp	Asn	Gln	Ser	Ser 10	Thr	Pro	Gly	Phe	Leu 15	Leu
Leu	Gly	Phe	Ser	Glu	His	Pro	Gly	Leu	Gly 25	Arg	Thr	Leu	Phe 30	Val	Asp
Val	Ile	Thr	Ser	Tyr	Leu	Leu	Thr	Leu	Val	Gly	Asn	Thr	Leu 45	Ile	Ile
Leu	Leu	Ser	Ala	Leu	Asp	Thr	Lys	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe
Leu 65	Ser	Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Cys	Val 80
Pro	Gln	Met	Leu	Ala	Asn	Leu	Trp	Gly	Pro	Lys	Lys	Thr	Ile	Ser	Phe
Leu	Asp	Cys	Ser	Val	Gln	Ile	Phe	Ile	Phe	Leu	Ser	Leu	Gly	Thr	Thr
Glu	Cys	Ile	Leu	Met	Lys	Val	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Val
Cys	Gln	Pro	Leu	His	Tyr	Ala	Thr	Ile	Ile	His	Pro	Arg	Leu	Cys	Trp
Gln 145	Leu	Ala	Ser	Val	Ala	Trp	Val	Ile	Gly	Leu	Val	Gly	Ser	Val	Val 160
Gln	Thr	Pro	Ser	Thr	Leu	His	Leu	Pro	Phe	Cys	Pro	Asp	Arg	Gln	Val
Asp	Asp	Phe	Val	Cys	Glu	Val	Pro	Ala	Leu	Ile	Arg	Leu	Ser	Cys	Glu
Asp	Thr	Ser	Tyr	Asn	Glu	Ile	Gln	Val	Ala	Val	Ala	Ser	Val	Phe	Ile

195	200	205
Leu Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr		
210	215	220
Trp Ala Val Leu Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe		
225	230	235
Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser		
	245	250
Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg		
	260	265
Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn		
	275	280
Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg		
	290	295
Arg Leu Leu Gly Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala		
305	310	315
		320

&lt;210&gt; 2588

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (3093312-dir-1364-13 conceptual translation of range 136584-137530)

&lt;400&gt;2588

Val Ala Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu		
1	5	10
Leu Gly Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Val Ile		
	20	25
Ile Phe Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val		
	35	40
Leu Val Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe		
	50	55
Leu Ser Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val		
	65	70
Pro Gln Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr		
	85	90
Ile Gly Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr		
	100	105
Glu Tyr Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val		
	115	120
Cys His Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu		
	130	135
Gln Leu Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile		
	145	150
Gln Ser Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val		
	165	170
Asp Asp Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr		
	180	185
Asp Thr Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu		
	195	200
Leu Val Met Pro Leu Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala		
	210	215
Lys Ala Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe		
	225	230
Gly Thr Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr		
	245	250
Val Thr Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp		
	260	265
Gly Lys Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn		
	275	280
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile		
	290	295
		300

Arg Leu Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn  
305 310 315

<210> 2589

<211> 348

<212> PRT

<213> Unknown (5262456-dir-612-12 conceptual translation of range 61285-62326)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400>2589

Leu	Ile	Phe	Cys	Pro	Met	Ala	Asn	Thr	Leu	Ser	Ser	Leu	Asn	Ser	Cys
1				5					10				15		
Asn	Val	Phe	Leu	Leu	Val	Leu	Asn	Arg	Val	Met	Gly	Met	Thr	Asn	Ser
		20						25					30		
Ser	Val	Lys	Gly	Asp	Phe	Ile	Leu	Val	Gly	Phe	Ser	His	Gln	Pro	His
		35					40					45			
Leu	Glu	Lys	Ile	Leu	Phe	Val	Ala	Val	Leu	Ile	Ser	Tyr	Leu	Leu	Thr
	50					55					60				
Leu	Val	Gly	Asn	Thr	Val	Ile	Ile	Leu	Ile	Cys	Ser	Val	Asp	Pro	Lys
65					70					75				80	
Leu	Lys	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His	Leu	Ser	Leu	Val	Asp
				85					90					95	
Ile	Cys	Phe	Thr	Thr	Ser	Ile	Val	Pro	Gln	Leu	Leu	Trp	Asn	Leu	Lys
			100					105					110		
Gly	Pro	Asp	Lys	Thr	Ile	Thr	Phe	Leu	Gly	Cys	Val	Ile	Gln	Leu	Tyr
		115					120					125			
Ile	Ser	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	Val	Leu	Leu	Ala	Val	Met
	130					135					140				
Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Lys	Pro	Leu	His	Tyr	Thr	Ala
145					150					155				160	
Val	Met	Asn	Pro	Gln	Leu	Cys	Gln	Ala	Leu	Ala	Gly	Val	Ala	Trp	Leu
				165					170					175	
Ser	Gly	Val	Gly	Asn	Thr	Leu	Ile	Gln	Gly	Thr	Val	Thr	Leu	Trp	Leu
			180					185					190		
Pro	Arg	Cys	Gly	His	Arg	Leu	Leu	Gln	His	Phe	Phe	Cys	Glu	Val	Pro
		195				200						205			
Ser	Met	Ile	Lys	Leu	Ala	Cys	Val	Asp	Ile	His	Asp	Asn	Glu	Val	Gln
	210					215					220				
Leu	Phe	Val	Ala	Ser	Leu	Val	Leu	Leu	Leu	Leu	Pro	Leu	Val	Leu	Ile
225					230					235				240	
Leu	Leu	Ser	Tyr	Gly	His	Ile	Ala	Lys	Val	Val	Ile	Arg	Ile	Lys	Ser
			245						250					255	
Val	Gln	Ala	Trp	Cys	Lys	Gly	Leu	Gly	Thr	Cys	Gly	Ser	His	Leu	Ile
			260					265					270		
Val	Val	Ser	Leu	Phe	Cys	Gly	Thr	Ile	Thr	Ala	Val	Tyr	Ile	Gln	Ser
		275					280					285			
Asn	Ser	Ser	Tyr	Ala	His	Ala	His	Gly	Lys	Phe	Ile	Ser	Leu	Phe	Tyr
	290					295					300				
Thr	Val	Val	Thr	Pro	Thr	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn
305					310					315				320	
Asn	Asp	Val	Lys	Gly	Ala	Leu	Arg	Leu	Phe	Asn	Arg	Asp	Leu	Gly	Thr
			325						330					335	
Xaa	Lys	Met	Lys	Gln	Ser	Thr	Gln	Arg	Ser	Thr	Phe				
			340					345							

<210> 2590

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (200153-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2590

```

Met Glu Val Asp Ser Asn Ser Ser Ser Gly Thr Phe Ile Leu Met Gly
 1           5           10           15
Val Ser Asp His Pro His Leu Glu Ile Ile Phe Phe Ala Val Ile Leu
          20           25           30
Ala Ser Tyr Leu Leu Thr Leu Val Gly Asn Leu Thr Ile Ile Leu Leu
          35           40           45
Ser Arg Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Thr Thr Ser Ser Val Pro Gln
65           70           75           80
Met Leu Lys Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Gly Gly
          85           90           95
Cys Val Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
          100          105          110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
          115          120          125
Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys Trp Gly Leu
          130          135          140
Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
145          150          155          160
Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys Val Asp Asn
          165          170          175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
          180          185          190
Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Val
          195          200          205
Val Pro Val Ser Val Ile Leu Val Ser Tyr Cys Phe Ile Ala Gln Ala
          210          215          220
Val Met Lys Ile Arg Ser Val Glu Gly Arg Arg Lys Ala Phe Asn Thr
225          230          235          240
Cys Val Ser His Leu Val Val Val Phe Leu Phe Tyr Gly Ser Ala Ile
          245          250          255
Tyr Gly Tyr Leu Leu Pro Ala Lys Ser Ser Asn Gln Ser Gln Gly Lys
          260          265          270
Phe Ile Ser Leu Phe Tyr Ser Val Val Thr Pro Met Val Asn Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Leu
          290          295          300
Leu Gly Lys Gly Arg Gly Ala Ser
305          310

```

&lt;210&gt; 2591

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (902728-dir-0-6 conceptual translation of range 2-472)

&lt;400&gt;2591

```

Val Cys Arg Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys
 1           5           10           15
Trp Val Leu Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val
          20           25           30
Ile Gln Ser Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys
          35           40           45
Val Asp Asn Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys
          50           55           60
Gly Asp Thr Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe

```

65					70					75				80
Phe	Thr	Ala	Val	Pro	Leu	Ser	Ile	Ile	Leu	Val	Ser	Tyr	Cys	Phe Ile
				85					90					95
Ala	Gln	Ala	Val	Met	Lys	Ile	Arg	Ser	Val	Glu	Gly	Arg	Arg	Lys Ala
			100					105					110	
Phe	Asn	Thr	Cys	Val	Ser	His	Leu	Val	Val	Val	Phe	Leu	Phe	Tyr Gly
		115					120					125		
Ser	Ala	Ile	Tyr	Gly	Tyr	Leu	Leu	Pro	Ala	Lys	Ser	Ser	Asn	Gln Asp
		130					135					140		
Gln	Gly	Lys	Phe	Ile	Ser	Leu	Phe	Tyr	Ser	Val	Val	Thr		
145					150					155				

&lt;210&gt; 2592

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (p146-dir-0-11 conceptual translation of range 1-936)

&lt;400&gt;2592

Met	Asp	Gly	Val	Asn	Asp	Ser	Ser	Leu	Gln	Gly	Phe	Val	Leu	Met	Ser
1				5					10					15	
Ile	Ser	Asp	His	Pro	Gln	Leu	Glu	Met	Ile	Phe	Phe	Ile	Ala	Ile	Leu
		20						25					30		
Phe	Ser	Tyr	Leu	Leu	Thr	Leu	Leu	Gly	Asn	Ser	Thr	Ile	Ile	Leu	Leu
		35					40					45			
Ser	Arg	Leu	Glu	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
		50					55				60				
Asn	Leu	Ser	Ser	Leu	Asp	Leu	Ala	Phe	Ala	Thr	Ser	Ser	Val	Pro	Gln
65					70					75					80
Met	Leu	Ile	Asn	Leu	Trp	Gly	Pro	Gly	Lys	Thr	Ile	Ser	Tyr	Gly	Gly
			85						90					95	
Cys	Ile	Thr	Gln	Leu	Tyr	Val	Phe	Leu	Trp	Leu	Gly	Ala	Thr	Glu	Cys
			100					105					110		
Ile	Leu	Leu	Val	Val	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Val	Cys	Arg
		115					120					125			
Pro	Leu	Arg	Tyr	Thr	Ala	Ile	Met	Asn	Pro	Gln	Leu	Cys	Trp	Leu	Leu
		130					135					140			
Ala	Val	Ile	Ala	Trp	Leu	Gly	Gly	Leu	Gly	Asn	Ser	Val	Ile	Gln	Ser
145					150					155					160
Thr	Phe	Thr	Leu	Gln	Leu	Pro	Leu	Cys	Gly	His	Arg	Arg	Val	Glu	Gly
			165						170					175	
Phe	Leu	Cys	Glu	Val	Pro	Ala	Met	Ile	Lys	Leu	Ala	Cys	Gly	Asp	Thr
			180					185					190		
Ser	Leu	Asn	Gln	Ala	Val	Leu	Asn	Gly	Val	Cys	Thr	Phe	Phe	Thr	Ala
		195					200					205			
Val	Pro	Leu	Ser	Ile	Ile	Val	Ile	Ser	Tyr	Cys	Leu	Ile	Ala	Gln	Ala
		210					215					220			
Val	Leu	Lys	Ile	His	Ser	Ala	Glu	Gly	Arg	Arg	Lys	Ala	Phe	Asn	Thr
225					230					235					240
Cys	Leu	Ser	His	Leu	Val	Val	Phe	Leu	Phe	Tyr	Gly	Ser	Ala	Ser	
			245						250				255		
Tyr	Gly	Tyr	Leu	Leu	Pro	Ala	Lys	Asn	Ser	Lys	Gln	Asp	Gln	Gly	Lys
			260					265					270		
Phe	Ile	Ser	Leu	Phe	Tyr	Ser	Leu	Val	Thr	Pro	Met	Val	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Thr	Leu	Arg	Asn	Met	Glu	Val	Lys	Gly	Ala	Leu	Arg	Arg	Leu
		290					295					300			
Leu	Gly	Lys	Gly	Arg	Glu	Val	Gly								
305					310										

&lt;210&gt; 2593

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921701-dir-0-8 conceptual translation of range 2-648)

&lt;400&gt;2593

```

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1          5          10          15
Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20          25          30
Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35          40          45
Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50          55          60
Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65          70          75          80
Ser Arg Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85          90          95
Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100         105         110
Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115         120         125
Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130         135         140
Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145         150         155         160
Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165         170         175
His Leu Ile Val Val Ser Leu Phe Lys Gly Thr Ala Val Ser Val Tyr
 180         185         190
Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195         200         205
Leu Phe Tyr Gly Ile Ile Ala Pro
 210         215

```

&lt;210&gt; 2594

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921699-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2594

```

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1          5          10          15
Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20          25          30
Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35          40          45
Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50          55          60
Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65          70          75          80
Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85          90          95
Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100         105         110
Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115         120         125
Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130         135         140
Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145         150         155         160
Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165         170         175

```

His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val Ser Val Tyr  
                   180                  185                  190  
 Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser  
                   195                  200                  205  
 Leu Phe Tyr Gly Ile Ile Ala Pro  
                   210                  215

&lt;210&gt; 2595

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921706-dir-0-8 conceptual translation of range 2-646)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(215)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2595

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val  
   1                  5                  10                  15  
 Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala  
                   20                  25                  30  
 Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu  
                   35                  40                  45  
 Ala Val Thr Ser Leu Ile Gly Cys Ser Tyr Cys Arg Pro Leu His Tyr  
                   50                  55                  60  
 Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala Ser  
   65                  70                  75                  80  
 Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr Leu  
                   85                  90                  95  
 Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys Glu  
                   100                  105                  110  
 Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn Glu  
                   115                  120                  125  
 Ala Glu Leu Phe Leu Asp Ser Glu Leu Phe His Leu Ile Pro Leu Thr  
                   130                  135                  140  
 Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg Ile  
   145                  150                  155                  160  
 Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser His  
                   165                  170                  175  
 Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val Ser Val Tyr Leu  
                   180                  185                  190  
 Xaa Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser Leu  
                   195                  200                  205  
 Phe Tyr Gly Ile Ile Ala Pro  
                   210                  215

&lt;210&gt; 2596

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Unknown (1142995-dir-0-5 conceptual translation of range 1-336)

&lt;400&gt;2596

Arg Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln  
   1                  5                  10                  15  
 Leu Ala Ala Val Ser Trp Ile Ile Gly Phe Gly Asn Ser Val Trp Leu  
                   20                  25                  30  
 Ser Ile Leu Thr Leu Gln Leu Pro Arg Cys Gly His Tyr Val Ile Asp  
                   35                  40                  45  
 His Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp  
                   50                  55                  60

Val Thr Ala Asn Glu Ala Glu Leu Phe Phe Val Ser Val Phe Phe His  
 65 70 75 80  
 Leu Thr Pro Leu Ser Leu Ile Leu Thr Ser Tyr Ala Phe Ile Ala Arg  
 85 90 95  
 Ala Ile Leu Lys Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly  
 100 105 110

&lt;210&gt; 2597

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (3080457-rev-750-12 conceptual translation of range 75137-76079)

&lt;400&gt;2597

Asn Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu  
 1 5 10 15  
 Val Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe  
 20 25 30  
 Leu Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu  
 35 40 45  
 Val Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu  
 50 55 60  
 Ser Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro  
 65 70 75 80  
 Gln Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly  
 85 90 95  
 Gly Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu  
 100 105 110  
 Cys Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln  
 130 135 140  
 Leu Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln  
 145 150 155 160  
 Ser Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp  
 165 170 175  
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp  
 180 185 190  
 Thr Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu  
 195 200 205  
 Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln  
 210 215 220  
 Ala Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly  
 225 230 235 240  
 Thr Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala  
 245 250 255  
 Ile Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly  
 260 265 270  
 Lys Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg  
 290 295 300  
 Leu Leu Gln Arg Val Phe Leu Ile Lys Lys  
 305 310

&lt;210&gt; 2598

&lt;211&gt; 343

&lt;212&gt; PRT

&lt;213&gt; Unknown (506841-dir-0-12 conceptual translation of range 60-1090)

&lt;220&gt;



&lt;221&gt; VARIANT

&lt;222&gt; (1)...(343)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2598

```

Cys Ile Ile Tyr Met Ser Val Ala Asn Glu Ser Ile Ser Arg Glu Phe
 1           5           10           15
Ile Leu Leu Gly Phe Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe
          20           25           30
Val Val Phe Leu Val Ser Tyr Ile Leu Thr Ile Phe Gly Asn Met Met
          35           40           45
Ile Ile Leu Val Ser Arg Leu Asp Ser Lys Leu His Thr Pro Met Tyr
          50           55           60
Phe Phe Leu Thr Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser
65           70           75           80
Thr Val Pro Gln Met Leu Ile Asn Ile Cys Ser Thr Arg Lys Val Ile
          85           90           95
Ser Tyr Gly Gly Cys Val Val Gln Leu Phe Ile Phe Leu Ser Leu Gly
          100          105          110
Ser Thr Glu Cys Phe Leu Leu Gly Val Met Ser Leu Asp Arg Phe Leu
          115          120          125
Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met His Gln Arg Arg
          130          135          140
Cys Leu His Leu Ala Ala Ala Cys Trp Ile Ser Gly Phe Ser Asn Ser
145          150          155          160
Val Leu Gln Ser Thr Trp Thr Leu Gln Met Pro Leu Cys Gly His Lys
          165          170          175
Glu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser
          180          185          190
Cys Val Asp Thr Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val
          195          200          205
Leu Phe Leu Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe
          210          215          220
Ile Val Gln Ala Val Leu Lys Ile Arg Ser Ala Glu Cys Arg Arg Lys
225          230          235          240
Ala Phe Gly Thr Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr
          245          250          255
Gly Thr Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser Pro Ser Lys
          260          265          270
Asp Arg Gly Lys Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Pro Met
          275          280          285
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Gly Ala
          290          295          300
Phe Lys Arg Leu Met Lys Arg Ile Ile Leu Ile Gly Lys Xaa Gly Val
305          310          315          320
Pro Glu Xaa Xaa Pro Tyr Xaa Tyr Lys Tyr Ile Phe Ile Ala Cys Lys
          325          330          335
Leu Tyr Cys Phe Leu Leu Cys
          340

```

&lt;210&gt; 2599

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Unknown (3093312-rev-75-13 conceptual translation of range 7680-8721)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(348)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2599

Leu Ile Ala Phe Leu Ser Tyr Ile Phe Leu Gly Val Arg Asn Lys Xaa  
 1 5 10 15  
 Val Ile Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu  
 20 25 30  
 Leu Gly Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val  
 35 40 45  
 Leu Leu Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met  
 50 55 60  
 Met Val Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe  
 65 70 75 80  
 Leu Thr Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val  
 85 90 95  
 Pro His Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr  
 100 105 110  
 Ala Gly Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr  
 115 120 125  
 Glu Cys Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val  
 130 135 140  
 Cys Arg Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu  
 145 150 155 160  
 Arg Met Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu  
 165 170 175  
 Gln Ser Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val  
 180 185 190  
 Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala  
 195 200 205  
 Asp Thr Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile  
 210 215 220  
 Leu Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala  
 225 230 235 240  
 Gln Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe  
 245 250 255  
 Gly Thr Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr  
 260 265 270  
 Ala Ile Tyr Met Tyr Leu Gln Pro Ser Ser Thr Ser Lys Asp Trp  
 275 280 285  
 Gly Lys Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn  
 290 295 300  
 Ser Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Phe Lys  
 305 310 315 320  
 Arg Leu Met Pro Arg Ile Phe Phe Cys Lys Lys Xaa Arg Ser Thr Pro  
 325 330 335  
 Ser Val Met Arg Ile Phe Leu Val Phe Pro Tyr Leu  
 340 345

&lt;210&gt; 2600

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Unknown (5262456-rev-0-10 conceptual translation of range 184-1000)

&lt;400&gt;2600

Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly  
 1 5 10 15  
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val  
 20 25 30  
 Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser  
 35 40 45  
 His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn  
 50 55 60  
 Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met  
 65 70 75 80

```

Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
      85                      90                      95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
      100                    105                    110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
      115                    120                    125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
      130                    135                    140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
      145                    150                    155                    160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
      165                    170                    175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
      180                    185                    190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met
      195                    200                    205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
      210                    215                    220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
      225                    230                    235                    240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
      245                    250                    255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
      260                    265                    270

```

&lt;210&gt; 2601

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Unknown (3093312-dir-1027-12 conceptual translation of range 102817-103865)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(350)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2601

```

Phe Leu Ser Gly Asn Arg Lys Xaa Met Met Met Glu Lys Xaa Asn Ala
  1                      5                      10                      15
Ser Ser Glu Gly Tyr Phe Ile Leu Val Gly Phe Ser Asn Trp Pro Tyr
      20                    25                    30
Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Cys Leu Met Thr
      35                    40                    45
Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Thr Tyr Leu Asp Ser His
      50                    55                    60
Leu His Thr Pro Leu Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp
      65                    70                    75                    80
Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val Ser Leu Trp
      85                    90                    95
Gly Val Glu Lys Thr Ile Ser Tyr Ala Gly Cys Met Val Gln Leu Tyr
      100                    105                    110
Phe Phe Leu Thr Leu Gly Thr Thr Glu Cys Val Leu Leu Val Val Met
      115                    120                    125
Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His Tyr Thr Val
      130                    135                    140
Leu Met His Ser Arg Phe Cys His Leu Leu Ala Val Ala Ser Trp Val
      145                    150                    155                    160
Ser Gly Phe Thr Asn Pro Ala Leu His Ser Ser Phe Thr Phe Trp Val
      165                    170                    175
Pro Leu Cys Gly His Arg Gln Ile Asp His Phe Phe Cys Glu Val Pro
      180                    185                    190

```

Ala Leu Leu Xaa Leu Ser Phe Val Asn Thr Arg Glu Asn Lys Leu Thr  
 195 200 205  
 Leu Met Ile Thr Ser Ser Ile Phe Val Leu Leu Leu Thr Leu Ile  
 210 215 220  
 Phe Thr Ser Tyr Gly Ala Ile Ala Gln Ala Val Leu Arg Met Gln Ser  
 225 230 235 240  
 Thr Thr Gly Leu Gln Lys Val Phe Gly Thr Cys Gly Ala His His Met  
 245 250 255  
 Val Val Ser Leu Phe Phe Ile Pro Ala Met Cys Met Tyr Leu Gln Pro  
 260 265 270  
 Pro Ser Gly Asn Ser Gln Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr  
 275 280 285  
 Thr Val Val Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn  
 290 295 300  
 Lys Asp Val Arg Gly Val Val Lys Arg Leu Arg Gly Trp Glu Xaa Ala  
 305 310 315 320  
 Cys Val Cys Val Ile Leu Thr Ile Xaa Trp Ser Leu Ser Ser Gln Xaa  
 325 330 335  
 Phe Ile His Leu Phe Ile Tyr Gln Pro Phe Phe Tyr Ser Leu  
 340 345 350

&lt;210&gt; 2602

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Unknown (5262456-dir-273-9 conceptual translation of range 27452-28066)

&lt;400&gt;2602

Gln Lys Ile Ala Lys Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met  
 1 5 10 15  
 Leu Leu Gly Phe Pro Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly  
 20 25 30  
 Val Val Phe Phe Phe Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu  
 35 40 45  
 Ile Leu Leu Pro Leu Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe  
 50 55 60  
 Phe Leu Arg Asn Leu Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile  
 65 70 75 80  
 Val Pro Gln Met Leu Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr  
 85 90 95  
 Phe Gly Gly Cys Ala Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr  
 100 105 110  
 Val Glu Cys Met Leu Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala  
 115 120 125  
 Val Cys Lys Pro Leu Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys  
 130 135 140  
 Gln Gly Leu Val Ala Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met  
 145 150 155 160  
 Ile Leu Ser Pro Cys Pro Val Ser Leu Pro Arg Cys Gly Asp His His  
 165 170 175  
 Leu Asp His Tyr Phe Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys  
 180 185 190  
 Gly Ala Thr Thr Val Met Glu Glu Thr Val Arg Val Lys  
 195 200 205

&lt;210&gt; 2603

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Unknown (2924249-rev-741-9 conceptual translation of range 74285-74912)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2603

```

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1           5           10           15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
      20           25           30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
      35           40           45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
      50           55           60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65           70           75           80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
      85           90           95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Ile Glu
      100          105          110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
      115          120          125
Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Cys Leu His
130          135          140
Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
145          150          155          160
Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
      165          170          175
Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
      180          185          190
Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
      195          200          205
Glu Leu
      210

```

&lt;210&gt; 2604

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Unknown (4156137-rev-1191-9 conceptual translation of range 119253-119880)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(210)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2604

```

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1           5           10           15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
      20           25           30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
      35           40           45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
      50           55           60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65           70           75           80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
      85           90           95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Thr Glu
      100          105          110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
      115          120          125

```

Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Tyr Leu His  
 130 135 140  
 Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln  
 145 150 155 160  
 Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile  
 165 170 175  
 Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr  
 180 185 190  
 Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly  
 195 200 205  
 Glu Leu  
 210

&lt;210&gt; 2605

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921643-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2605

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala  
 1 5 10 15  
 His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala  
 20 25 30  
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu  
 35 40 45  
 Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg  
 50 55 60  
 Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr  
 65 70 75 80  
 Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr  
 85 90 95  
 Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys  
 100 105 110  
 Glu Leu Leu Ala Val Val Arg Leu Ala Arg Val Asp Thr Ser Ser Asn  
 115 120 125  
 Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe  
 130 135 140  
 Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys  
 145 150 155 160  
 Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser  
 165 170 175  
 His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr  
 180 185 190  
 Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser  
 195 200 205  
 Val Phe Tyr Ala Ile Leu Thr Pro  
 210 215

&lt;210&gt; 2606

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921711-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2606

Leu Val Asp Val Ser Cys Ala Thr Ser Val Val Pro Gln Leu Leu Ala  
 1 5 10 15  
 His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala  
 20 25 30  
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu  
 35 40 45  
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg

50		55		60	
Tyr Ser Ala Ile Met	His Gly Gly Leu Cys	Ala Arg Leu Ala Ile Thr			
65	70	75	80		
Ser Trp Val Ser Gly	Phe Ile Ser Ser	Pro Val Gln Thr Ala Ile Thr			
85	90	95			
Phe Gln Leu Pro Met	Cys Arg Asn Lys	Phe Ile Asp His Ile Ser Cys			
100	105	110			
Glu Leu Leu Ala Val	Val Arg Leu Ala Cys	Val Asp Thr Ser Ser Asn			
115	120	125			
Glu Val Thr Ile Met	Val Ser Ile Val Leu	Leu Met Thr Pro Phe			
130	135	140			
Cys Leu Val Leu Leu	Ser Tyr Ile Gln Ile	Ile Ser Thr Ile Leu Lys			
145	150	155	160		
Ile Gln Ser Arg Glu	Gly Arg Lys Lys	Ala Phe His Thr Cys Ala Ser			
165	170	175			
His Leu Thr Val Ala	Leu Cys Tyr Gly	Val Ala Ile Phe Thr Tyr			
180	185	190			
Ile Gln Pro His Ser	Ser Pro Ser Val	Leu Gln Glu Lys Leu Phe Ser			
195	200	205			
Val Phe Tyr Ala Ile	Leu Thr Pro				
210	215				

&lt;210&gt; 2607

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (1336042-dir-0-11 conceptual translation of range 1-951)

&lt;400&gt;2607

Met Gly Thr Asp Asn	Gln Thr Trp Val	Ser Glu Phe Ile Leu Leu Gly	
1	5	10	15
Leu Ser Ser Asp Trp	Asp Thr Arg Val	Ser Leu Phe Val Leu Phe Leu	
20	25	30	
Val Met Tyr Val Val	Thr Val Leu Gly	Asn Cys Leu Ile Val Leu Leu	
35	40	45	
Ile Arg Leu Asp Ser	Arg Leu His Thr	Pro Met Tyr Phe Phe Leu Thr	
50	55	60	
Asn Leu Ser Leu Val	Asp Val Ser Tyr	Ala Thr Ser Val Val Pro Gln	
65	70	75	80
Leu Leu Ala His Phe	Leu Ala Glu His	Lys Ala Ile Pro Phe Gln Ser	
85	90	95	
Cys Ala Ala Gln Leu	Phe Phe Ser Leu	Ala Leu Gly Gly Ile Glu Phe	
100	105	110	
Val Leu Leu Ala Val	Met Ala Tyr Asp	Arg Tyr Val Ala Val Cys Asp	
115	120	125	
Ala Leu Arg Tyr Ser	Ala Ile Met His	Gly Gly Leu Cys Ala Arg Leu	
130	135	140	
Ala Ile Thr Ser Trp	Val Ser Gly Phe	Ile Ser Ser Pro Val Gln Thr	
145	150	155	160
Ala Ile Thr Phe Gln	Leu Pro Met Cys	Arg Asn Lys Phe Ile Asp His	
165	170	175	
Ile Ser Cys Glu Leu	Leu Ala Val Val	Arg Leu Ala Cys Val Asp Thr	
180	185	190	
Ser Ser Asn Glu Val	Thr Ile Met Val	Ser Ser Ile Val Leu Leu Met	
195	200	205	
Thr Pro Leu Cys Leu	Val Leu Leu Ser	Tyr Ile Gln Ile Ile Ser Thr	
210	215	220	
Ile Leu Lys Ile Gln	Ser Arg Glu Gly	Arg Lys Lys Ala Phe His Thr	
225	230	235	240
Cys Ala Ser His Leu	Thr Val Val Ala	Leu Cys Tyr Gly Val Ala Ile	
245	250	255	
Phe Thr Tyr Ile Gln	Pro His Ser Ser	Pro Ser Val Leu Gln Glu Lys	

	260		265		270										
Leu	Phe	Ser	Val	Phe	Tyr	Ala	Ile	Leu	Thr	Pro	Met	Leu	Asn	Pro	Met
	275						280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Trp	Gln	Lys	Leu
	290					295					300				
Leu	Trp	Lys	Phe	Ser	Gly	Leu	Thr	Ser	Lys	Leu	Ala	Thr			
305					310					315					

&lt;210&gt; 2608

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921713-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2608

Leu	Val	Asp	Val	Ser	Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala
1			5					10					15		
His	Phe	Leu	Ala	Glu	His	Lys	Ala	Thr	Pro	Phe	Gln	Ser	Cys	Ala	Ala
		20					25					30			
Gln	Leu	Phe	Phe	Ser	Leu	Ala	Leu	Gly	Gly	Ile	Glu	Phe	Val	Leu	Leu
	35					40					45				
Ala	Val	Met	Thr	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys	Asp	Ala	Leu	Arg
	50				55						60				
Tyr	Ser	Ala	Ile	Met	His	Gly	Gly	Leu	Cys	Ala	Arg	Leu	Ala	Ile	Thr
65				70					75					80	
Ser	Trp	Val	Ser	Gly	Phe	Ile	Ser	Ser	Pro	Val	Gln	Thr	Ala	Ile	Thr
			85				90						95		
Phe	Gln	Leu	Pro	Met	Cys	Arg	Asn	Lys	Phe	Ile	Asp	His	Ile	Ser	Cys
		100					105						110		
Glu	Leu	Leu	Ala	Val	Val	Arg	Leu	Ala	Cys	Val	Asp	Thr	Ser	Ser	Asn
	115					120						125			
Glu	Val	Thr	Ile	Met	Val	Ser	Ser	Val	Val	Leu	Leu	Met	Thr	Pro	Phe
	130				135						140				
Cys	Leu	Val	Leu	Leu	Ser	Tyr	Ile	Gln	Ile	Asn	Ser	Thr	Ile	Leu	Lys
145					150					155				160	
Ile	Gln	Ser	Arg	Glu	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr	Cys	Ala	Ser
			165					170					175		
His	Leu	Thr	Val	Ala	Leu	Cys	Tyr	Gly	Val	Ala	Ile	Phe	Thr	Tyr	
		180				185						190			
Ile	Gln	Pro	His	Ser	Ser	Pro	Ser	Val	Leu	Gln	Glu	Lys	Leu	Phe	Ser
	195					200						205			
Val	Phe	Tyr	Ala	Ile	Leu	Thr	Pro								
	210				215										

&lt;210&gt; 2609

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Unknown (p161-dir-0-11 conceptual translation of range 2-903)

&lt;400&gt;2609

Trp	Val	Ser	Glu	Phe	Ile	Leu	Leu	Gly	Leu	Ser	Ser	Asp	Trp	Asp	Thr
1			5					10					15		
Gln	Val	Ser	Leu	Phe	Val	Leu	Phe	Leu	Val	Met	Tyr	Val	Val	Thr	Val
		20					25					30			
Leu	Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu	Ile	Arg	Leu	Asp	Ser	Arg	Leu
	35					40					45				
His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Asn	Leu	Ser	Leu	Val	Asp	Val
	50				55					60					
Ser	Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala	His	Phe	Leu	Ala
65				70					75				80		
Glu	His	Lys	Ala	Ile	Ser	Phe	Gln	Ser	Cys	Ala	Ala	Gln	Leu	Phe	Phe
			85					90					95		



Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala  
                   100                  105                  110  
 Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg Tyr Ser Ala Ile  
                   115                  120                  125  
 Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser  
                   130                  135                  140  
 Gly Phe Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe Gln Leu Pro  
                   145                  150                  155                  160  
 Met Cys Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala  
                   165                  170                  175  
 Val Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile  
                   180                  185                  190  
 Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu  
                   195                  200                  205  
 Leu Ser Tyr Ile Gln Ile Thr Ser Thr Ile Leu Lys Ile Gln Ser Arg  
                   210                  215                  220  
 Glu Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val  
                   225                  230                  235                  240  
 Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His  
                   245                  250                  255  
 Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser Val Phe Tyr Ala  
                   260                  265                  270  
 Ile Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys  
                   275                  280                  285  
 Glu Val Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe  
                   290                  295                  300

&lt;210&gt; 2610

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Unknown (3766130-dir-170-13 conceptual translation of range 17111-18112)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(334)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2610

Phe Cys Phe Phe Leu Thr Leu Ser Thr Asp Xaa Tyr Ser Ser His Phe  
   1                  5                  10                  15  
 Xaa Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu  
                   20                  25                  30  
 Gly Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe  
                   35                  40                  45  
 Leu Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu  
                   50                  55                  60  
 Leu Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu  
                   65                  70                  75                  80  
 Thr Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro  
                   85                  90                  95  
 Gln Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln  
                   100                  105                  110  
 Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu  
                   115                  120                  125  
 Phe Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser  
                   130                  135                  140  
 Asp Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg  
                   145                  150                  155                  160  
 Leu Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln  
                   165                  170                  175

Thr Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp  
 180 185 190  
 His Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp  
 195 200 205  
 Thr Ser Ser Asn Glu Ala Ala Ile Met Val Ser Ser Ile Val Leu Leu  
 210 215 220  
 Met Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser  
 225 230 235 240  
 Thr Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His  
 245 250 255  
 Thr Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Thr Thr  
 260 265 270  
 Ile Phe Thr Tyr Ile Gln Pro His Ser Gly Pro Ser Val Leu Gln Glu  
 275 280 285  
 Lys Leu Ile Ser Val Phe Tyr Ala Ile Val Met Pro Leu Leu Asn Pro  
 290 295 300  
 Val Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp His Lys  
 305 310 315 320  
 Leu Leu Glu Lys Phe Ser Gly Leu Thr Ser Lys Leu Gly Thr  
 325 330

&lt;210&gt; 2611

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (p172-dir-0-10 conceptual translation of range 2-895)

&lt;400&gt;2611

Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val Ser  
 1 5 10 15  
 Leu Phe Val Leu Phe Leu Val Met Cys Met Val Thr Met Leu Gly Asn  
 20 25 30  
 Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro  
 35 40 45  
 Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr Ala  
 50 55 60  
 Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His Lys  
 65 70 75 80  
 Ser Ile Pro Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala  
 85 90 95  
 Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp Arg  
 100 105 110  
 Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His Gly  
 115 120 125  
 Ala Pro Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe Ile  
 130 135 140  
 Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys Thr  
 145 150 155 160  
 Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile Arg  
 165 170 175  
 Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val Ser  
 180 185 190  
 Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr  
 195 200 205  
 Ile Trp Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly Arg  
 210 215 220  
 Lys Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala Leu  
 225 230 235 240  
 Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser Leu  
 245 250 255  
 Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu Thr  
 260 265 270

Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys  
           275                          280                          285  
 Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe  
           290                          295

<210> 2612

<211> 298

<212> PRT

<213> Unknown (p171-dir-0-10 conceptual translation of range 3-896)

<220>

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400>2612

Ser Asp Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val  
   1                          5                          10                          15  
 Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly  
           20                          25                          30  
 Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr  
           35                          40                          45  
 Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr  
           50                          55                          60  
 Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His  
   65                          70                          75                          80  
 Lys Ser Ile Pro Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu  
           85                          90                          95  
 Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp  
           100                          105                          110  
 Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His  
           115                          120                          125  
 Gly Ala Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe  
           130                          135                          140  
 Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys  
   145                          150                          155                          160  
 Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile  
           165                          170                          175  
 Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val  
           180                          185                          190  
 Ser Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser  
           195                          200                          205  
 Tyr Ile Xaa Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly  
           210                          215                          220  
 Arg Lys Lys Ala Phe His Thr Tyr Ala Ser His Leu Thr Val Val Ala  
   225                          230                          235                          240  
 Leu Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser  
           245                          250                          255  
 Leu Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu  
           260                          265                          270  
 Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val  
           275                          280                          285  
 Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys  
           290                          295

<210> 2613

<211> 299

<212> PRT

<213> Unknown (p173-dir-0-11 conceptual translation of range 4-900)

<400>2613

```

Val Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
1      5      10      15
Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
20      25      30
Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
35      40      45
Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
50      55      60
Ala Ile Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
65      70      75      80
Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
85      90      95
Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
100      105      110
Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His
115      120      125
Gly Ala Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe
130      135      140
Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys
145      150      155      160
Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile
165      170      175
Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val
180      185      190
Ser Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser
195      200      205
Tyr Ile Trp Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly
210      215      220
Arg Lys Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala
225      230      235      240
Leu Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser
245      250      255
Leu Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu
260      265      270
Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
275      280      285
Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
290      295

```

&lt;210&gt; 2614

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Unknown (p142-dir-0-11 conceptual translation of range 2-900)

&lt;400&gt;2614

```

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
1      5      10      15
Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
20      25      30
Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
35      40      45
Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
50      55      60
Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
65      70      75      80
His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
85      90      95
Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
100      105      110
Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
115      120      125

```

His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly  
 130 135 140  
 Ser Ile Asn Ser Leu Val His Thr Thr Ile Thr Phe Gln Leu Pro Met  
 145 150 155 160  
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val  
 165 170 175  
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met  
 180 185 190  
 Val Phe Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu  
 195 200 205  
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu  
 210 215 220  
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Met Val  
 225 230 235 240  
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser  
 245 250 255  
 Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile  
 260 265 270  
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Ser Lys Glu  
 275 280 285  
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe  
 290 295 300

&lt;210&gt; 2615

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Unknown (p162-dir-0-10 conceptual translation of range 1-899)

&lt;400&gt;2615

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln  
 1 5 10 15  
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu  
 20 25 30  
 Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His  
 35 40 45  
 Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser  
 50 55 60  
 Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu  
 65 70 75 80  
 His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser  
 85 90 95  
 Leu Ala Leu Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr  
 100 105 110  
 Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met  
 115 120 125  
 His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly  
 130 135 140  
 Ser Ile Asn Ser Leu Ala His Thr Thr Ile Thr Phe Gln Leu Pro Met  
 145 150 155 160  
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val  
 165 170 175  
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met  
 180 185 190  
 Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu  
 195 200 205  
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu  
 210 215 220  
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Val Val  
 225 230 235 240  
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser  
 245 250 255

Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Thr  
 260 265 270  
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu  
 275 280 285  
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe  
 290 295 300

&lt;210&gt; 2616

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Unknown (p160-dir-0-11 conceptual translation of range 3-901)

&lt;400&gt;2616

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln  
 1 5 10 15  
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu  
 20 25 30  
 Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His  
 35 40 45  
 Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser  
 50 55 60  
 Tyr Val Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu  
 65 70 75 80  
 His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser  
 85 90 95  
 Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr  
 100 105 110  
 Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met  
 115 120 125  
 His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly  
 130 135 140  
 Ser Ile Asn Ser Leu Val His Thr Thr Thr Thr Phe Gln Leu Pro Met  
 145 150 155 160  
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val  
 165 170 175  
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met  
 180 185 190  
 Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu  
 195 200 205  
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Lys  
 210 215 220  
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Val Val  
 225 230 235 240  
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser  
 245 250 255  
 Asn Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile  
 260 265 270  
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu  
 275 280 285  
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe  
 290 295 300

&lt;210&gt; 2617

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Unknown (p165-dir-0-10 conceptual translation of range 1-893)

&lt;400&gt;2617

Val Ser Glu Phe Ile Ile Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln  
 1 5 10 15  
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Val Leu

<400>2618															
Val	Ser	Glu	Phe	Ile	Ile	Leu	Gly	Leu	Ser	Ser	Asp	Trp	Asp	Thr	Gln
1				5					10					15	
Val	Ser	Leu	Phe	Val	Leu	Phe	Leu	Val	Met	Tyr	Val	Val	Thr	Val	Leu
			20					25					30		
Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu	Ile	Arg	Leu	Asp	Ser	Arg	Leu	His
		35					40					45			
Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Asn	Leu	Ser	Leu	Val	Asp	Val	Ser
	50					55					60				
Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala	His	Phe	Leu	Ala	Glu
65					70					75					80
His	Lys	Ala	Ile	Pro	Phe	Gln	Ser	Cys	Ala	Ala	Gln	Leu	Phe	Phe	Ser
			85						90					95	
Leu	Ala	Leu	Gly	Ile	Glu	Phe	Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	
			100				105					110			

```

Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
      115                120                125
His Ala Gly Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
      130                135                140
Ser Ile Asn Ser Leu Val His Thr Ala Ile Thr Phe Gln Leu Pro Arg
145      150                155                160
Cys Arg Asn Lys Phe Ile Glu His Ile Ser Cys Glu Ile Leu Ala Val
      165                170                175
Ile Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
      180                185                190
Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
      195                200                205
Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
210      215                220
Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val
225      230                235                240
Ala Leu Xaa Tyr Gly Val Ala Ile Phe Thr Xaa Ile Gln Pro His Ser
      245                250                255
Ser Pro Ser Val Ile Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile
      260                265                270
Val Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Ile Arg Asn Lys Glu
275      280                285
Val Lys Gly Ala Trp Gln Lys Ile Leu Trp Lys
290                295

```

&lt;210&gt; 2619

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Unknown (p174-dir-0-11 conceptual translation of range 4-900)

&lt;400&gt;2619

```

Val Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
1      5                10                15
Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
      20                25                30
Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His Thr
35      40                45
Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
50      55                60
Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
65      70                75                80
Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
      85                90                95
Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
100      105                110
Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Val Ile Met His
115      120                125
Gly Ala Leu Cys Ala Lys Leu Ala Ile Thr Ser Trp Val Ser Gly Ser
130      135                140
Ile Asn Ser Arg Met His Thr Thr Ile Thr Phe Gln Leu Pro Met Cys
145      150                155                160
Thr Asn Lys Phe Ile Asp His Ile Phe Cys Glu Ile Leu Ala Leu Ile
      165                170                175
Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Ile Val
180      185                190
Ser Ser Ile Val Leu Leu Met Thr Pro Leu Cys Leu Val Leu Leu Ser
195      200                205
Tyr Ile Arg Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu Gly
210      215                220
Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala
225      230                235                240

```



Leu Cys Tyr Gly Met Ala Ile Phe Thr Tyr Ile His Pro His Ser Ser  
                   245                  250                  255  
 Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile Leu  
                   260                  265                  270  
 Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val  
                   275                  280                  285  
 Lys Gly Ala Trp Lys Lys Leu Leu Trp Lys Phe  
                   290                  295

<210> 2620

<211> 317

<212> PRT

<213> Unknown (1314664-dir-0-11 conceptual translation of range 1-951)

<400>2620

Met Gly Thr Gly Asn Gln Thr Trp Val Arg Glu Phe Val Leu Leu Gly  
 1                  5                  10                  15  
 Leu Ser Ser Asp Trp Asp Thr Glu Val Ser Leu Phe Val Leu Phe Leu  
                   20                  25                  30  
 Ile Thr Tyr Met Val Thr Val Leu Gly Asn Phe Leu Ile Ile Leu Leu  
                   35                  40                  45  
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr  
                   50                  55                  60  
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Ile Pro Gln  
 65                  70                  75                  80  
 Met Leu Ala His Leu Leu Ala Ala His Lys Ala Ile Pro Phe Val Ser  
                   85                  90                  95  
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Gly Leu Gly Gly Ile Glu Phe  
                   100                  105                  110  
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp  
                   115                  120                  125  
 Pro Leu Arg Tyr Ser Val Ile Met His Gly Gly Leu Cys Thr Arg Leu  
                   130                  135                  140  
 Ala Ile Thr Ser Trp Val Ser Gly Ser Met Asn Ser Leu Met Gln Thr  
 145                  150                  155                  160  
 Val Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Tyr Ile Asp His  
                   165                  170                  175  
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr  
                   180                  185                  190  
 Ser Ser Asn Glu Ile Ala Ile Met Val Ser Ser Ile Val Leu Leu Met  
                   195                  200                  205  
 Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr  
                   210                  215                  220  
 Ile Leu Lys Ile Gln Ser Thr Glu Gly Arg Lys Lys Ala Phe His Thr  
 225                  230                  235                  240  
 Cys Ala Ser His Leu Thr Val Val Val Leu Cys Tyr Gly Met Ala Ile  
                   245                  250                  255  
 Phe Thr Tyr Ile Gln Pro Arg Ser Ser Pro Ser Val Leu Gln Glu Lys  
                   260                  265                  270  
 Leu Ile Ser Leu Phe Tyr Ser Val Leu Thr Pro Met Leu Asn Pro Met  
                   275                  280                  285  
 Ile Tyr Ser Val Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu  
                   290                  295                  300  
 Leu Gly Gln Leu Thr Gly Ile Thr Ser Lys Leu Ala Thr  
 305                  310                  315

<210> 2621

<211> 349

<212> PRT

<213> Unknown (3766130-dir-627-13 conceptual translation of range 62771-63818)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(349)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2621

```

Leu Leu Ile Leu His Phe His Asp Trp Leu Phe Leu His Leu Xaa Cys
 1              5              10              15
Gly Pro Trp Lys Leu Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val
      20              25              30
Ser Glu Phe Ile Leu Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val
      35              40              45
Ser Leu Phe Ala Leu Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly
      50              55              60
Asn Thr Leu Ile Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
      65              70              75              80
Pro Met Tyr Phe Ser Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr
      85              90              95
Thr Lys Ser Ile Val Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg
      100             105             110
Lys Ser Ile Pro Phe Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu
      115             120             125
Ala Leu Cys Gly Ser Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp
      130             135             140
Arg Tyr Val Ala Val Cys His Pro Leu His Tyr Thr Val Ile Met His
      145             150             155             160
Gly Gly Leu Cys Leu Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe
      165             170             175
Ser Asn Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser
      180             185             190
Arg Phe Ile Asn His Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu
      195             200             205
Ala Cys Val Asp Val Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly
      210             215             220
Phe Leu Val Ile Leu Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala
      225             230             235             240
Cys Ile Val Ala Thr Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys
      245             250             255
Lys Ala Phe Gly Thr Cys Ala Ser His Leu Ile Val Val Cys Met Cys
      260             265             270
Phe Gly Ala Thr Ile Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser
      275             280             285
Ala Glu Glu Glu Lys Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro
      290             295             300
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala
      305             310             315             320
Ala Val Arg Lys Val Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu
      325             330             335
Arg Thr Ser Cys Tyr Leu Ser Ser Lys Pro Lys Arg Arg
      340             345

```

&lt;210&gt; 2622

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Unknown (hg27-dir-0-8 conceptual translation of range 1-642)

&lt;400&gt;2622

```

Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu Val
 1              5              10              15
His Leu Leu Ser Arg Lys Lys Val Ile Val Phe Thr Leu Cys Ala Ala

```

```

      20      25      30
Arg Leu Leu Phe Leu Leu Ile Gly Cys Thr Gln Cys Ala Leu Leu
   35      40      45
Gly Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
   50      55      60
Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr Ala
   65      70      75      80
Pro Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe Thr
      85      90      95
Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Trp Cys
      100      105      110
Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala Ser
      115      120      125
Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro Val
      130      135      140
Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val Lys
      145      150      155      160
Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr Tyr
      180      185      190
Met Thr Pro Lys Ser Ser Lys Gln Glu Lys Ser Val Ser Val Phe
      195      200      205
Tyr Pro Ile Val Thr Pro
      210

```

&lt;210&gt; 2623

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (p51-dir-0-8 conceptual translation of range 1-651)

&lt;400&gt;2623

```

Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu
   1      5      10      15
Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu Cys Ala
      20      25      30
Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys Ala Leu
      35      40      45
Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
      50      55      60
Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr
      65      70      75      80
Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe
      85      90      95
Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Phe
      100      105      110
Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala
      115      120      125
Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro
      130      135      140
Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val
      145      150      155      160
Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly
      165      170      175
Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr
      180      185      190
Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val
      195      200      205
Phe Tyr Ala Ile Val Thr Pro Met Leu
      210      215

```

&lt;210&gt; 2624

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (2564517-dir-0-6 conceptual translation of range 1-474)

&lt;400&gt;2624

```

Ile Ser Phe Pro Leu Arg Tyr Thr Ile Ile Met Ser Arg Ser Ile Cys
 1           5           10           15
Ile Thr Met Val Ser Cys Cys Trp Ile Ser Gly Ser Leu Ile Ala Leu
          20           25           30
Val Val Ile Val Phe Thr Leu Gln Leu Pro Leu Cys Gly Ala Asn Val
          35           40           45
Ile Asn His Phe Phe Cys Glu Ala Thr Thr Leu Val Gly Met Ala Cys
          50           55           60
Val Asp Thr Phe Val Thr Glu Met Val Ile Phe Ser Ala Gly Ile Phe
          65           70           75           80
Thr Leu Leu Leu Pro Ser Ile Leu Thr Leu Leu Ser Tyr Ile Cys Ile
          85           90           95
Ile Val Ala Ile Val Gly Ile Arg Ser Ser Ala Gly Arg Tyr Lys Ala
          100          105          110
Phe Ser Thr Cys Ala Ser His Leu Ile Ile Val Thr Ile Phe Tyr Gly
          115          120          125
Thr Ala Ile Phe Gly Tyr Met Lys Pro Val Ser Lys Asn Ser Gly Asn
          130          135          140
Gln Asp Lys Met Thr Ser Val Phe Tyr Thr Val Thr Pro Pro
          145          150          155

```

&lt;210&gt; 2625

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Unknown (p102-dir-0-8 conceptual translation of range 2-646)

&lt;400&gt;2625

```

Phe Leu Asp Ile Cys Tyr Ile Ser Ala Ser Val Pro Gln Met Ile Val
 1           5           10           15
Asn Cys Leu Val Arg Ile Pro Ile Ile Ser Leu Gly Gln Cys Leu Ala
          20           25           30
Gln Met Cys Ala Gly Leu Tyr Leu Gly Val Val Glu Cys Leu Leu Leu
          35           40           45
Ala Val Met Ala Tyr Asp Arg Cys Ile Ala Ile Gly Asp Pro Leu Arg
          50           55           60
Tyr Ser Val Arg Met Gly Pro Gln Leu Cys Ala Gln Leu Ala Gly Ala
          65           70           75           80
Ser Trp Val Ser Ala Phe Leu Leu Thr Val Val Pro Val Leu Thr Met
          85           90           95
Pro Leu Glu Phe Cys Gly Gln His Ile Ile Asn His Phe Ser Cys Glu
          100          105          110
Leu Leu Ala Val Leu Lys Leu Ala Cys Asn Asp Leu Trp Ile Tyr Glu
          115          120          125
Leu Leu Ile Met Val Thr Ser Ser Leu Thr Leu Leu Ala Pro Phe Ala
          130          135          140
Phe Ile Leu Ala Ser Tyr Gly Cys Ile Leu Gly Ala Val Leu Lys Met
          145          150          155          160
His Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His
          165          170          175
Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ala Ile Ser Met Tyr Met
          180          185          190
Met Pro Gln Asp Lys Ala Ser Arg Asp Lys Asp Lys Ile Ile Ser Met
          195          200          205
Leu Tyr Gly Ile Val Thr Pro
          210          215

```

&lt;210&gt; 2626

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921715-dir-0-8 conceptual translation of range 2-652)

&lt;400&gt;2626

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
130          135          140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
145          150          155          160
Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
165          170          175
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
180          185          190
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
195          200          205
Ser Leu Phe Tyr Ser Leu Phe Asn Pro
210          215

```

&lt;210&gt; 2627

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (2921709-dir-0-8 conceptual translation of range 2-652)

&lt;400&gt;2627

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr
1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
130          135          140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu

```



Leu Val Leu Val Ser Tyr Leu Arg Ile Leu Ala Ala Ile Leu Arg Ile  
 145 150 155 160  
 Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His  
 165 170 175  
 Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met  
 180 185 190  
 Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu  
 195 200 205  
 Phe Tyr Ser Leu Phe Asn Pro  
 210 215

<210> 2630

<211> 352

<212> PRT

<213> Unknown (4156187-rev-1021-13 conceptual translation of range 102238-103293)

<220>

<221> VARIANT

<222> (1)...(352)

<223> Xaa = Any Amino Acid

<400>2630

Leu Leu Val Phe Cys Leu Phe Leu Cys Leu Phe Phe Ser Ser Glu Met  
 1 5 10 15  
 Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu  
 20 25 30  
 Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe  
 35 40 45  
 Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser  
 50 55 60  
 Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu  
 65 70 75 80  
 Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu  
 85 90 95  
 Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met  
 100 105 110  
 Thr Xaa Thr Phe Leu Phe Leu Ser Phe Ala His Thr Glu Cys Leu Leu  
 115 120 125  
 Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu  
 130 135 140  
 Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile  
 145 150 155 160  
 Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val His Val Ser Leu  
 165 170 175  
 Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile Asn His Phe Phe  
 180 185 190  
 Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp Leu  
 195 200 205  
 Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly Pro  
 210 215 220  
 Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile Leu  
 225 230 235 240  
 Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser  
 245 250 255  
 Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met  
 260 265 270  
 Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu  
 275 280 285  
 Phe Leu Phe Tyr Ser Ser Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr  
 290 295 300

Asn Leu Arg Asn Val Glu Val Lys Gly Ala Leu Arg Arg Ala Leu Cys  
 305 310 315 320  
 Lys Glu Ser His Ser Xaa Glu Val Xaa His Leu Asn Cys Gln Pro Gln  
 325 330 335  
 Leu Ser Arg Gly Leu Leu Met Pro Asn Tyr Cys Leu Asn Pro Glu Lys  
 340 345 350

<210> 2631

<211> 314

<212> PRT

<213> Unknown (4156187-rev-834-13 conceptual translation of range 83640-84581)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400>2631

Glu Met Gly Glu Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly  
 1 5 10 15  
 Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser  
 20 25 30  
 Leu Phe Tyr Ile Phe Thr Leu Leu Gly Asn Gly Ala Ile Leu Gly Leu  
 35 40 45  
 Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 His Leu Ala Val Val Asp Ile Ala Tyr Thr Arg Asn Thr Val Pro Gln  
 65 70 75 80  
 Met Leu Ala Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly  
 85 90 95  
 Cys Met Thr Gln Thr Phe Leu Cys Leu Ser Phe Gly His Ser Glu Cys  
 100 105 110  
 Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Arg Tyr Ser Val Ile Met Thr Trp Arg Val Cys Ile Thr Leu  
 130 135 140  
 Ala Val Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Leu Ala His Val  
 145 150 155 160  
 Val Leu Ile Leu Arg Leu Pro Phe Ser Gly Pro His Glu Ile Asn His  
 165 170 175  
 Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr  
 180 185 190  
 Trp Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Phe Leu Val  
 195 200 205  
 Gly Pro Pro Ser Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala  
 210 215 220  
 Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile  
 245 250 255  
 Ile Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys  
 260 265 270  
 Val Phe Phe Leu Phe Tyr Ser Phe Phe Asn Pro Thr Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gly Glu Val Lys Gly Ala Leu Arg Arg Ala  
 290 295 300  
 Leu Gly Lys Glu Ser His Ser Xaa Leu Val  
 305 310

<210> 2632



&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Unknown (3983369-dir-0-8 conceptual translation of range 1-669)

&lt;400&gt;2632

```

Ser His Leu Ala Ile Val Asp Met Ala Tyr Ala Cys Asn Thr Val Pro
1      5      10      15
Gln Thr Leu Ile Asn Leu Leu Asp Glu Thr Arg Pro Ile Thr Phe Ala
      20      25      30
Gly Cys Met Thr Gln Thr Tyr Leu Phe Leu Thr Phe Ala Ile Thr Glu
      35      40      45
Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys
      50      55      60
His Pro Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Ile
65      70      75      80
Met Ala Ala Val Ser Trp Ile Val Ser Phe Leu Leu Ser Leu Val His
      85      90      95
Leu Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn
      100     105     110
His Phe Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp
      115     120     125
Thr Thr Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Thr Leu
      130     135     140
Val Gly Pro Leu Cys Phe Val Leu Val Ser Tyr Thr Arg Ile Leu Val
145     150     155     160
Ala Ile Leu Arg Ile Gln Ser Gly Glu Arg Arg Arg Lys Ala Phe Ser
      165     170     175
Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala
      180     185     190
Ile Val Met Tyr Met Ala Pro Lys Ser Gln His Pro Gly Glu Gln Gln
      195     200     205
Lys Ile Leu Phe Leu Phe Tyr Ser Phe Phe Asn Pro Met Leu Asn
      210     215     220

```

&lt;210&gt; 2633

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Unknown (OST008-dir-0-8 conceptual translation of range 2-649)

&lt;400&gt;2633

```

Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Ala
1      5      10      15
Asn Leu Met Asn Gln Lys Arg Thr Ile Ser Phe Val Pro Cys Ile Met
      20      25      30
Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu Ile Leu
      35      40      45
Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Phe Gln
      50      55      60
Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Val Leu Thr
65      70      75      80
Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Glu Ile Leu Leu
      85      90      95
Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu Phe Cys
      100     105     110
Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Val Asn
      115     120     125
Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly Pro Leu
      130     135     140
Ser Leu Ile Leu Val Ser Tyr Met His Ile Leu Gly Ala Ile Leu Lys
145     150     155     160
Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys Ser Ser

```

```
<210> 2634
<211> 310
<212> PRT
<213> Unknown (4156187-dir-87-12 conceptual translation of range 8841-9771)
```

[illegible]

1604

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(339)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2635

```

Ile Cys Phe Xaa Thr Leu Leu Leu Asn His Glu His Xaa Leu Asp Phe
 1          5          10          15
Leu Cys His Arg Asp Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe
          20          25          30
Leu Leu Leu Gly Phe Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe
          35          40          45
Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr
          50          55          60
Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr
65          70          75          80
Phe Phe Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
          85          90          95
Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
          100          105          110
Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
          115          120          125
Val Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val
          130          135          140
Ala Ile Cys His Pro Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
145          150          155          160
Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
          165          170          175
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
          180          185          190
Lys Ile Tyr His Phe Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
          195          200          205
Cys Ala Asp Thr His Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile
          210          215          220
Ser Gly Leu Val Gly Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys
225          230          235          240
Ile Leu Cys Ala Ile Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys
          245          250          255
Ala Phe Cys Thr Cys Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr
          260          265          270
Gly Thr Ala Ile Ile Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys
          275          280          285
Glu Gln Lys Lys Tyr Leu Leu Phe His Ser Leu Phe Asn Pro Met
          290          295          300
Leu Asn Pro Leu Ile Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr
305          310          315          320
Leu Lys Arg Val Leu Gly Val Glu Arg Ala Leu Xaa Lys Gly Leu Trp
          325          330          335
His Cys Asp

```

&lt;210&gt; 2636

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Unknown (4156166-dir-1014-13 conceptual translation of range 101536-102552)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(339)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2636

```

Ile Cys Phe Xaa Thr Leu Leu Leu Asn His Glu His Xaa Leu Asp Phe
 1           5           10           15
Leu Cys His Arg Asp Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe
          20           25           30
Leu Leu Leu Gly Phe Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe
          35           40           45
Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr
          50           55           60
Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr
65           70           75           80
Phe Phe Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
          85           90           95
Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
          100          105          110
Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
          115          120          125
Val Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val
          130          135          140
Ala Ile Cys His Pro Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
145          150          155          160
Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
          165          170          175
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
          180          185          190
Lys Ile Tyr His Phe Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
          195          200          205
Cys Ala Asp Thr His Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile
          210          215          220
Ser Gly Leu Val Gly Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys
225          230          235          240
Ile Leu Cys Ala Ile Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys
          245          250          255
Ala Phe Arg Thr Cys Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr
          260          265          270
Gly Thr Ala Ile Ile Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys
          275          280          285
Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met
          290          295          300
Leu Asn Pro Leu Ile Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr
305          310          315          320
Leu Lys Arg Val Leu Gly Val Glu Arg Ala Leu Xaa Lys Gly Leu Trp
          325          330          335
His Cys Asp

```

&lt;210&gt; 2637

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (293753-dir-0-8 conceptual translation of range 2-667)

&lt;400&gt;2637

```

Phe Phe Leu Ser His Leu Ala Ile Val Asp Ile Ala Tyr Ala Cys Asn
 1           5           10           15
Thr Val Pro Gln Met Leu Val Asn Leu Leu Asp Pro Val Lys Pro Ile
          20           25           30
Ser Tyr Ala Gly Cys Met Thr Gln Thr Phe Leu Phe Leu Thr Phe Ala
          35           40           45
Ile Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val
          50           55           60

```

Ala Ile Cys His Pro Leu Arg Tyr Ser Ala Ile Met Ser Trp Arg Val  
 65 70 75 80  
 Cys Ser Thr Met Ala Val Thr Ser Trp Ile Ile Gly Val Leu Leu Ser  
 85 90 95  
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Val Ser Gln  
 100 105 110  
 Lys Val Asn His Phe Phe Cys Glu Ile Thr Ala Ile Leu Lys Leu Ala  
 115 120 125  
 Cys Ala Asp Thr His Leu Asn Glu Thr Met Val Leu Ala Gly Ala Val  
 130 135 140  
 Ser Val Leu Val Gly Pro Phe Ser Ser Ile Val Val Ser Tyr Ala Cys  
 145 150 155 160  
 Ile Leu Gly Ala Ile Leu Lys Ile Gln Ser Glu Glu Gly Gln Arg Lys  
 165 170 175  
 Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Tyr  
 180 185 190  
 Gly Thr Ala Ile Val Met Tyr Val Gly Pro Arg His Gly Ser Pro Lys  
 195 200 205  
 Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn  
 210 215 220

&lt;210&gt; 2638

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Unknown (892-dir-0-5 conceptual translation of range 2-343)

&lt;400&gt;2638

Ile Cys His Pro Leu Arg Tyr Lys Val Ile Met Ser Arg Trp Met Cys  
 1 5 10 15  
 Leu Leu Met Val Gly Ile Cys Gly Val Tyr Gly Val Val Gly Ser Leu  
 20 25 30  
 Cys Tyr Thr Phe Phe Ala Met Arg Leu Pro Tyr Cys Gly Pro Asn Glu  
 35 40 45  
 Ile Asp His Tyr Phe Cys Glu Val Pro Ala Val Leu Lys Leu Ala Cys  
 50 55 60  
 Ala Asp Thr Ser Leu Asn Asp Leu Val Asp Phe Ile Thr Gly Phe Asn  
 65 70 75 80  
 Val Ile Val Val Pro Leu Thr Leu Val Val Ile Val Tyr Ala Asn Ile  
 85 90 95  
 Phe Ala Thr Ile Met Lys Ile Arg Ser Ala Gln Gly Gln Ile Lys Ala  
 100 105 110  
 Phe Ser

&lt;210&gt; 2639

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Unknown (2331266-dir-0-13 conceptual translation of range 111-1160)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(350)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2639

Leu Ala Gln Asn Ile Lys Arg Lys Thr Ala Met Asn Ser Val Asn Ala  
 1 5 10 15  
 Ser Phe Tyr Gln Asn Ile Ser Ile Val Arg Pro Glu Tyr Phe Phe Ile  
 20 25 30  
 Ser Gly Leu Ser Gly Ile Pro Tyr Ser Ser Tyr Tyr Tyr Ile Phe Leu  
 35 40 45

```

Phe Val Val Tyr Phe Ile Ser Val Ile Gly Asn Ser Val Val Leu Leu
 50          55          60
Ile Ile Ala Val Asp Arg Ser Leu His Ser Pro Lys Tyr Ile Gly Val
65          70          75          80
Phe Asn Leu Ala Leu Ala Asp Ile Gly Glu Thr Asn Ala Leu Ile Pro
 85          90          95
Asn Met Met Lys Thr Phe Leu Phe Asn Ser Gln Tyr Ile Ser Tyr Asn
100         105         110
Gly Cys Met Ala Asn Met Phe Phe Val Val Leu Phe Asn Ser Ile Gln
115         120         125
Ser Phe Thr Leu Val Ala Leu Ala Tyr Asp Arg Phe Ile Ala Ile Cys
130         135         140
Leu Pro Leu Arg Tyr His Ala Ile Val Asn Asn Thr Ser Met Ile Leu
145         150         155         160
Ile Phe Leu Ala Ile Trp Ala Phe Asn Ser Ser Val Val Ala Ser Met
165         170         175
Val Ser Met Ile Thr Arg Leu Ser Ile Cys Lys Ser Asn Val Ile Pro
180         185         190
Ser Tyr Phe Cys Asp His Gly Pro Ile Phe Arg Leu Ala Cys Asn Asp
195         200         205
Ile Lys Ile Asn Glu Phe Phe Ala Phe Phe Ile Ser Ile Leu Tyr Leu
210         215         220
Thr Met Pro Met Val Ile Ile Ala Leu Ser Tyr Leu Asn Ile Phe Leu
225         230         235         240
Ala Leu Ile Lys Ile Thr Thr Trp Glu Gly Arg Leu Lys Ala Leu Lys
245         250         255
Thr Cys Val Ser His Leu Leu Leu Val Gly Ile Phe Phe Leu Pro Leu
260         265         270
Leu Cys Thr Tyr Ile Ala Gln Val Leu Leu Ala Leu Thr Pro Asn Ala
275         280         285
Arg Val Ile Ser Thr Ser Leu Ser Tyr Ala Ile Pro Pro Met Leu Asn
290         295         300
Pro Ile Ile Tyr Val Leu Asn Thr Ala Glu Ile Lys Tyr Ile Ile Arg
305         310         315         320
Lys Leu Phe Lys Arg Arg Leu Arg Ser Val Ser Asp Asn Ile Ser Lys
325         330         335
Xaa Phe Cys Ser Cys Trp Gly Leu Tyr Gln Ser Lys Lys Lys
340         345         350

```

&lt;210&gt; 2640

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Unknown (2331262-dir-1-13 conceptual translation of range 199-1257)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(353)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2640

```

Val Gln Asn Thr Lys Cys Lys Val Ala Met Ser Ser Leu Asn Ala Ser
 1          5          10         15
Phe Ser Leu Asn Ile Ser Val Val Arg Pro Glu Tyr Phe Phe Ile Leu
20         25         30
Gly Leu Ser Gly Ile Pro Tyr Ser Asn Leu Tyr Tyr Ile Phe Ile Phe
35         40         45
Ile Ile Thr Phe Ile Thr Val Ile Gly Asn Phe Leu Val Ile Leu Leu
50         55         60
Ile Val Leu Asp Arg Ser Leu His Ser Pro Lys Tyr Ile Gly Val Phe
65         70         75         80
Asn Leu Ala Leu Ala Asp Ile Gly Glu Thr Asn Ala Leu Ile Pro Asn

```

```
<210> 2641
<211> 351
<212> PRT
<213> Unknown (4726083-dir-262-12 conceptual translation of range 26289-
27340)

<220>
<221> VARIANT
<222> (1)...(351)
<223> Xaa = Any Amino Acid
```

<400>2641																
Leu	Ser	Pro	Ser	Leu	Lys	Pro	Ser	Cys	Asn	Cys	Asp	Pro	Thr	Met	Trp	
1				5					10					15		
Pro	Asn	Ser	Ser	Asp	Ala	Pro	Phe	Leu	Leu	Thr	Gly	Phe	Leu	Gly	Leu	
			20					25					30			
Glu	Met	Ile	His	His	Trp	Ile	Ser	Ile	Pro	Phe	Phe	Val	Ile	Tyr	Phe	
		35					40					45				
Ser	Ile	Ile	Val	Gly	Asn	Gly	Thr	Leu	Leu	Phe	Ile	Ile	Trp	Ser	Asp	
	50					55					60					
His	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe	Leu	Ala	Val	Leu	Ala	Ser	
65					70				75					80		
Met	Asp	Leu	Gly	Met	Thr	Leu	Thr	Thr	Met	Pro	Thr	Val	Leu	Gly	Val	
				85					90					95		
Leu	Val	Leu	Asn	Gln	Arg	Glu	Ile	Val	His	Gly	Ala	Cys	Phe	Ile	Gln	

```
<210> 2642
<211> 159
<212> PRT
<213> Unknown (4680279-dir-0-6 conceptual translation of range 2-478)
```

<210> 2643  
<211> 160



&lt;212&gt; PRT

&lt;213&gt; Unknown (902668-dir-0-6 conceptual translation of range 2-481)

&lt;400&gt;2643

```

Ile Ser Asn Pro Leu Arg Tyr Ala Ser Val Leu Thr Asn Asn Val Ile
 1           5           10           15
Ile Arg Ile Gly Val Ala Ile Thr Thr Arg Ala Thr Leu Ser Leu Leu
          20           25           30
Pro Leu Pro Phe Leu Leu Lys Arg Leu Asn Tyr Cys Pro Gly Lys Ile
          35           40           45
Leu Leu Ser His Ser Phe Cys Phe His Ala Asp Val Met Lys Leu Ala
          50           55           60
Cys Ala Asp Ile Thr Val Asn Ile Leu Tyr Gly Leu Tyr Val Val Leu
65          70          75          80
Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Val Met Ser Tyr Ser Leu
          85          90          95
Ile Leu His Thr Val Met Gly Leu Ala Ser Pro Arg Glu Arg Val Arg
          100          105          110
Thr Leu Asn Thr Cys Val Ser His Ile Ser Ala Val Leu Val Phe Tyr
          115          120          125
Ile Pro Val Ile Gly Val Ser Met Ile His Arg Phe Gly Lys His Leu
          130          135          140
Pro His Ile Val His Ala Leu Val Ala Tyr Val Tyr Leu Val Val Pro
145          150          155          160

```

&lt;210&gt; 2644

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Unknown (3927807-dir-288-13 conceptual translation of range 29007-29954)

&lt;400&gt;2644

```

Leu Asn Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu
 1           5           10           15
Ala Gly Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro
          20           25           30
Phe Gly Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu
          35           40           45
Leu Val Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe
          50           55           60
Leu Leu Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu
65          70          75          80
Pro Thr Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe
          85          90          95
Pro Ala Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala
          130          135          140
Gln Ile Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro
145          150          155          160
Leu Ile Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu
          165          170          175
Ser His Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr
          180          185          190
Asp Ala Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala
          195          200          205
Ile Leu Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Il Phe Arg
          210          215          220
Thr Val Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn

```

```
<210> 2645
<211> 316
<212> PRT
<213> Unknown (4761596-dir-254-13 conceptual translation of range 25614-26561)
```

Phe	His	Asn	Asp	Thr	Asn	Pro	Gln	Asp	Val	Trp	Tyr	Val	Leu	Ile	Gly
1				5					10					15	
Ile	Pro	Gly	Leu	Glu	Asp	Leu	His	Ser	Trp	Ile	Ala	Ile	Pro	Ile	Cys
		20						25					30		
Ser	Met	Tyr	Ile	Val	Ala	Val	Ile	Gly	Asn	Val	Leu	Leu	Ile	Phe	Leu
		35					40					45			
Ile	Val	Thr	Glu	Arg	Ser	Leu	His	Glu	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
Met	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Leu	Ser	Thr	Ala	Thr	Ala	Pro	Lys
65					70					75				80	
Met	Leu	Ala	Ile	Phe	Trp	Phe	His	Ser	Arg	Gly	Ile	Ser	Phe	Gly	Ser
				85					90					95	
Cys	Val	Ser	Gln	Met	Phe	Phe	Ile	His	Phe	Ile	Phe	Val	Ala	Glu	Ser
			100					105					110		
Ala	Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Tyr
		115					120					125			
Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Ser	Ser	Val	Ile	Gly	Lys	Ile
	130					135					140				
Gly	Thr	Ala	Ala	Val	Val	Arg	Ser	Phe	Leu	Ile	Cys	Phe	Pro	Phe	Ile
145					150					155				160	
Phe	Leu	Val	Tyr	Arg	Leu	Leu	Tyr	Cys	Gly	Lys	His	Ile	Ile	Pro	His
				165					170					175	
Ser	Tyr	Cys	Glu	His	Met	Gly	Ile	Ala	Arg	Leu	Ala	Cys	Asp	Asn	Ile
			180					185					190		
Thr	Val	Asn	Ile	Ile	Tyr	Gly	Leu	Thr	Met	Ala	Leu	Leu	Ser	Thr	Gly
		195					200					205			
Leu	Asp	Ile	Leu	Leu	Ile	Ile	Ile	Ser	Tyr	Thr	Met	Ile	Leu	Arg	Thr
	210					215					220				
Val	Phe	Gln	Ile	Pro	Ser	Trp	Ala	Ala	Arg	Tyr	Lys	Ala	Leu	Asn	Thr
225					230					235				240	
Cys	Gly	Ser	His	Ile	Cys	Val	Ile	Leu	Leu	Phe	Tyr	Thr	Pro	Ala	Phe
				245					250					255	
Phe	Ser	Phe	Phe	Ala	His	Arg	Phe	Gly	Gly	Lys	Thr	Val	Pro	Arg	His
			260					265					270		
Ile	His	Ile	Leu	Val	Ala	Asn	Leu	Tyr	Val	Val	Val	Pro	Pro	Met	Leu
		275					280					285			
Asn	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr	Lys	Gln	Ile	Gln	Asp	Arg	Val
		290				295						300			
Val	Phe	Leu	Phe	Ser	Ser	Val	Ser	Thr	Cys	Gln	His				
305					310					315					

**<210> 2646**

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Unknown (2564519-dir-0-6 conceptual translation of range 1-477)

&lt;400&gt;2646

```

Ile Cys Asn Pro Leu Arg Tyr Ala Val Met Leu Thr Asn Ile Val Ile
 1             5             10             15
Arg Lys Ile Ala Ile Leu Ala Val Val Arg Gly Leu Cys Val Val Ala
      20             25             30
Pro Phe Thr Phe Leu Leu His Arg Leu Pro Tyr Cys Gln Asn Asn Val
      35             40             45
Val Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ala Cys
      50             55             60
Ala Asp Val Thr Val Asn Ser Val Tyr Gly Leu Thr Ile Ala Leu Ser
65             70             75             80
Ile Thr Gly Leu Asp Ala Ala Leu Val Val Ala Ser Tyr Val Leu Ile
      85             90             95
Leu Arg Ala Val Leu Asn Met Asn Ser Met Thr Ala Arg His Lys Ala
      100            105            110
Leu Ser Thr Cys Ala Ser His Val Cys Val Ile Ile Leu Phe Cys Val
      115            120            125
Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Lys Asn Ile Pro
      130            135            140
Leu Asn Val His Ile Phe Val Ala Asn Leu Tyr Ile Leu Leu Pro
145            150            155

```

&lt;210&gt; 2647

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (1644474-dir-0-6 conceptual translation of range 1-474)

&lt;400&gt;2647

```

Lys Pro Leu His Tyr Asn Glu Ile Met Asn Ser Ser Met Phe Leu Lys
 1             5             10             15
Leu Phe Leu Phe Thr Leu Ile Arg Ser Gly Thr Ile Met Ser Thr Leu
      20             25             30
Val Ala Leu Ala Ser Pro Leu Ser Phe Cys Gly Ser Asn Val Ile Tyr
      35             40             45
His Cys Tyr Cys Asp His Met Ala Leu Val Ser Leu Ala Cys Asp Ser
      50             55             60
Ile Ala Gln Asn Gln Thr Met Gly Leu Ile Val Ile Ile Cys Phe Val
65             70             75             80
Gly Ile Asp Thr Ser Val Ile Phe Phe Ser Tyr Val Lys Ile Leu His
      85             90             95
Val Val Leu Gly Thr Ala Ala Gly Glu Asp Arg Trp Lys Ala Phe His
      100            105            110
Thr Cys Gly Thr His Leu Met Val Met Ile Cys Phe Tyr Phe Val Gly
      115            120            125
Ser Val Thr Phe Leu Ser Arg Asn Leu Asn Ile Pro Ile Pro Ile Asp
      130            135            140
Val Asn Thr Phe Leu Gly Val Met Tyr Ile Val Phe Pro Ala
145            150            155

```

&lt;210&gt; 2648

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Unknown (4877304-dir-0-6 conceptual translation of range 2-484)

&lt;400&gt;2648

```

Leu Ala Ile Cys Tyr Pro Leu His Tyr Ser Ala Leu Met Thr Asn Lys
 1             5             10             15

```

```

His Ala Ile Arg Leu Ser Cys Leu Cys Trp Ile Ile Gly Phe Leu Ile
      20      25      30
Leu Ile Met Asn Leu Cys Phe Ile Arg Gln Thr Leu Phe Cys Gly Pro
      35      40      45
Asn Glu Val Pro His Tyr Phe Cys Asp Tyr Ser Ala Val Ala Ala Leu
      50      55      60
Ala Cys Asn Asp Ile Ser Ile Tyr Ala Ala Val Gly Phe Ala Ile Ala
      65      70      75      80
Met Cys Val Ile Cys Ser Val Leu Leu Cys Leu Val Tyr Ser Tyr Val
      85      90      95
Lys Ile Val Ala Ser Val Leu Lys Ile Ala Ser Thr Asp Gly Arg Gln
      100     105     110
Lys Ala Phe Ser Thr Cys Val Ser His Leu Phe Val Val Ser Val Phe
      115     120     125
Ser Ile Leu Ala Ala Phe Val Phe Val Ser Tyr Arg Ile Glu Glu Phe
      130     135     140
Ser Glu Asp Ala Arg Met Ile Ile His Val Val Gln Asn Thr Phe Pro
      145     150     155     160
Ser

```

&lt;210&gt; 2649

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Unknown (5262456-dir-284-6 conceptual translation of range 28407-28908)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(168)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt;2649

```

Gly Phe Trp Leu Gly Cys Tyr Leu Trp Phe Met Val Val Leu Thr Leu
  1      5      10      15
Ala Ile Arg Leu Arg Pro Phe Gly Leu Gly Gly Phe Leu Leu Lys Xaa
      20      25      30
Thr Ile Glu Xaa Gly Ala Cys Pro Arg Xaa Val Met Leu Leu Leu Cys
      35      40      45
Gln Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile Phe Leu
      50      55      60
Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala Val Ala
      65      70      75      80
Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe Gly Thr
      85      90      95
Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr Val Arg
      100     105     110
Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu Gly Lys
      115     120     125
Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn Pro Tyr
      130     135     140
Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu Ile Gly
      145     150     155     160
Lys Glu Lys Gly Ser Gly Asp Thr
      165

```

&lt;210&gt; 2650

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (3941546-dir-0-12 conceptual translation of range 37-972)

&lt;400&gt;2650

```

Asn Val Ser Phe Tyr Asn Phe Lys Cys Thr Leu Ser Glu Leu Thr Gln
 1          5          10          15
Pro Gln Arg Val Leu Ile Trp Val Phe Thr Ile Ile Ile Thr Ile
 20          25          30
Thr Val Val Gly Asn Ile Leu Thr Ile Val Ser Ile Leu Tyr Phe Arg
 35          40          45
Gln Leu Gln Thr Arg Thr Asn Val Leu Ala Leu Ser Leu Ala Leu Ala
 50          55          60
Asp Phe Leu Val Gly Cys Leu Ile Met Pro Phe Ser Val Met Arg Thr
 65          70          75          80
Ala Tyr Ser Cys Trp Phe Tyr Gly Gln Leu Met Cys Arg Ile His Thr
 85          90          95
Trp Leu Asp Tyr Thr Phe Thr Thr Cys Ser Ile Phe Asn Leu Ala Cys
 100          105          110
Ile Ser Ile Asp Arg Tyr Val Ala Ile Ser Asp Pro Leu Arg Tyr Asp
 115          120          125
Gln Arg Val Thr Tyr Arg Ile Leu Ala Val Met Leu Thr Ile Cys Trp
 130          135          140
Gly Asn Ile Ile Pro Tyr Gly Val Ser Tyr Met Leu Lys Leu Asn Ile
 145          150          155          160
Asn Gly Ile Glu Ser Val Val Ala Ala Lys Ser Cys Pro Asp Asn Cys
 165          170          175
Ser Val Phe Met Asn Val Pro Phe Gly Leu Ala Asn Ser Met Gly Ala
 180          185          190
Tyr Val Leu Pro Met Leu Phe Ile Met Ala Ala Tyr Ser Arg Ile Tyr
 195          200          205
Val Met Ala Arg Asn Gln Ala Lys Arg Ile Ser Ser Leu Gly Asp Gln
 210          215          220
Val Arg Ala Ser Asn Ala Ser Asp Leu Thr Met Gln Ser Lys Trp Asn
 225          230          235          240
Ala Met Lys Arg Asp His Asn Ala Thr Lys Thr Leu Gly Met Ile Met
 245          250          255
Val Val Leu Phe Ile Val Trp Leu Pro Phe Ile Val Val Val Ala Thr
 260          265          270
Glu Pro Val Ile Gly Tyr Arg Met Asp Ser Thr Val Trp Asp Val Ala
 275          280          285
Asn Trp Phe Thr Tyr Phe Asn Ser Arg Met Asn Pro Ile Leu Phe Ala
 290          295          300
Ser Phe Asn Asn Ser Phe Arg Ser
305          310

```

&lt;210&gt; 2651

&lt;211&gt; 314

&lt;212&gt; PRT

<213> Unknown (17-2 (HGMP07I 400671 OL1A 438389 P30953 OLFI 1804351A S20572)  
Parmentier-M 92)

&lt;400&gt;2651

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20          25          30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35          40          45
Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65          70          75          80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85          90          95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser

```

100	105	110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe		
115	120	125
Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu		
130	135	140
Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr		
145	150	155
Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His		
165	170	175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr		
180	185	190
Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val		
195	200	205
Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser		
210	215	220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile		
245	250	255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr		
260	265	270
Val Met Ala Met Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe		
275	280	285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val		
290	295	300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu		
305	310	

&lt;210&gt; 2652

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (17-4 (OLFR1 425221 482560 A48413 HSHGM07EG) Schurmans-S 93)

&lt;400&gt;2652

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly	
1	5
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu	
20	25
Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala	
35	40
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala	
50	55
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys	
65	70
Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly	
85	90
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn	
100	105
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys	
115	120
Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu	
130	135
Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr	
145	150
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr	
165	170
Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile	
180	185
Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe L u	
195	200
Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala	
	205

```

      210              215              220
Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
      245              250              255
Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
      260              265              270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
      275              280              285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
      290              295              300
Asp Lys His Phe Lys Arg Leu Thr
305              310

```

&lt;210&gt; 2653

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (17-40 (OL1E 516320 2209308A 1588713))

&lt;400&gt;2653

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
1              5              10              15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val
      20              25              30
Leu Phe Leu Phe Ala Tyr Leu Val Thr Val Arg Gly Asn Leu Ser Ile
      35              40              45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Thr Pro Met Tyr Phe
      50              55              60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Ser Val Thr
      65              70              75              80
Val Pro Ser Met Leu Ser Arg Leu Leu Ser Arg Lys Arg Ala Val Pro
      85              90              95
Cys Gly Ala Cys Leu Thr Gln Leu Phe Phe Phe His Leu Phe Val Gly
      100              105              110
Val Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Phe Leu Ala
      115              120              125
Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
      130              135              140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
      145              150              155              160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Val
      165              170              175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
      180              185              190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile
      195              200              205
Met Ala Gly Thr Pro Met Ala Leu Ile Val Ile Ser Tyr Ile His Val
      210              215              220
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
      225              230              235              240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly
      245              250              255
Ser Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Thr Lys Leu Ser Asp
      260              265              270
Lys Asp Lys Ala Val Gly Ile Phe Asn Thr Val Ile Asn Pro Met Leu
      275              280              285
Asn Pro Ile Ile Tyr Ser Phe Arg Asn Pro Asp Val Gln Ser Ala Ile
      290              295              300
Trp Arg Met Leu Thr Gly Arg Arg Ser Leu Ala
305              310              315

```

<210> 2654  
 <211> 323  
 <212> PRT  
 <213> Unknown (17-93)

<400>2654

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
          20          25          30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
          35          40          45
Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
          85          90          95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
          100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
          130          135          140
Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
          145          150          155          160
Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
          165          170          175
Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
          180          185          190
Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
          195          200          205
Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
          210          215          220
Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
          225          230          235          240
Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
          245          250          255
Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
          260          265          270
Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
          275          280          285
Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
          290          295          300
Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
          305          310          315          320
Phe Leu Leu

```

<210> 2655  
 <211> 316  
 <212> PRT  
 <213> Unknown (FAT11 (HUMORLMHC A57069 601919 1097174 1362875) Fan-W 95)

<400>2655

```

Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1          5          10          15
Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
          20          25          30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
          35          40          45

```



Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu  
 50 55 60  
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu  
 65 70 75 80  
 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser  
 85 90 95  
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu  
 100 105 110  
 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu  
 115 120 125  
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser  
 130 135 140  
 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser  
 145 150 155 160  
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val  
 165 170 175  
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr  
 180 185 190  
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro  
 195 200 205  
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu  
 210 215 220  
 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser  
 225 230 235 240  
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val  
 245 250 255  
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe  
 260 265 270  
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr  
 275 280 285  
 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly  
 290 295 300  
 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala  
 305 310 315

&lt;210&gt; 2656

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Unknown (H8 (432510) Selbie-LA 92)

&lt;400&gt;2656

Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Gly Phe  
 1 5 10 15  
 Ile Ser Thr Ile Ile Pro Lys Met Leu Asp His Ile Ser Ser Gly Ile  
 20 25 30  
 Lys Leu Ile Ser Tyr Gly Glu Cys Leu Thr Gln Leu Tyr Phe Ser Gly  
 35 40 45  
 Leu Phe Ala Asp Leu Asp Asn Asn Phe Leu Leu Ala Val Met Ala Ile  
 50 55 60  
 Asp Arg Tyr Val Ala Ile Ser His Pro Leu His Tyr Ala Leu Thr Met  
 65 70 75 80  
 Asn Ser Gln Arg Cys Val Leu Leu Val Ala Val Ser Trp Val Ile Thr  
 85 90 95  
 Ile Leu His Ala Leu Val His Thr Leu Leu Val Thr Arg Leu Ser Phe  
 100 105 110  
 Cys Gly Pro Asn Ile Ile Pro His Phe Phe Cys Asp Leu Val Pro Leu  
 115 120 125  
 Leu Lys Leu Ala Cys Ser Ser Thr Cys Val Asn Asp Leu Val Leu Ile  
 130 135 140  
 Leu Val Pro Gly Thr Leu Leu Ile Ala Pro Phe Val Cys Ile Leu Met  
 145 150 155 160

Ser Tyr Phe Tyr Ile Ala Leu Ala Ile Leu Arg Ile Asp Ser Pro Arg  
 165 170 175  
 Gly Lys Gln Arg Ala Phe Ser Ser Cys Thr Ser His Leu Ser Val Val  
 180 185 190  
 Ser Leu Phe Tyr Ser Thr Ala Ile Gly Val Tyr Leu Cys Pro Pro Ser  
 195 200 205  
 Ser His Ser Asp Gly Lys Asp Arg Val Phe Ser Val Met Tyr Thr Val  
 210 215 220  
 Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp  
 225 230 235 240  
 Met Lys Gly Ala Leu Gly Lys Leu Leu Gly Ile Lys Thr Ser  
 245 250

&lt;210&gt; 2657

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Unknown (G3 (432509) Selbie-LA 92)

&lt;400&gt;2657

Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Asp Leu Gln Pro Val  
 1 5 10 15  
 Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu  
 20 25 30  
 Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His  
 35 40 45  
 Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Pro Asp Ile Gly  
 50 55 60  
 Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp Thr Gln Ser His  
 65 70 75 80  
 Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu  
 85 90 95  
 Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr  
 100 105 110  
 Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr Pro Ile Ile Val  
 115 120 125  
 Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser  
 130 135 140  
 Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Leu Thr Ile  
 145 150 155 160  
 Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp Pro Ser Gln Leu  
 165 170 175  
 Leu Lys Leu Ala Cys Ser Asp Ser Val Leu Thr Asn Ile Phe Ile Tyr  
 180 185 190  
 Ser Ile Gly  
 195

&lt;210&gt; 2658

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (HsOLF1 (1336041 HSU56420) Issel-Tarver-L 97 11q11)

&lt;400&gt;2658

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu  
 1 5 10 15  
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met  
 20 25 30  
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met  
 35 40 45  
 Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Il Val

```

65          70          75          80
Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
      85          90          95
Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
      100        105        110
Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
      115        120        125
Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
      130        135        140
Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val
      145        150        155        160
His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
      165        170        175
Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
      180        185        190
Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
      195        200        205
Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
      210        215        220
Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
      225        230        235        240
Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
      245        250        255
Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
      260        265        270
Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn
      275        280        285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu
      290        295        300
Lys Val Leu Arg Ser Lys Val Asp Ser Ser
305          310

```

&lt;210&gt; 2659

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (HsOLF3 (1336043 HSU56421) Issel-Tarver-L 97 7q35)

&lt;400&gt;2659

```

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
1          5          10          15
Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
      20        25        30
Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
      35        40        45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50        55        60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
      65        70        75        80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
      85        90        95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
      100        105        110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
      115        120        125
Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
      130        135        140
Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
      145        150        155        160
Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
      165        170        175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

```

```

      180      185      190
Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
      195      200      205
Thr Pro Leu Cys Leu Val Leu Ser Tyr Ile Gln Ile Ile S r Thr
      210      215      220
Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
      225      230      235      240
Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
      245      250      255
Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
      260      265      270
Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
      290      295      300
Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
      305      310      315

```

&lt;210&gt; 2660

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (OLFMF gi|2370145|gnl|PID|e334200 olfactory receptor protein)

&lt;400&gt;2660

```

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
  1      5      10      15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
      20      25      30
Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
      35      40      45
Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
      65      70      75      80
Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
      85      90      95
Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
      115      120      125
Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
      130      135      140
Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
      145      150      155      160
Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
      165      170      175
Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asn Thr
      180      185      190
His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
      195      200      205
Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
      210      215      220
Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
      245      250      255
Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
      260      265      270
Met Ala Thr Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val

```

290 295 300  
 Ile Gly Arg Val Val Phe Ser Val  
 305 310

&lt;210&gt; 2661

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Unknown (OLFMF2 gi|2808536|emb|AJ003145|HSAJ03145 Homo sapiens mRNA for )

&lt;400&gt;2661

Val Gln Thr Tyr Glu Arg Asp Lys Pro Val Ser Val Ser Glu Phe Leu  
 1 5 10 15  
 Leu Leu Gly Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val  
 20 25 30  
 Phe Phe Leu Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile  
 35 40 45  
 Ile Leu Ala Ile Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe  
 50 55 60  
 Phe Leu Ser Asn Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val  
 65 70 75 80  
 Pro Lys Met Leu Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe  
 85 90 95  
 Ser Gly Cys Leu Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met  
 100 105 110  
 Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val  
 115 120 125  
 Cys Arg Pro Leu His Tyr Thr Ala Lys Met Ile His Gln Leu Cys Ala  
 130 135 140  
 Leu Leu Val Thr Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu  
 145 150 155 160  
 His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile  
 165 170 175  
 Pro His Ile Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser  
 180 185 190  
 Asp Thr His Leu Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val  
 195 200 205  
 Thr Ile Thr Pro Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr  
 210 215 220  
 Cys Val Val Leu Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe  
 225 230 235 240  
 Ser Thr Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr  
 245 250 255  
 Ile Met Ser Pro Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg  
 260 265 270  
 Asp Ile Ala Ala Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn  
 275 280 285  
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val  
 290 295 300  
 Lys Val Val Ala Val Lys Phe Phe Ser Val Gln  
 305 310 315

&lt;210&gt; 2662

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (CFDTMT)

&lt;400&gt;2662

Met Thr Glu Lys Asn Gln Thr Val Val Ser Glu Phe Val Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Asp Pro Asp Gln Arg Asp Leu Phe Tyr Ala Leu Phe Leu

```
<210> 2663
<211> 309
<212> PRT
<213> Unknown (CF0LP4 (CFU53682) Issel-Tarver-L 97)
```

Met	Glu	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Pro	Glu	Phe	Leu	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Glu	Glu	Pro	Lys	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu
			20					25					30		
Ser	Met	Tyr	Leu	Val	Thr	Ile	Leu	Gly	Asn	Leu	Leu	Leu	Ile	Leu	Ala
		35					40					45			
Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
		50				55					60				
Asn	Leu	Ser	Phe	Val	Asp	Ile	Cys	Phe	Thr	Cys	Thr	Thr	Ile	Pro	Lys
65					70					75					80
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Arg	Lys	Val	Ile	Thr	Tyr	Glu	Ser
			85						90					95	
Cys	Ile	Ile	Gln	Met	Tyr	Phe	Phe	Glu	Leu	Phe	Ala	Gly	Ile	Asp	Asn
			100					105					110		
Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Tyr
		115					120					125			
Pro	Leu	His	Tyr	Met	Val	Ile	Met	Asn	Pro	Gln	Leu	Cys	Ser	Leu	Leu

```

      130              135              140
Leu Leu Val Ser Trp Ile Met Ser Ala Leu His Ser Leu Leu Gln Thr
145              150              155              160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr His Phe Gln Ile Pro His
      165              170              175
Phe Phe Cys Glu Leu Asn Gln Met Ile Gln Leu Ala Cys Ser Asp Thr
      180              185              190
Phe Leu Asn Asn Met Met Leu Tyr Phe Ala Ala Ile Leu Leu Gly Val
      195              200              205
Ala Pro Leu Val Gly Val Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser
      210              215              220
Ile Arg Gly Ile Ser Ser Ala His Ser Lys Tyr Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu
      245              250              255
Gly Val Tyr Leu Ser Ser Ala Ala Pro Gln Ser Thr His Thr Ser Ser
      260              265              270
Val Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Asn Val Phe
      290              295              300
Phe Arg Gly Lys Pro
305

```

&lt;210&gt; 2664

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (CfOLF3 (CFU53681) Issel-Tarver-L 97)

&lt;400&gt;2664

```

Met Gly Thr Gly Asn Gln Thr Trp Val Arg Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Ser Ser Asp Trp Asp Thr Glu Val Ser Leu Phe Val Leu Phe Leu
      20      25      30
Ile Thr Tyr Met Val Thr Val Leu Gly Asn Phe Leu Ile Ile Leu Leu
      35      40      45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Ile Pro Gln
65      70      75      80
Met Leu Ala His Leu Leu Ala Ala His Lys Ala Ile Pro Phe Val Ser
      85      90      95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Gly Leu Gly Gly Ile Glu Phe
      100      105      110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
      115      120      125
Pro Leu Arg Tyr Ser Val Ile Met His Gly Gly Leu Cys Thr Arg Leu
      130      135      140
Ala Ile Thr Ser Trp Val Ser Gly Ser Met Asn Ser Leu Met Gln Thr
145      150      155      160
Val Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Tyr Ile Asp His
      165      170      175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
      180      185      190
Ser Ser Asn Glu Ile Ala Ile Met Val Ser Ser Ile Val Leu Leu Met
      195      200      205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
      210      215      220
Ile Leu Lys Ile Gln Ser Thr Glu Gly Arg Lys Lys Ala Phe His Thr
225      230      235      240
Cys Ala Ser His Leu Thr Val Val Val Leu Cys Tyr Gly Met Ala Ile

```

<213> Unknown (CfOLF2 (1314663 CFU53680) Issel-Tarver-L 97)

<213> Unknown (CfOLF1 (1314661 CFU53679) Issel-Tarver-L 97)



&lt;400&gt;2666

```

Met Asp Gly Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Phe
 1          5          10          15
Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Val Phe Leu Thr
      20          25          30
Leu Tyr Gly Ile Ile Leu Thr Gly Asn Ile Gly Leu Met Met Leu Ile
      35          40          45
Arg Thr Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50          55          60
Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Ala Ile Val Pro Lys Met
      65          70          75          80
Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Leu Tyr Gly Cys
      85          90          95
Ala Leu Gln Phe Tyr Phe Ser Cys Ala Phe Ala Asp Thr Glu Ser Phe
      100          105          110
Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
      115          120          125
Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Val Trp Leu Ile
      130          135          140
Val Leu Ser Tyr Ile Gly Gly Asn Met Ser Ser Leu Val His Thr Ser
      145          150          155          160
Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile Asn His Phe
      165          170          175
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
      180          185          190
Val Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val Glu Ile Phe
      195          200          205
Cys Phe Ile Val Ile Val Ile Ser Tyr Tyr Phe Ile Leu Arg Ser Val
      210          215          220
Leu Arg Ile Arg Ser Ser Ser Gly Arg Lys Lys Thr Phe Ser Thr Cys
      225          230          235          240
Ala Ser His Leu Thr Ser Val Ala Ile Tyr Gln Gly Thr Leu Leu Phe
      245          250          255
Ile Tyr Ser Arg Pro Thr Tyr Leu Tyr Thr Pro Asn Thr Asp Lys Ile
      260          265          270
Ile Ser Val Phe Tyr Thr Ile Ile Ile Pro Val Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Lys Arg Ala Val
      290          295          300
Arg Leu Lys Val Asp Ser Ser
      305          310

```

&lt;210&gt; 2667

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU42392)

&lt;400&gt;2667

```

Asn Pro Leu Arg Tyr Pro Ala Val Met Thr Ser Asn Met Val Val His
 1          5          10          15
Leu Ser Ala Ala Ala Trp Gly Val Ala Val Val Leu Val Gly Ile Leu
      20          25          30
Ile Gly Leu Thr Val Arg Leu Ser Phe Cys Arg Ser Val Ile Glu Asn
      35          40          45
Pro Phe Cys Asp Asn Ala Ser Leu Phe Lys Leu Ser Cys Glu Ser Thr
      50          55          60
Ala Ile Asn Asn Ile Tyr Gly Leu Ser Phe Thr Val Val Leu Leu Thr
      65          70          75          80
Ser Ser Leu Gly Ser Ile Ala Leu Thr Tyr Leu Arg Ile Ala Ile Val
      85          90          95

```

Cys Phe Lys Ser Lys Asn Lys Ala Thr Asn Ser Lys Ala Ile Lys Thr  
 100 105 110  
 Cys Ser Thr His Leu Ala Val Tyr Leu Ile Met Met Val Ser Gly Leu  
 115 120 125  
 Thr Thr Ile Thr Leu His Arg Phe Pro Glu Leu Ser Asp Ser Arg Lys  
 130 135 140  
 Leu Ser Ser Ile Ile Lys His Ile Val Pro Pro  
 145 150 155

&lt;210&gt; 2668

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU42394)

&lt;400&gt;2668

Asn Pro Leu Arg Tyr Gln Thr Ile Met Thr Asn Lys Thr Val Ile Thr  
 1 5 10 15  
 Leu Ser Ala Leu Ala Trp Gly Ile Ala Leu Leu Phe Ile Ser Ile Leu  
 20 25 30  
 Ile Gly Leu Thr Leu Arg Leu Ser Arg Cys Arg Thr Phe Ile Ser Asn  
 35 40 45  
 Pro Phe Cys Asp Asn Ala Ser Leu Phe Lys Leu Ser Cys Glu Asp Val  
 50 55 60  
 Thr Ile Asn Asn Leu Tyr Gly Leu Ile Tyr Thr Val Leu Leu Phe Gly  
 65 70 75 80  
 Ser Ser Met Gly Ser Ile Ala Val Thr Tyr Ile Lys Ile Thr Ala Val  
 85 90 95  
 Cys Leu Val Thr Lys Ser Lys Met Leu Asn Ser Arg Ala Leu Lys Thr  
 100 105 110  
 Cys Ser Thr His Leu Ser Leu Tyr Leu Ile Met Leu Ile Ser Gly Leu  
 115 120 125  
 Ile Ile Ile Val Leu His Arg Phe Pro Ala Tyr Ser Asp Tyr Arg Lys  
 130 135 140  
 Ile Ala Ser Leu Leu Phe His Ile Ile Pro Ser  
 145 150 155

&lt;210&gt; 2669

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU42395)

&lt;400&gt;2669

Leu Pro Leu Arg Tyr His Ala Ile Val Asn Asn Ser Ser Ile Thr Leu  
 1 5 10 15  
 Ile Leu Ser Ala Lys Trp Ala Phe Asn Ser Ser Ile Val Ala Leu Met  
 20 25 30  
 Val Ser Leu Ile Thr Arg Ile Ser Phe Cys Asp Ser Asn Val Ile Gln  
 35 40 45  
 Ser Tyr Phe Cys Asp His Gly Pro Val Tyr Arg Leu Ala Cys Asn Asp  
 50 55 60  
 Asn Ser Ile Asn Arg Phe Met Gly Ser Phe Ile Thr Cys Leu Tyr Leu  
 65 70 75 80  
 Val Val Pro Leu Gly Ile Ile Ile Leu Ser Tyr Ile Gly Ile Phe Leu  
 85 90 95  
 Ala Leu Asn Lys Ile Thr Thr Trp Glu Ser Arg Leu Lys Ala Leu Lys  
 100 105 110  
 Thr Cys Val Ser His Leu Leu Leu Val Gly Ile Tyr Phe Leu Pro Met  
 115 120 125  
 Ser Cys Thr Tyr Ile Ala Ala Trp Leu Leu Ala Leu Ala Pro Asn Ala  
 130 135 140  
 Arg Val Ile Thr Thr Ser Leu Ala Tyr Thr Ile Ser Gln

145

150

155

&lt;210&gt; 2670

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU42396)

&lt;400&gt;2670

```

Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Val Ile Val Asn Asn
 1           5           10           15
Thr Ser Met Ile Ser Ile Phe Ser Ala Val Phe Met Phe Asn Ser Ile
      20           25           30
Ile Val Ala Ser Met Val Ser Leu Val Thr Asn Ile Ser Phe Cys Lys
      35           40           45
Ser Asn Val Ile Gln Ser Tyr Phe Cys Asp His Gly Pro Met Phe Arg
 50           55           60
Met Ala Cys Asn Asp Asn Asn Ile Asn Lys Ile Met Gly Phe Leu Tyr
65           70           75           80
Thr Thr Leu Tyr Leu Ile Ala Pro Met Leu Val Ile Phe Leu Ser Tyr
      85           90           95
Leu Gly Ile Phe Leu Val Val Ser Lys Ile Ala Thr Trp Glu Arg Arg
      100           105           110
Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu Leu Leu Val Gly Ile
      115           120           125
Tyr Phe Leu Pro Ile Phe Phe Thr Tyr Leu Thr Ser Leu Leu Leu Phe
 130           135           140
Ser Thr Ser Asn Ser Arg
145           150

```

&lt;210&gt; 2671

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU42397 (odorant receptor 8; 1644478) Weth-F 96)

&lt;400&gt;2671

```

Asn Pro Leu Arg Tyr Pro Asn Ile Val Thr Lys Trp Asn Ile Phe Tyr
 1           5           10           15
Leu Cys Leu Ile Ser Trp Val Ile Ala Asn Val Thr Pro Leu Met Met
      20           25           30
Val Ile Arg Ala Tyr Pro Leu Pro Tyr Cys Ala Glu Asn Thr Ile Ile
      35           40           45
Gln Cys Tyr Cys Asp His Ile Ser Ile Thr Ser Leu Ala Cys Thr Asn
 50           55           60
Arg Ala Pro Tyr Ser Ile Pro Ala Phe Val Leu Ala Met Val Ala Leu
65           70           75           80
Leu Thr Pro Leu Ala Phe Ile Val Phe Ser Tyr Cys Ala Ile Ile Leu
      85           90           95
Ala Val Leu Arg Ile Ser Ser Thr Gln Ala Arg Leu Lys Thr Phe Ser
      100           105           110
Thr Cys Ser Pro Gln Leu Ile Ile Ala Leu Tyr Phe Leu Pro Arg
      115           120           125
Cys Phe Ile Tyr Leu Ser Ser Asn Ile Gly Ile Tyr Phe Ser Thr Asp
 130           135           140
Leu Arg Leu Ala Ile Ile Met Met Tyr Ser Leu Phe Pro Pro
145           150           155

```

&lt;210&gt; 2672

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU42398 (1151131))

&lt;400&gt;2672

```

Arg Pro Leu Glu Tyr His Ser Ile Met Thr Asp Gln Arg Ile Ile Glu
 1           5           10           15
Cys Ile Leu Phe Cys Trp Leu Thr Pro Phe Phe Cys Met Ala Val Leu
          20           25           30
Ile Gly Leu Thr Ala Arg Leu Thr Leu Cys Gly Ser Ala Ile Glu Lys
          35           40           45
Leu Tyr Cys Glu Asn Trp Ser Val Val Lys Leu Ser Cys Phe Ser Thr
          50           55           60
Thr Val Asn Asn Val Val Gly Tyr Val Ile Ile Val Tyr Phe Gly
65           70           75           80
His Ala Val Leu Ile Phe Cys Ser Tyr Ile Tyr Leu Val Val Lys Cys
          85           90           95
Arg Lys Ser Thr Glu Ser Arg His Lys Phe Ile Gln Thr Cys Val Pro
          100          105          110
His Leu Leu Ala Leu Leu Asn Val Thr Val Ala Leu Leu Phe Asp Val
          115          120          125
Leu Tyr Ser Arg Tyr Gly Ser Lys Ser Leu Pro Gln Asp Leu Arg Asn
          130          135          140
Phe Met Ser Leu Glu Phe Leu Leu Val Pro Pro
145           150           155

```

&lt;210&gt; 2673

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU44439)

&lt;400&gt;2673

```

Met Ala Tyr Asp Arg Leu Ile Ala Ile Cys Trp Pro Leu Arg Tyr Ser
 1           5           10           15
Thr Ile Asn Thr Asn Leu Arg Met Leu Ile Ile Ala Leu Ile Trp
          20           25           30
Ile Leu Val Thr Leu Leu Asp Ile Phe Pro Val Ile Phe Ala Ser Arg
          35           40           45
Leu Pro Tyr Cys Ser Ser Arg Ala Val Leu Ser Cys Cys Cys Glu His
          50           55           60
Gly Pro Val Tyr Arg Leu Ala Cys Thr Asp Thr Tyr Asn Arg Gln
65           70           75           80
Leu Gly Thr Val Lys Thr Met Ile Thr Leu Leu Gly Pro Leu Phe Phe
          85           90           95
Ile Val Phe Thr Tyr Val Ile Val Val Ile Ala Val Met Arg Ile Ala
          100          105          110
Ser Val Thr Gln Arg Trp Lys Ala Phe His Thr Cys Leu Thr His Met
          115          120          125
Met Leu Val Met Leu Tyr Tyr Met Pro Ile Ile Ile Ala Cys Val Leu
          130          135          140
Gly Asn Leu Arg Leu Val Gln Asn Val Asp Leu Leu Thr Ala Ile Leu
145           150           155           160
Thr Arg Ser Val Thr Val Pro Ala Met Leu Asn Pro Ile Ile
          165           170

```

&lt;210&gt; 2674

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU44440)

&lt;400&gt;2674

```

Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His
 1           5           10           15
Ser Ile Val Asn Asn Ser Asn Met Ile Leu Ile Phe Ser Ala Ile Trp
          20           25           30

```

```

Ala Phe Asn Ser Ser Val Val Ala Leu Met Val Ser Leu Ile Asp Arg
    35                      40                      45
Leu Ser Phe Cys Glu Ser Asn Met Ile Gln Ser Tyr Phe Cys Asp His
    50                      55                      60
Gly Pro Val Tyr Arg Leu Ala Cys Ser Asp Ile Ser Lys Asn Lys Ile
    65                      70                      75                      80
Met Ala Tyr Val Ile Ser Ala Met Tyr Ile Ile Ala Pro Met Val Val
    85                      90                      95
Ile Val Phe Ser Tyr Leu Gly Ile Phe Leu Ala Leu Ile Lys Ile Thr
    100                     105                     110
Thr Trp Glu Gly Arg Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu
    115                     120                     125
Leu Leu Val Gly Ile Phe Phe Leu Pro Leu Phe Cys Thr Tyr Leu Ala
    130                     135                     140
Gln Leu Leu Leu Ser Leu Asn Pro Asn Ala Arg Val Ile Ser Thr Ser
    145                     150                     155                     160
Leu Ser Tyr Ala Ile Pro Pro Met Leu Asn Pro Ile Ile
    165                     170

```

&lt;210&gt; 2675

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Unknown (DRU44441)

&lt;400&gt;2675

```

Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His
    1                      5                      10                      15
Val Ile Val Asn Asn Thr Ser Met Ile Ser Ile Phe Ser Ala Val Phe
    20                      25                      30
Met Phe Asn Ser Ile Ile Val Ala Ser Met Val Ser Leu Val Thr Asn
    35                      40                      45
Ile Ser Phe Cys Lys Ser Asn Val Ile Gln Ser Tyr Phe Cys Asp His
    50                      55                      60
Gly Pro Met Phe Arg Met Ala Cys Asn Asp Asn Ile Ile His Glu Ile
    65                      70                      75                      80
Met Gly Phe Leu Tyr Thr Thr Leu Tyr Leu Ile Ala Pro Met Leu Val
    85                      90                      95
Ile Phe Leu Ser Tyr Leu Gly Ile Phe Leu Val Val Ser Lys Ile Ala
    100                     105                     110
Thr Trp Glu Arg Arg Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu
    115                     120                     125
Leu Phe Val Gly Ile Tyr Phe Leu Pro Ile Phe Phe Thr Tyr Leu Thr
    130                     135                     140
Ser Leu Leu Leu Phe Ser Thr Ser Asn Ser Arg Val Ile Ser Thr Ser
    145                     150                     155                     160
Leu Ala Tyr Ala Ile Pro Pro Met Leu Asn Pro Ile Ile
    165                     170

```

&lt;210&gt; 2676

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDA (fish1 L09217 1079242) Ngai-J 93)

&lt;400&gt;2676

```

Met Thr Ser Val Leu Asn Ala Leu Ser Ala Asn Ala Thr Phe Ile Arg
    1                      5                      10                      15
Pro Ser Thr Phe Tyr Ile Asn Gly Phe Tyr Asn Ile Pro His Thr Lys
    20                      25                      30
Tyr Tyr Tyr Ala Phe Leu Cys Ile Ala Tyr Ala Val Thr Val Leu Gly
    35                      40                      45
Asn Ser Phe Ile Met Cys Thr Ile Tyr Leu Ala Arg Ser Leu His Thr

```

50 55 60  
 Ala Lys Tyr Ile Thr Val Phe Asn Leu Ala Leu Ser Asp Leu Gly Gly  
 65 70 75 80  
 Ser Ser Ala Leu Ile Pro Lys Leu Ile Asp Thr Phe Leu Phe Glu Asn  
 85 90 95  
 Gln Val Ile Ser Tyr Glu Ala Cys Leu Ala Asn Met Phe Phe Val Leu  
 100 105 110  
 Phe Phe Met Thr Val Gln Ser Leu Thr Leu Leu Val Met Ala Tyr Asp  
 115 120 125  
 Arg Val Val Ala Ile Cys Phe Pro Leu Arg Tyr Asn Val Ile Val Thr  
 130 135 140  
 Lys Glu Ala Met Thr Leu Ile Ile Val Ile Thr Trp Ile Phe Ser Ile  
 145 150 155 160  
 Ser Ile Ile Ala Leu Leu Val Ala Leu Ile Thr Arg Leu Ser Phe Cys  
 165 170 175  
 Arg Ser Val Ile Ile Asn Ser Tyr Phe Cys Asp His Gly Pro Ile Leu  
 180 185 190  
 Ile Leu Ala Cys Asn Asp Lys Phe Ile Asn Arg Val Met Ala Ile Gly  
 195 200 205  
 Cys Phe Val Val Leu Asp Cys Val Pro Phe Leu Leu Ile Ile Val Ser  
 210 215 220  
 Tyr Ile Cys Ile Gly Ile Ala Leu Met Asn Ile Ser His Gly Leu Glu  
 225 230 235 240  
 Arg Arg Lys Ala Met Lys Thr Cys Thr Ser His Leu Ile Leu Val Ala  
 245 250 255  
 Leu Phe Tyr Leu Pro Phe Ile Gly Thr Asn Ile Thr Ser Leu Thr Ser  
 260 265 270  
 Ser Ile Asn Ala Asn Asp Arg Ile Leu Asn Ser Thr Leu Thr Gln Ile  
 275 280 285  
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Lys Thr Glu Glu  
 290 295 300  
 Val Met Gln Ala Val Lys Val Leu Tyr Lys Arg Ala Lys Ala Val Val  
 305 310 315 320  
 Ile Cys Asp Ile Pro Asn Gly Gln Val Phe Gln Pro Trp Val Gly Val  
 325 330 335  
 Asp Ser Lys Lys Lys Thr Phe Cys  
 340

&lt;210&gt; 2677

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDB (fish3 L09218 1079244) Ngai-J 93)

&lt;400&gt;2677

Met Ala Asp Asn Ile Thr Ser Ile Leu Ser Leu Thr Ser Thr Asn Ala  
 1 5 10 15  
 Thr Phe Ile Arg Pro Ser Thr Phe Tyr Ile Thr Gly Leu Tyr Asn Ile  
 20 25 30  
 Pro His Ala Lys Tyr Tyr Tyr Leu Phe Leu Cys Phe Val Tyr Thr Val  
 35 40 45  
 Thr Phe Leu Gly Asn Ser Phe Ile Met Gly Thr Ile Tyr Leu Ala Arg  
 50 55 60  
 Ser Leu His Thr Ala Lys Tyr Ile Ala Val Phe Asn Leu Ala Leu Ser  
 65 70 75 80  
 Asp Leu Cys Gly Ser Ser Ala Leu Ile Pro Lys Leu Leu Asp Met Leu  
 85 90 95  
 Leu Phe Glu Asn Gln Ser Ile Ser Tyr Glu Ala Cys Leu Ser Asn Met  
 100 105 110  
 Phe Phe Val Tyr Cys Phe Met Thr Leu Gln Cys Leu Thr Leu Leu Ala  
 115 120 125  
 Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Tyr Pro Leu Arg Tyr His

130 135 140  
 Ala Ile Val Thr Lys Ala Ala Met Ile Phe Ile Ile Gly Ala Met Trp  
 145 150 155 160  
 Val Leu Ser Val Ser Val Asn Ala Val Leu Val Ala Leu Ile Thr Arg  
 165 170 175  
 Leu Ser Phe Cys Arg Ser Thr Thr Val Tyr Ser Tyr Phe Cys Asp His  
 180 185 190  
 Gly Pro Ile Tyr Lys Leu Ala Cys Asn Asp Asn Thr Ile Asn Ser Ile  
 195 200 205  
 Met Gly Asn Val Cys Thr Ala Thr Leu Leu Tyr Phe Pro Leu Ile Leu  
 210 215 220  
 Ile Ile Ala Ser Tyr Val Cys Ile Gly Phe Ala Leu Gln Lys Ile Ala  
 225 230 235 240  
 His Gly Val Glu Gln Val Lys Ala Met Lys Thr Cys Thr Ser His Leu  
 245 250 255  
 Ile Leu Val Ala Met Phe Tyr Leu Pro Ile Ile Ser Val Tyr Thr Val  
 260 265 270  
 Ala Leu Thr Thr Arg Ile Asp Thr Asn Ile Arg Ile Ile Asn Thr Ala  
 275 280 285  
 Leu Thr Gln Thr Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu  
 290 295 300  
 Lys Thr Glu Glu Val Met Gln Ala Ile Lys Leu Leu Tyr Lys His Ile  
 305 310 315 320  
 Arg

&lt;210&gt; 2678

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDC (fish32A L09219 1079245) Ngai-J 93)

&lt;400&gt;2678

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg  
 1 5 10 15  
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln  
 20 25 30  
 Tyr Tyr Phe Ala Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly  
 35 40 45  
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile  
 50 55 60  
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu  
 65 70 75 80  
 Thr Asn Val Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser  
 85 90 95  
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Leu Thr Phe  
 100 105 110  
 Phe Phe Ser Ser Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp  
 115 120 125  
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr Asn Ala Ile Val Asn  
 130 135 140  
 Asn Ser Phe Met Phe Ala Ser Leu Thr Ala Ile Trp Ile Phe Asn Val  
 145 150 155 160  
 Val Met Asn Gly Thr Leu Val Val Leu Ile Thr Arg Leu Ser Phe Cys  
 165 170 175  
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr  
 180 185 190  
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu  
 195 200 205  
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Phe Ser  
 210 215 220  
 Tyr Leu Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser

```

225          230          235          240
Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
          245          250          255
Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Val Thr Phe
          260          265          270
Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
          275          280          285
Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
          290          295          300
Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Ile Ile
305          310          315          320
Ser Gln Val His Ala Leu Ala Lys
          325

```

&lt;210&gt; 2679

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDD (fish22 fish202 L09220 1079243) Ngai-J 93)

&lt;400&gt;2679

```

Met Pro Glu Gly Asn Ile Thr Asn Val Lys Asn Phe Val Ile Leu Gly
1          5          10          15
Phe Pro Gly Leu Pro Pro Asn Tyr Tyr Gly Leu Val Ser Val Val Met
          20          25          30
Phe Phe Val Tyr Val Cys Thr Leu Ile Gly Asn Cys Thr Phe Phe Thr
          35          40          45
Leu Phe Leu Arg Glu Lys Ser Leu Gln Lys Pro Met Tyr Tyr Ile Met
          50          55          60
Leu Asn Leu Ala Ala Ser Asp Val Leu Phe Ser Thr Thr Thr Leu Pro
65          70          75          80
Lys Ile Ile Ala Arg Tyr Trp Phe Gly Asp Gly Ser Ile Ser Phe Val
          85          90          95
Gly Cys Phe Ile Gln Met Gln Phe Val His Tyr Phe Ala Thr Val Asn
          100          105          110
Ala Leu Val Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
          115          120          125
Asn Pro Leu Arg Tyr Val Asn Ile Val Lys Glu Ser Thr Ile Leu Gly
          130          135          140
Leu Cys Val Val Ser Trp Leu Leu Ala Glu Pro Thr Val Leu Thr Thr
145          150          155          160
Val Ile Arg Ala Thr Ser Leu Pro Tyr Cys Ala Ser Asn Thr Val Ile
          165          170          175
Gln Cys Tyr Cys Asp His Val Ser Val Thr Lys Leu Ala Cys Ile Asp
          180          185          190
Arg Thr Pro Tyr Ala Phe Pro Ala Leu Val Ser Ala Leu Val Met Leu
195          200          205
Leu Thr Pro Leu Ala Phe Ile Leu Phe Ser Tyr Gly Ser Ile Ile Val
210          215          220
Thr Val Phe Arg Thr Ser Ser Thr Arg Gly Arg Leu Lys Thr Leu Ser
225          230          235          240
Thr Cys Ser Ser Gln Leu Ile Ile Ile Thr Leu Phe Phe Leu Pro Arg
          245          250          255
Cys Leu Asn Tyr Leu Ser Ser Ser Leu Gly Ile His Ile Asn Ala Asp
          260          265          270
Ile Gln Ile Leu Val Ile Met Leu Tyr Ser Leu Leu Pro Pro Met Ile
          275          280          285
Asn Pro Val Ile Tyr Cys Leu Arg Thr Lys Glu Ala Lys Glu Cys Leu
290          295          300
Lys Arg Ser Leu Asn Arg Ser Ser Phe Val Gln Phe Leu Lys Ile Asn
305          310          315          320
Val Gln Val Ser Thr Leu Ser Asn

```



325

&lt;210&gt; 2680

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDE (fish47 L09221 1079249) Ngai-J 93)

&lt;400&gt;2680

```

Met Asn Ser Thr Asn Ser Thr Asp Ser Phe Asp Lys Gly Phe Tyr Leu
1      5      10      15
Ile Ala Tyr Asn Ser Leu Gly Asn Lys Asn Tyr Leu Ile Leu Ala Leu
20      25      30
Gly Ile Ile Tyr Leu Ile Thr Leu Leu Cys Asn Phe Thr Leu Leu Ala
35      40      45
Ile Ile Leu Met Asn Ser Ser Leu Gln Asn Pro Lys Phe Leu Ala Val
50      55      60
Phe Asn Leu Ala Val Val Asp Ile Ser Ile Asn Ser Val Ile Ile Pro
65      70      75      80
Gln Met Val Pro Val Phe Val Phe Asn Leu Asn His Ile Ser Phe Glu
85      90      95
Ser Cys Phe Ser Gln Met Phe Phe Met His Phe Phe Gly Asp Met Glu
100     105     110
Ser Phe Ser Leu Ala Leu Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys
115     120     125
Phe Pro Leu Arg Tyr Pro Thr Ile Asn Thr Asn Met Arg Met Val Leu
130     135     140
Ile Ile Ala Ser Leu Trp Phe Leu Val Phe Leu Ile Glu Leu Tyr Pro
145     150     155     160
Val Ala Leu Ala Ser Gly Leu Ser Tyr Cys Arg Ser Arg Val Val Pro
165     170     175
Ser Cys Cys Cys Glu His Gly Pro Val Tyr Asn Leu Ala Cys Gly Asp
180     185     190
Ile Ser Tyr Asn Lys Arg Leu Ala Leu Ala Lys Thr Leu Val Val Leu
195     200     205
Leu Gly Pro Leu Thr Phe Ile Ile Cys Ser Tyr Val Ile Val Val Val
210     215     220
Ala Val Leu Arg Ile Ala Ser Pro Thr Gln Cys Trp Lys Ala Phe Asn
225     230     235     240
Thr Cys Leu Thr His Met Ile Leu Val Leu Ile Tyr Tyr Leu Pro Ile
245     250     255
Ile Leu Ala Tyr Ile Leu Gly Asn Leu Lys Leu Leu Gln Ser Ala Asp
260     265     270
Leu Tyr Thr Ala Gly Leu Thr Val Cys Val Thr Leu Pro Ala Met Leu
275     280     285
Asn Pro Ile Ile Tyr Ser Leu Lys Thr Glu Glu Leu Gln Asp Lys Leu
290     295     300
Leu Lys Phe Ile Lys Pro Gln Lys Val Ser Asn Thr Val
305     310     315

```

&lt;210&gt; 2681

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDF (fish8 L09222 1079250) Ngai-J 93)

&lt;400&gt;2681

```

Met Leu Ala Pro Val Gln Asn Ile Ser Phe Thr Thr Phe Thr Leu Thr
1      5      10      15
Gly Phe His Asp Leu Gly Glu Trp Gly Pro Ile Leu Ser Ile Pro Tyr
20      25      30
Leu Leu Met Phe Leu Leu Ser Ser Thr Ser Asn Leu Thr Leu Ile Tyr
35      40      45

```

Leu Ile Ile Ser Gln Arg Ala Leu His Ser Pro Met Cys Ile Leu Ile  
 50 55 60  
 Gly Leu Met Ala Val Val Asp Leu Ser Met Pro Ile Phe Cys Val Pro  
 65 70 75 80  
 Asn Met Leu Leu Ser Phe Leu Phe Asn Trp Lys Gly Ile Ser Leu Val  
 85 90 95  
 Gly Cys Leu Val Gln Met Phe Cys Ile His Cys Ala Gly Thr Phe Gln  
 100 105 110  
 Ser Thr Ile Leu Leu Trp Met Ala Leu Asp Arg Phe Phe Ala Ile Cys  
 115 120 125  
 Arg Pro Leu Tyr Tyr Gln Lys Tyr Met Gly Met Pro Asn Phe Leu Lys  
 130 135 140  
 Phe Ile Ile Phe Pro Val Ile Arg Asn Leu Phe Phe Ile Thr Thr Ile  
 145 150 155 160  
 Val Ser Trp Ala Gly Lys Leu Thr Phe Cys Glu Thr Asn Glu Ile Asp  
 165 170 175  
 His Cys Val Cys Glu His Met Ala Leu Val Gln Leu Ala Cys Gly Asp  
 180 185 190  
 Ile Ser Ile Asn Asn Ala Leu Gly Leu Leu Thr Val Phe Leu Thr Ile  
 195 200 205  
 Thr Ala Asp Phe Ile Phe Ile Thr Ile Ser Tyr Ile Val Ile Leu Val  
 210 215 220  
 Ser Ile Leu Arg Ser Gly Lys Ala Cys Leu Lys Ala Val Asn Thr Cys  
 225 230 235 240  
 Ile Thr His Ile Ile Val Met Thr Val Ser Leu Thr Phe Ala Leu Ile  
 245 250 255  
 Ala Phe Leu Ser Tyr Arg Ile Arg Asn Phe Ser Pro Ser Ser Arg Val  
 260 265 270  
 Phe Leu Ser Thr Met Tyr Leu Phe Ile Pro Ser Cys Phe Asn Pro Ile  
 275 280 285  
 Ile Tyr Gly Val Arg Thr Lys Glu Ile Arg Glu Gln Phe Leu Lys Leu  
 290 295 300  
 Met Lys Tyr Val Lys Val Phe Pro Lys  
 305 310

&lt;210&gt; 2682

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDG (fish32D L09223 1079248) Ngai-J 93)

&lt;400&gt;2682

Met Asn Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg  
 1 5 10 15  
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln  
 20 25 30  
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly  
 35 40 45  
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile  
 50 55 60  
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu  
 65 70 75 80  
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser  
 85 90 95  
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Phe Thr Phe  
 100 105 110  
 Phe Phe Phe Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp  
 115 120 125  
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn  
 130 135 140  
 Asn Ser Phe Met Phe Ala Thr Leu Thr Ala Ile Trp Val Phe Asn Leu  
 145 150 155 160

Val Met Ile Gly Thr Leu Val Val Leu Ile Thr Arg Leu Ser Phe Cys  
 165 170 175  
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr  
 180 185 190  
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu  
 195 200 205  
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser  
 210 215 220  
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser  
 225 230 235 240  
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly  
 245 250 255  
 Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Leu Thr Phe  
 260 265 270  
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr  
 275 280 285  
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp  
 290 295 300  
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Lys Ile  
 305 310 315 320  
 Ser Gln Val His Ala Leu Ala Lys  
 325

&lt;210&gt; 2683

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDH (fish32C L09224 1079247) Ngai-J 93)

&lt;400&gt;2683

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg  
 1 5 10 15  
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln  
 20 25 30  
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly  
 35 40 45  
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile  
 50 55 60  
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Ile Gly Glu  
 65 70 75 80  
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser  
 85 90 95  
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Thr Asn Met Phe Phe Thr Phe  
 100 105 110  
 Phe Phe Ser Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp  
 115 120 125  
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn  
 130 135 140  
 Asn Ser Phe Met Phe Ala Thr Leu Thr Ala Ile Trp Val Phe Asn Leu  
 145 150 155 160  
 Val Ile Phe Gly Thr Thr Val Val Phe Ile Thr Arg Leu Ser Phe Cys  
 165 170 175  
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr  
 180 185 190  
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu  
 195 200 205  
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser  
 210 215 220  
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser  
 225 230 235 240  
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly  
 245 250 255

Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Leu Thr Phe  
 260 265 270  
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr  
 275 280 285  
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp  
 290 295 300  
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Lys Ile  
 305 310 315 320  
 Ser Gln Val His Ala Leu Ala Lys  
 325

&lt;210&gt; 2684

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Unknown (ICTORDII (fish32B L09225 1079246) Ngai-J 93)

&lt;400&gt;2684

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg  
 1 5 10 15  
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln  
 20 25 30  
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly  
 35 40 45  
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile  
 50 55 60  
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu  
 65 70 75 80  
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser  
 85 90 95  
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Phe Thr Phe  
 100 105 110  
 Phe Phe Ala Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp  
 115 120 125  
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn  
 130 135 140  
 Asn Ser Phe Met Phe Val Thr Leu Ile Ala Ile Trp Val Phe Asn Val  
 145 150 155 160  
 Val Ile Ile Gly Thr Thr Val Val Phe Ile Thr Arg Leu Ser Phe Cys  
 165 170 175  
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr  
 180 185 190  
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Tyr Phe  
 195 200 205  
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser  
 210 215 220  
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser  
 225 230 235 240  
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly  
 245 250 255  
 Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Val Thr Phe  
 260 265 270  
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr  
 275 280 285  
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp  
 290 295 300  
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Ile Ile  
 305 310 315 320  
 Ser Gln Val His Ala Leu Ala Lys  
 325

&lt;210&gt; 2685

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (ol1 (RATOL1RECE L34074) Guillaume-D 94)

&lt;400&gt;2685

```

Met Ser Val Ala Asn Glu Ser Ile Ser Arg Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Val Val Phe Leu
 20          25          30
Val Ser Tyr Ile Leu Thr Ile Phe Gly Asn Met Met Ile Ile Leu Val
 35          40          45
Ser Arg Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
 65          70          75          80
Met Leu Ile Asn Ile Cys Ser Thr Arg Lys Val Ile Ser Tyr Gly Gly
 85          90          95
Cys Val Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Ser Thr Glu Cys
 100         105         110
Phe Leu Leu Gly Val Met Ser Leu Asp Arg Phe Leu Ala Ile Cys Arg
 115         120         125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Arg Cys Leu His Leu
 130         135         140
Ala Ala Ala Cys Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
 145         150         155         160
Thr Trp Thr Leu Gln Met Pro Leu Cys Gly His Lys Glu Val Asp His
 165         170         175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
 180         185         190
Thr Ala Asn Glu Ala Glu Leu Phe Ile Ser Val Leu Phe Leu Leu
 195         200         205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
 210         215         220
Val Leu Lys Ile Arg Ser Ala Glu Cys Arg Arg Lys Ala Phe Gly Thr
 225         230         235         240
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Thr Ala Ile
 245         250         255
Tyr Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
 260         265         270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Pro Met Leu Asn Pro Leu
 275         280         285
Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Gly Ala Phe Lys Arg Leu
 290         295         300
Met Lys Arg Ile Ile Leu Ile Gly Lys
 305         310

```

&lt;210&gt; 2686

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Unknown (F3 (RATOLFPROB M64376 RNOLFP15 A23701) Buck-L 91)

&lt;400&gt;2686

```

Met Asp Ser Ser Asn Arg Thr Arg Val Ser Glu Phe Leu Leu Leu Gly
 1          5          10          15
Phe Val Glu Asn Lys Asp Leu Gln Pro Leu Ile Tyr Gly Leu Phe Leu
 20          25          30
Ser Met Tyr Leu Val Thr Val Ile Gly Asn Ile Ser Ile Ile Val Ala
 35          40          45
Ile Ile Ser Asp Pro Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

```

65          70          75          80
Met Leu Val Asn Ile Gln Thr Gln Asn Asn Val Ile Thr Tyr Ala Gly
      85          90          95
Cys Ile Thr Gln Ile Tyr Phe Phe Leu Leu Phe Val Glu Leu Asp Asn
      100          105          110
Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Met His Tyr Thr Val Ile Met Asn Tyr Lys Leu Cys Gly Phe Leu
      130          135          140
Val Leu Val Ser Trp Ile Val Ser Val Leu His Ala Leu Phe Gln Ser
145          150          155          160
Leu Met Met Leu Ala Leu Pro Phe Cys Thr His Leu Glu Ile Pro His
      165          170          175
Tyr Phe Cys Glu Pro Asn Gln Val Ile Gln Leu Thr Cys Ser Asp Ala
      180          185          190
Phe Leu Asn Asp Leu Val Ile Tyr Phe Thr Leu Val Leu Leu Ala Thr
      195          200          205
Val Pro Leu Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Val Ser Ser
      210          215          220
Ile Cys Ala Ile Ser Ser Val His Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu
      245          250          255
Gly Val Tyr Leu Ser Ser Ala Ala Asn Asn Ser Ser Gln Ala Ser Ala
      260          265          270
Thr Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Val Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Val Leu Lys Lys Thr
      290          295          300
Leu Cys Glu Glu Val Ile Arg Ser Pro Pro Ser Leu Leu His Phe Phe
305          310          315          320
Leu Val Leu Cys His Leu Pro Cys Phe Ile Phe Cys Tyr
      325          330

```

&lt;210&gt; 2687

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown (F5 (RATOLFPROC M64377 RNOLFPP17 OLF5 P23266 B23701) Buck-L 91)

&lt;400&gt;2687

```

Met Ser Ser Thr Asn Gln Ser Ser Val Thr Glu Phe Leu Leu Leu Gly
1          5          10          15
Leu Ser Arg Gln Pro Gln Gln Gln Gln Leu Leu Phe Leu Leu Phe Leu
      20          25          30
Ile Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35          40          45
Ile Gly Thr Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50          55          60
Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys
65          70          75          80
Val Leu Ala Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly
      85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Ala Val Phe Gly Asn Met Asp Asn
      100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu
      130          135          140
Val Val Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His

```

```

      165      170      175
Phe Phe Cys Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
      180      185      190
His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val
      195      200      205
Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala
      210      215      220
Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile
      245      250      255
Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met
      260      265      270
Ala Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu Arg Lys Val
      290      295      300
Leu Ala Met Arg Phe Pro Ser Lys Gln
      305      310

```

&lt;210&gt; 2688

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (F6 (RATOLFFPROD RNOLFP01 M64378) Buck-L 91)

&lt;400&gt;2688

```

Met Ala Trp Ser Thr Gly Gln Asn Leu Ser Thr Pro Gly Pro Phe Ile
  1      5      10      15
Leu Leu Gly Phe Pro Gly Pro Arg Ser Met Arg Ile Gly Leu Phe Leu
      20      25      30
Leu Phe Leu Val Met Tyr Leu Leu Thr Val Val Gly Asn Leu Ala Ile
      35      40      45
Ile Ser Leu Val Gly Ala His Arg Cys Leu Gln Thr Pro Met Tyr Phe
      50      55      60
Phe Leu Cys Asn Leu Ser Phe Leu Glu Ile Trp Phe Thr Thr Ala Cys
      65      70      75      80
Val Pro Lys Thr Leu Ala Thr Phe Ala Pro Arg Gly Gly Val Ile Ser
      85      90      95
Leu Ala Gly Cys Ala Thr Gln Met Tyr Phe Val Phe Ser Leu Gly Cys
      100      105      110
Thr Glu Tyr Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala
      115      120      125
Ile Cys Leu Pro Leu Arg Tyr Gly Gly Ile Met Thr Pro Gly Leu Ala
      130      135      140
Met Arg Leu Ala Leu Gly Ser Trp Leu Cys Gly Phe Ser Ala Ile Thr
      145      150      155      160
Val Pro Ala Thr Leu Ile Ala Arg Leu Ser Phe Cys Gly Ser Arg Val
      165      170      175
Ile Asn His Phe Phe Cys Asp Ile Ser Pro Trp Ile Val Leu Ser Cys
      180      185      190
Thr Asp Thr Gln Val Val Glu Leu Val Ser Phe Gly Ile Ala Phe Cys
      195      200      205
Val Ile Leu Gly Ser Cys Gly Ile Thr Leu Val Ser Tyr Ala Tyr Ile
      210      215      220
Ile Thr Thr Ile Ile Lys Ile Pro Ser Ala Arg Gly Arg His Arg Ala
      225      230      235      240
Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly
      245      250      255
Ser Thr Ile Phe Leu His Val Arg Thr Ser Val Glu Ser Ser Leu Asp
      260      265      270
Leu Thr Lys Ala Ile Thr Val Leu Asn Thr Ile Val Thr Pro Val Leu

```

275                      280                      285  
 Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Leu  
 290                      295                      300  
 Arg Arg Thr Val Lys Gly Lys  
 305                      310

&lt;210&gt; 2689

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Unknown (F12 (RATOLFPROG OLF2 P23268 M64381 D23701) Buck-L 91)

&lt;400&gt;2689

Met Glu Ser Gly Asn Ser Thr Arg Arg Phe Ser Ser Phe Phe Leu Leu  
 1                      5                      10                      15  
 Gly Phe Thr Glu Asn Pro Gln Leu His Phe Leu Ile Phe Ala Leu Phe  
 20                      25                      30  
 Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Met  
 35                      40                      45  
 Ala Ile Ile Thr Gln Ser His Leu His Thr Pro Met Tyr Phe Phe Leu  
 50                      55                      60  
 Ala Asn Leu Ser Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro  
 65                      70                      75                      80  
 Lys Met Leu Val Asn Ile Tyr Thr Gln Ser Lys Ser Ile Thr Tyr Glu  
 85                      90                      95  
 Asp Cys Ile Ser Gln Met Cys Val Phe Leu Val Phe Ala Glu Leu Gly  
 100                      105                      110  
 Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Arg Cys  
 115                      120                      125  
 His Pro Leu Cys Tyr Thr Val Ile Val Asn His Arg Leu Cys Ile Leu  
 130                      135                      140  
 Leu Leu Leu Leu Ser Trp Val Ile Ser Ile Phe His Ala Phe Ile Gln  
 145                      150                      155                      160  
 Ser Leu Ile Val Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro  
 165                      170                      175  
 His Phe Phe Cys Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp  
 180                      185                      190  
 Asn Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala  
 195                      200                      205  
 Ala Ile Ser Phe Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser  
 210                      215                      220  
 Ser Ile His Ser Ile Ser Thr Val Gln Gly Lys Tyr Lys Ala Phe Ser  
 225                      230                      235                      240  
 Thr Cys Ala Ser His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly  
 245                      250                      255  
 Leu Gly Val Tyr Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala  
 260                      265                      270  
 Ala Ser Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro  
 275                      280                      285  
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ala Leu Glu Arg  
 290                      295                      300  
 Leu Leu Glu Gly Asn Cys Lys Val His His Trp Thr Gly  
 305                      310                      315

&lt;210&gt; 2690

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (I3 (RATOLFPROK OLF0 P23269 M64385 RNOLFPO8 E23701) Buck-L 91)

&lt;400&gt;2690

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro  
 1                      5                      10                      15



```

Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
      20      25      30
Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
      35      40      45
Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
      50      55      60
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
      65      70      75      80
Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
      85      90      95
Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
      100      105      110
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
      115      120      125
His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
      130      135      140
Leu Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu
      145      150      155      160
Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
      165      170      175
Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
      180      185      190
Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
      195      200      205
Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
      210      215      220
Lys Val Pro Ser Thr Gln Gly Ile Cys Lys Val Phe Ser Thr Cys Gly
      225      230      235      240
Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
      245      250      255
Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
      260      265      270
Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
      275      280      285
Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
      290      295      300
Ser Met Lys Ile Thr Leu
      305      310

```

&lt;210&gt; 2691

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (I8 (RATOLFPROM M64387 RNOLFP09) Buck-L 91)

&lt;400&gt;2691

```

Met Asn Asn Lys Thr Val Ile Thr His Phe Leu Leu Leu Gly Leu Pro
  1      5      10      15
Ile Pro Pro Glu His Gln Gln Leu Phe Phe Ala Leu Phe Leu Ile Met
      20      25      30
Tyr Leu Thr Thr Phe Leu Gly Asn Leu Leu Ile Val Val Leu Val Gln
      35      40      45
Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
      50      55      60
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu Lys Leu Leu
      65      70      75      80
Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala Gly Cys Leu
      85      90      95
Thr Gln Ile Phe Phe Phe Leu Leu Phe Gly Tyr Leu Gly Asn Phe Leu
      100      105      110
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
      115      120      125

```

His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys Leu Leu Leu  
 130 135 140  
 Val Phe Trp Ile Met Thr Ser Ser His Ala Met Met His Thr Leu Leu  
 145 150 155 160  
 Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu Asn Phe Phe  
 165 170 175  
 Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val  
 180 185 190  
 Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile Val Ile Pro  
 195 200 205  
 Phe Val Leu Ile Val Ile Ser Tyr Ala Lys Ile Ile Ser Ser Ile Leu  
 210 215 220  
 Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser Thr Cys Gly  
 225 230 235 240  
 Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu  
 245 250 255  
 Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly Ser Ala Met  
 260 265 270  
 Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Arg Asp Met Lys Gln Ala Leu Ile Arg Val Thr Cys  
 290 295 300  
 Ser Lys Lys Ile Ser Leu Pro Trp  
 305 310

&lt;210&gt; 2692

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (I9 (RATOLFPRON OLF9 H23701 M64388 RNOLFP10 P23272) Buck-L 91)

&lt;400&gt;2692

Met Thr Arg Arg Asn Gln Thr Ala Ile Ser Gln Phe Phe Leu Leu Gly  
 1 5 10 15  
 Leu Pro Phe Pro Pro Glu Tyr Gln His Leu Phe Tyr Ala Leu Phe Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Ile Ile Ile Leu  
 35 40 45  
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly  
 85 90 95  
 Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu  
 130 135 140  
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His  
 165 170 175  
 Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr  
 180 185 190  
 His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val  
 195 200 205  
 Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser  
 210 215 220  
 Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr  
 225 230 235 240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
                                   245                                  250                                  255  
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr  
                                   260                                  265                                  270  
 Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe  
                                   275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Asp Ala Leu Glu Lys Ile  
                                   290                                  295                                  300  
 Met Cys Lys Lys Gln Ile Pro Ser Phe Leu  
 305                                  310

&lt;210&gt; 2693

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (I14 (RATOLFFPROQ OLF4 I23701 P23273 M64391 RNOLFP14) Buck-L 91)

&lt;400&gt;2693

Met Thr Gly Asn Asn Gln Thr Leu Ile Leu Glu Phe Leu Leu Leu Gly  
   1                                  5                                  10                                  15  
 Leu Pro Ile Pro Ser Glu Tyr His Leu Leu Phe Tyr Ala Leu Phe Leu  
                                   20                                  25                                  30  
 Ala Met Tyr Leu Thr Ile Ile Leu Gly Asn Leu Leu Ile Ile Val Leu  
                                   35                                  40                                  45  
 Val Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Phe Leu Ser  
                                   50                                  55                                  60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
                                   65                                  70                                  75                                  80  
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Thr Gly  
                                   85                                  90                                  95  
 Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser  
                                   100                                  105                                  110  
 Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
                                   115                                  120                                  125  
 Pro Leu Arg Tyr Thr Thr Ile Met Ser Thr Lys Phe Cys Ala Ser Leu  
                                   130                                  135                                  140  
 Val Leu Leu Leu Trp Met Leu Thr Met Thr His Ala Leu Leu His Thr  
                                   145                                  150                                  155                                  160  
 Leu Leu Ile Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His  
                                   165                                  170                                  175  
 Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile  
                                   180                                  185                                  190  
 Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu Ile Ile Ile  
                                   195                                  200                                  205  
 Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser  
                                   210                                  215                                  220  
 Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val Phe Ser Thr  
                                   225                                  230                                  235                                  240  
 Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Phe  
                                   245                                  250                                  255  
 Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu Ile  
                                   260                                  265                                  270  
 Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe  
                                   275                                  280                                  285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val  
                                   290                                  295                                  300  
 Ile Cys Thr Lys Lys Ile Ser Leu  
 305                                  310

&lt;210&gt; 2694

&lt;211&gt; 314

&lt;212&gt; PRT

<213> Unknown (I15 (RATOLFPROR A37286 M64391 RNOLFP16) Buck-L 91)

<400>2694

```

Met Thr Glu Glu Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Phe
 1          5          10          15
Leu Pro Ile Pro Ser Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
          20          25          30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45
Ile His Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Phe Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu Ser
          100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
          130          135          140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
          165          170          175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
          180          185          190
His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
          195          200          205
Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
          210          215          220
Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
          245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
          260          265          270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Ile Arg Val
          290          295          300
Leu Cys Lys Lys Lys Ile Thr Phe Cys Leu
305          310

```

<210> 2695

<211> 309

<212> PRT

<213> Unknown (RNOLP4 (517366 631861 1083741 S51356) Gat-U 94)

<400>2695

```

Met Met Gly Thr Gly Asn His Ser Ala Val Val Val Phe Val Leu Val
 1          5          10          15
Gly Leu Thr Lys Gln Pro Glu Leu Leu Leu Pro Leu Phe Phe Leu Phe
          20          25          30
Leu Val Ile Tyr Val Leu Thr Val Val Gly Asn Leu Gly Met Ile Leu
          35          40          45
Leu Ile Ile Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu
          50          55          60
Ser Ser Leu Ser Phe Val Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro
65          70          75          80
Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Phe Ile Thr Tyr Ser

```

85 90 95  
 Glu Cys Met Ala Gln Phe Phe Phe Phe Ala Ile Phe Val Val Thr Glu  
 100 105 110  
 Gly Tyr Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys  
 115 120 125  
 Arg Pro Leu Leu Tyr Asn Val Ile Met Ser Ser Arg Ile Cys Ser Leu  
 130 135 140  
 Leu Val Leu Val Ala Phe Ser Leu Gly Leu Phe Ser Ala Val Val His  
 145 150 155 160  
 Thr Ser Ala Met Met Asn Leu Ser Phe Cys Lys Ser Tyr Ile Ile Ser  
 165 170 175  
 His Tyr Phe Cys Asp Ala Leu Pro Leu Leu Lys Leu Ala Cys Ser Asn  
 180 185 190  
 Thr His Leu Asn Glu Leu Leu Ile Phe Ile Ile Gly Gly Leu Asn Thr  
 195 200 205  
 Leu Val Pro Thr Leu Ala Val Ala Ile Ser Tyr Val Phe Ile Phe Cys  
 210 215 220  
 Ser Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly  
 225 230 235 240  
 Thr Cys Ser Ser His Leu Met Ala Val Gly Ile Phe Phe Gly Ser Ile  
 245 250 255  
 Thr Phe Met Tyr Leu Lys Pro Ser Ser Ser Asn Ser Leu Glu Gln Glu  
 260 265 270  
 Lys Val Ser Ser Val Phe Tyr Thr Val Ile Pro Met Leu Asn Pro  
 275 280 285  
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Gly Arg  
 290 295 300  
 Phe Ser Val Arg Ser  
 305

&lt;210&gt; 2696

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (TB641 (RNU50949 1256393) Thomas-MB 96)

&lt;400&gt;2696

Met Arg Arg Asn Arg Asn Thr Ser Leu Asp Thr Val Val Thr Asp Phe  
 1 5 10 15  
 Leu Leu Leu Gly Leu Ala His Pro Pro Asn Leu Arg Thr Phe Leu Phe  
 20 25 30  
 Leu Val Phe Leu Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu  
 35 40 45  
 Ile Leu Leu Thr Val Trp Ala Asp Pro Lys Leu His Ala Arg Pro Met  
 50 55 60  
 Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser  
 65 70 75 80  
 Val Ile Val Pro Arg Ile Ile Leu Asn Phe Thr Pro Ala Asn Lys Ala  
 85 90 95  
 Ile Ala Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu  
 100 105 110  
 Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr  
 115 120 125  
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Lys  
 130 135 140  
 Leu Cys Thr Ile Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His  
 145 150 155 160  
 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro  
 165 170 175  
 Lys Glu Val Asp Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu  
 180 185 190  
 Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Val Asp Ile

```
<210> 2697
<211> 315
<212> PRT
<213> Unknown (TB567 (RNU50948 1256391) Thomas-MB 96)
```

1648

305

310

315

&lt;210&gt; 2698

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Unknown (TB334 (RNU50947 1256389) Thomas-MB 96)

&lt;400&gt;2698

Met Glu Asn Gln Ser Ser Val Ser Glu Phe Phe Leu Arg Gly Ile Ser  
 1 5 10 15  
 Gly Phe Pro Glu Gln Gln Gln Leu Leu Tyr Gly Leu Phe Leu Cys Met  
 20 25 30  
 Tyr Leu Val Thr Leu Thr Gly Asn Val Leu Ile Ile Leu Ala Ile Gly  
 35 40 45  
 Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu  
 50 55 60  
 Ser Phe Ala Asp Met Gly Leu Ile Ser Ser Thr Val Thr Lys Met Leu  
 65 70 75 80  
 Phe Asn Val Gln Thr Gln Cys His Thr Ile Ser Tyr Thr Gly Cys Leu  
 85 90 95  
 Thr Gln Met Tyr Leu Phe Met Met Phe Gly Asp Leu Asp Ser Phe Phe  
 100 105 110  
 Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu  
 115 120 125  
 His Tyr Ser Thr Ile Met Asn Ala Arg Ile Cys Val Leu Met Leu Ile  
 130 135 140  
 Leu Cys Trp Ile Leu Thr Asn Val Val Ala Leu Thr His Thr Leu Leu  
 145 150 155 160  
 Met Ala Arg Leu Ser Phe Cys Val Val Gly Glu Ile Ala His Phe Phe  
 165 170 175  
 Cys Asp Val Thr Ser Val Met Lys Leu Ser Cys Ser Asp Thr His Val  
 180 185 190  
 Asn Glu Leu Val Leu Ser Gly Phe Gly Gly Thr Val Leu Met Val Pro  
 195 200 205  
 Phe Val Ser Ile Val Ile Ser Tyr Val His Ile Val Phe Ala Val Leu  
 210 215 220  
 Arg Ile Gln Ser Ser Gly Gly Ser Ser Lys Ala Phe Ser Thr Cys Ser  
 225 230 235 240  
 Ser His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Val  
 245 250 255  
 Tyr Leu Phe Pro Ser Ser Val Glu Thr Thr Glu Lys Asp Val Ala Ala  
 260 265 270  
 Ala Ala Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr  
 275 280 285  
 Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Lys Arg Leu Leu Ser  
 290 295 300  
 His Arg Arg Ile Leu Ser Ser  
 305 310

&lt;210&gt; 2699

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (OR12 (423700 S29708) Raming-K 93)

&lt;400&gt;2699

Met Ile Met Asn Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Pro Pro Glu His Trp His Leu Phe Tyr Thr Leu Leu Leu  
 20 25 30  
 Ala Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Ile Leu  
 35 40 45

Ile Leu Leu Asp Ser Asn Leu His Ile Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Asn Gln Asp Thr Ser Ile Thr Tyr Thr Gly  
 85 90 95  
 Cys Leu Thr Gln Met Tyr Phe Ser Met Val Phe Ala Gly Met Glu Ile  
 100 105 110  
 Phe Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu  
 115 120 125  
 Pro Leu His Tyr Thr Ser Ile Met Ser Pro Lys Phe Cys Val Cys Leu  
 130 135 140  
 Gly Ser Leu Ser Trp Val Phe Asn Val Leu Tyr Ser Met Leu His Thr  
 145 150 155 160  
 Leu Leu Leu Ala Arg Leu Ser Phe Cys Lys Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Tyr Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Gly Leu Leu Ile Val  
 195 200 205  
 Ile Pro Phe Leu Leu Ile Val Met Thr Tyr Val Gln Ile Val Cys Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Thr Arg Ala Ile Tyr Lys Ile Phe Ser Thr  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Thr Val Ser Leu Phe Tyr Gly Thr Val Ile  
 245 250 255  
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr  
 260 265 270  
 Val Met Ala Met Met Ile Thr Val Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Glu Ala Leu Val Arg Val  
 290 295 300  
 Leu Ile Lys Lys Lys Ile Ser Leu  
 305 310

&lt;210&gt; 2700

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Unknown (OR14 (423701) Raming-K 93)

&lt;400&gt;2700

Ser Val Thr Glu Phe Ile Leu Ala Gly Leu Thr Asp Gln Pro Gly Leu  
 1 5 10 15  
 Arg Met Pro Leu Phe Phe Leu Phe Leu Gly Phe Tyr Met Val Thr Val  
 20 25 30  
 Val Gly Asn Leu Ile Gly Leu Phe Leu Ile Gly Leu Asn Ser His Leu  
 35 40 45  
 His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Val Val Asp Phe  
 50 55 60  
 Cys Phe Ser Ser Thr Ile Ile Pro Lys Met Leu Met Ser Phe Ile Ser  
 65 70 75 80  
 Lys Lys Asn Ile Ile Ser His Ser Gly Cys Met Thr Gln Leu Phe Phe  
 85 90 95  
 Phe Cys Phe Phe Val Val Ser Glu Thr Phe Ile Leu Ser Ala Met Ala  
 100 105 110  
 Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Met Tyr Thr Val Thr  
 115 120 125  
 Met Ser Pro Gln Val Cys Leu Leu Leu Leu Gly Ala Tyr Val Met  
 130 135 140  
 Gly Phe Ser Glu Ala Met Ala His Thr Gly Asn Leu Met Asn Leu Thr  
 145 150 155 160



Phe Cys Ala Asp Asn Leu Val Asn His Phe Met Cys Asp Ile Leu Pro  
 165 170 175  
 Leu Leu Glu Leu Ser Cys Asn Ser Thr Phe Ile Asn Glu Leu Val Val  
 180 185 190  
 Phe Ile Val Val Ala Ile Asp Ile Ala Val Pro Ile Val Ser Ile Phe  
 195 200 205  
 Ile Ser Tyr Ala Leu Ile Leu Ser Ser Ile Leu Arg Met His Ser Thr  
 210 215 220  
 Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Val  
 225 230 235 240  
 Val Cys Leu Leu Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Leu Pro  
 245 250 255  
 Ser Ile Leu Pro Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr  
 260 265 270  
 Ile Val Val Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys  
 275 280 285  
 Asp Val Lys Val Ala Leu Arg Lys Thr Leu Gly Lys Ile Ile Leu Ser  
 290 295 300

&lt;210&gt; 2701

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Unknown (OR18 (423702) Raming-K 93)

&lt;400&gt;2701

Met Gly Glu Asn Asn Asn Ile Thr Glu Phe Ile Leu Leu Gly Leu Thr  
 1 5 10 15  
 Gln Asp Pro Asp Gly Arg Lys Ala Leu Phe Val Ile Phe Phe Leu Ile  
 20 25 30  
 Tyr Ile Val Thr Met Met Gly Asn Leu Leu Ile Val Val Thr Val Ile  
 35 40 45  
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu  
 50 55 60  
 Ser Leu Leu Asp Ala Leu Phe Ser Thr Ala Ile Ser Pro Lys Leu Ile  
 65 70 75 80  
 Ala Asp Leu Leu Tyr Asp Gln Lys Thr Ile Ser Phe Arg Ala Cys Met  
 85 90 95  
 Ser Gln Leu Phe Ile Glu His Leu Phe Gly Gly Val Asp Ile Val Ile  
 100 105 110  
 Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu  
 115 120 125  
 His Tyr Leu Ala Ile Met Asn Arg Arg Val Cys Ile Thr Leu Leu Ile  
 130 135 140  
 Phe Ala Trp Thr Gly Gly Phe Thr His Ser Leu Ile Gln Ile Val Phe  
 145 150 155 160  
 Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile  
 165 170 175  
 Cys Asp Met Ser Pro Leu Leu Val Leu Ala Cys Thr Asp Thr Tyr Phe  
 180 185 190  
 Ile Gly Leu Thr Val Ile Ala Asn Gly Gly Val Asn Cys Ile Val Ile  
 195 200 205  
 Phe Thr Leu Leu Leu Gly Ser Tyr Gly Ile Ile Leu Arg Ser Leu Lys  
 210 215 220  
 Thr Gln Ser Gln Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Ser Ser  
 225 230 235 240  
 His Ile Leu Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr  
 245 250 255  
 Ala Arg Pro Val Tyr Asn Phe Pro Ile Asp Lys Cys Ile Thr Val Phe  
 260 265 270  
 Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg  
 275 280 285

Asn Ser Glu Ile Lys Ser Cys Met Lys Lys Leu Trp Cys Lys Met Leu  
 290 295 300  
 His Ala Asp  
 305

<210> 2702  
 <211> 314  
 <212> PRT  
 <213> Unknown (OR5 (423703 444281) Raming-K 93)

<400>2702  
 Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Pro Pro Glu His Gln His Val Gly Tyr Ala Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu  
 35 40 45  
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly  
 85 90 95  
 Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu  
 130 135 140  
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr  
 145 150 155 160  
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His  
 165 170 175  
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr  
 180 185 190  
 Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val  
 195 200 205  
 Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser  
 210 215 220  
 Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Ser  
 225 230 235 240  
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile  
 245 250 255  
 Pro Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr  
 260 265 270  
 Val Met Ser Leu Met Tyr Thr Leu Val Thr Pro Met Leu Asn Pro Phe  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Ile Ile  
 290 295 300  
 Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu  
 305 310

<210> 2703  
 <211> 305  
 <212> PRT  
 <213> Unknown (OR37 (423699 S29711 265086) Raming-K 93)

<400>2703  
 Leu Leu Leu Gly Leu Ser Gly Tyr Pro Lys Thr Glu Ile Leu Tyr Phe  
 1 5 10 15  
 Val Ile Val Leu Val Met Tyr Leu Val Ile His Thr Gly Asn Gly Val

20 25 30  
 Leu Ile Ile Ala Ser Ile Phe Asp Ser His Leu His Thr Pro Met Tyr  
 35 40 45  
 Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser  
 50 55 60  
 Ser Val Pro Ser Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile  
 65 70 75 80  
 Ser Phe Ser Gly Cys Thr Val Gln Met Phe Val Gly Phe Ala Met Gly  
 85 90 95  
 Ser Thr Glu Cys Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val  
 100 105 110  
 Ala Ile Cys Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Glu Val  
 115 120 125  
 Tyr Val Ser Met Ala Ser Ala Ser Trp Phe Ser Gly Gly Ile Asn Ser  
 130 135 140  
 Val Val Gln Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn  
 145 150 155 160  
 Val Ile Asn His Phe Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala  
 165 170 175  
 Cys Ala Asp Ile Ser Leu Asn Ile Val Thr Met Val Ile Ser Asn Met  
 180 185 190  
 Ala Phe Leu Val Leu Pro Leu Leu Leu Ile Phe Phe Ser Tyr Val Leu  
 195 200 205  
 Ile Leu Tyr Thr Ile Leu Arg Met Asn Ser Ala Ser Gly Arg Arg Lys  
 210 215 220  
 Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr  
 225 230 235 240  
 Gly Thr Ile Phe Ser Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Thr  
 245 250 255  
 Gly Lys Asp Lys Phe Gln Thr Ser Asp Lys Ile Ile Ser Leu Phe Tyr  
 260 265 270  
 Gly Val Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn  
 275 280 285  
 Lys Asp Val Lys Ala Ala Val Lys Tyr Ile Leu Lys Gln Lys Tyr Ile  
 290 295 300  
 Pro  
 305

&lt;210&gt; 2704

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (RNOLFRECP (1504112) Raming-K 93)

&lt;400&gt;2704

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly  
 1 5 10 15  
 Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu  
 20 25 30  
 Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu  
 35 40 45  
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser  
 50 55 60  
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys  
 65 70 75 80  
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly  
 85 90 95  
 Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn  
 100 105 110  
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe  
 115 120 125  
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu

130	135	140
Val Val Leu Ser Trp	Val Leu Thr Thr Phe His	Ala Met Leu His Thr
145	150	155
Leu Leu Met Ala Arg	Leu Ser Phe Cys Glu Asp	Asn Val Ile Pro His
165	170	175
Phe Phe Cys Asp Met	Ser Ala Leu Leu Lys Leu	Ala Cys Ser Asp Thr
180	185	190
Arg Val Asn Glu Val	Val Ile Phe Ile Val Val	Ser Leu Phe Leu Val
195	200	205
Leu Pro Phe Ala Leu	Ile Ile Met Ser Tyr Val	Arg Ile Val Ser Ser
210	215	220
Ile Leu Lys Val Pro	Ser Ser Gln Gly Ile Tyr	Lys Ala Phe Ser Thr
225	230	235
Cys Gly Ser His Leu	Ser Val Val Ser Leu Phe	Tyr Gly Thr Val Ile
245	250	255
Gly Leu Tyr Leu Cys	Pro Ser Ser Asn Asn	Ser Thr Val Lys Glu Thr
260	265	270
Val Met Ser Leu Met	Tyr Thr Val Val Thr	Pro Met Leu Asn Pro Phe
275	280	285
Ile Tyr Ser Leu Arg	Asn Arg Asp Ile Lys	Gly Ala Met Glu Arg Ile
290	295	300
Phe Cys Lys Arg Lys	Ile Gln Leu Asn Leu	
305	310	

&lt;210&gt; 2705

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Unknown (1906335A (444281) Raming-K 93)

&lt;400&gt;2705

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
1 5 10 15
Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
20 25 30
Ser Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu
35 40 45
Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
50 55 60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65 70 75 80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
85 90 95
Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
100 105 110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
115 120 125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
130 135 140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145 150 155 160
Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
165 170 175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
180 185 190
Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
195 200 205
Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
210 215 220
Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Ser
225 230 235 240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile

```
<210> 2706
<211> 185
<212> PRT
<213> Unknown (PTE01 (544449) Abe-K 93)
```

Met	Tyr	Leu	Phe	Leu	Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Ser	Phe	Thr
1				5					10					15	
Ser	Thr	Thr	Leu	Pro	Lys	Met	Ile	Val	Asp	Ile	Gln	Thr	Asn	Asn	Arg
			20					25					30		
Ala	Ile	Ser	Tyr	Ser	Gly	Cys	Leu	Thr	Gln	Met	Ser	Phe	Phe	Met	Leu
		35					40					45			
Phe	Gly	Cys	Leu	Asp	Ser	Leu	Leu	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg
	50					55					60				
Phe	Val	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Gln	Val	Ile	Met	Asn	Pro
65					70					75				80	
Arg	Leu	Cys	Gly	Leu	Leu	Val	Phe	Leu	Ser	Ile	Leu	Ile	Ser	Leu	Leu
				85					90					95	
Val	Ser	Gln	Leu	His	Asn	Ser	Val	Val	Leu	Gln	Leu	Thr	Tyr	Phe	Lys
			100					105					110		
Ser	Val	Asp	Ile	Ser	His	Phe	Phe	Cys	Asp	Pro	Ser	Leu	Leu	Leu	Asn
		115					120					125			
Leu	Ala	Cys	Ser	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Val	Met	Tyr	Phe	Val
	130					135					140				
Gly	Ala	Ile	Ser	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Phe	Phe	Ser	Tyr
145					150					155				160	
Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu	Arg	Met	Pro	Ser	Pro	Gly	Gly	Lys
				165					170					175	
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser							
		180						185							

<210> 2707  
<211> 168  
<212> PRT  
<213> Unknown (PTE03 (544450) Abe-K 93)

Thr	Thr	Val	Pro	Lys	Met	Leu	Ile	Asn	Leu	Gln	Lys	Gln	Asn	Lys	Ala
1				5				10					15		
Ile	Ser	Tyr	Ala	Gly	Cys	Ile	Thr	Gln	Leu	Ser	Phe	Val	Leu	Leu	Phe
			20					25				30			
Ala	Gly	Met	Glu	Asn	Phe	Leu	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr
		35				40					45				
Val	Ala	Ile	Cys	Lys	Pro	Leu	Arg	Tyr	Thr	Ala	Ile	Met	Lys	Ala	His
	50					55					60				
Leu	Cys	Leu	Val	Met	Thr	Leu	Leu	Ser	Leu	Cys	Ile	Ser	Ile	Val	Asp
65					70				75					80	
Ala	Leu	Leu	His	Gly	Leu	Met	Ile	Leu	Arg	Leu	Ser	Phe	Cys	Thr	Phe
			85					90					95		
Leu	Glu	Ile	Pro	His	Tyr	Phe	Cys	Glu	Leu	Tyr	Gln	Val	Ile	Lys	Leu
			100					105				110			

Ser Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Val Tyr Thr Met Thr  
 115 120 125  
 Ser Thr Leu Gly Gly Val Pro Leu Gly Gly Ile Ile Phe Ser Tyr Phe  
 130 135 140  
 Lys Ile Ile Ser Ser Ile Leu Arg Met Pro Ser Ser Gly Ser Arg His  
 145 150 155 160  
 Arg Ala Phe Ser Thr Cys Gly Ser  
 165

&lt;210&gt; 2708

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Unknown (PTE33 (544451) Abe-K 93)

&lt;400&gt;2708

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Val Asp Ile Tyr Phe Ile  
 1 5 10 15  
 Ser Gly Thr Ile Pro Lys Ile Leu Val Asn Met Gln Ser Lys Thr Lys  
 20 25 30  
 Asp Ile Ser Tyr Ile Glu Cys Leu Thr Gln Val Tyr Phe Phe Asn Thr  
 35 40 45  
 Phe Val Gly Met Asp Asp Val Leu Arg Thr Leu Met Ala Tyr Asp Arg  
 50 55 60  
 Phe Val Ala Ile Cys Met Pro Leu Lys Tyr Thr Val Ile Met Asn Pro  
 65 70 75 80  
 Arg Val Cys Thr Leu Leu Val Leu Met Phe Trp Ile Ile Met Phe Cys  
 85 90 95  
 Ile Ser Leu Ile His Val Leu Leu Met Asn Glu Leu Asn Phe Ser Arg  
 100 105 110  
 Gly Thr Lys Ile Pro His Phe Phe Cys Glu Leu Ala Gln Val Leu Lys  
 115 120 125  
 Val Ser Asn Ser Asp Thr His Ile Asn Asn Ile Phe Met Tyr Val Leu  
 130 135 140  
 Ser Ser Leu Leu Gly Val Ile Pro Met Thr Gly Ile Leu Met Ser Tyr  
 145 150 155 160  
 Ser Gln Ile Val Ser Ser Leu Leu Arg Met Ser Ser Thr Val Ser Lys  
 165 170 175  
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Cys Val Val Cys Leu  
 180 185 190  
 Phe Tyr Gly Ser Val Ile Gly Val Tyr Phe Ser Ser Ser Val Val Leu  
 195 200 205  
 Ser Thr Gln Arg Ile Met Val Ala Ser Leu Met Tyr Thr Val Ile Ser  
 210 215 220  
 Pro Met Phe Asn Pro Phe Ile Tyr Ser Leu  
 225 230

&lt;210&gt; 2709

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Unknown (PTE38 (544452) Abe-K 93)

&lt;400&gt;2709

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Asn Asp Ile Cys Ile Ile  
 1 5 10 15  
 Thr Thr Thr Ile Pro Lys Met Leu Met Asn Val Gln Ser His Asp Gln  
 20 25 30  
 Ser Ile Thr Tyr Leu Gly Cys Leu Ser Gln Val Tyr Leu Ile Val Asn  
 35 40 45  
 Phe Gly Ser Ile Glu Ser Cys Leu Leu Ala Val Met Ala Tyr Asp Arg  
 50 55 60  
 Tyr Val Ala Ile Cys His Pro Leu Lys Tyr Thr Val Ile Met Asn His

65                      70                      75                      80  
 Tyr Phe Cys Val Met Leu Leu Leu Phe Ala Cys Ser Leu Ala Leu His  
                                  85                      90                      95  
 Met Cys Leu Phe His Ile Leu Met Val Leu Ile Leu Thr Phe Cys Thr  
                                  100                      105                      110  
 Lys Thr Glu Ile Pro His Phe Phe Cys Glu Leu Ala His Ile Ile Lys  
                                  115                      120                      125  
 Leu Thr Cys Ser Asp Asn Phe Ile Asn Tyr Leu Leu Ile Tyr Thr Val  
                                  130                      135                      140  
 Ser Val Leu Phe Phe Gly Val His Ile Val Gly Ile Ile Leu Ser Tyr  
 145                                   150                      155                      160  
 Ile Tyr Thr Val Ser Ser Val Leu Arg Met Ser Leu Leu Gly Gly Met  
                                  165                      170                      175  
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu  
                                  180                      185                      190  
 Phe Tyr Gly Thr Gly Phe Gly Val His Ile Ser Ser Pro Leu Thr Asp  
                                  195                      200                      205  
 Ser Pro Arg Lys Thr Val Val Ala Ser Val Met Tyr Thr Val Val Thr  
                                  210                      215                      220  
 Gln Met His Gly Pro Phe Ile Tyr Ser Leu  
 225                                   230

&lt;210&gt; 2710

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Unknown (PTE45 (544453) Abe-K 93)

&lt;400&gt;2710

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Ala Asp Ile Cys Leu Ile  
 1                      5                      10                      15  
 Ser Thr Thr Ile Pro Lys Met Leu Ala Asn Glu His Leu Asn His Lys  
                                  20                      25                      30  
 Ala Ile Thr Tyr Glu Gly Cys Ile Met Gln Ile Tyr Phe Phe Thr Leu  
                                  35                      40                      45  
 Phe Val Gly Leu Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg  
                                  50                      55                      60  
 Phe Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ser Ile Met Thr Pro  
 65                                   70                      75                      80  
 His Leu Cys His Ser Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu  
                                  85                      90                      95  
 Asn Ser Ser Leu Gln Ser Phe Leu Val Leu Gln Leu Ser Phe Cys Thr  
                                  100                      105                      110  
 Glu Val Glu Ile Pro His Phe Phe Cys Glu Leu Ser Met Leu Val His  
                                  115                      120                      125  
 Leu Ala Cys Ser Asp Thr Phe Leu Ser Asp Met Ala Met Asn Val Leu  
                                  130                      135                      140  
 Ala Ala Leu Leu Gly Gly Gly Cys Leu Val Gly Ile Leu Tyr Ser Tyr  
 145                                   150                      155                      160  
 Ser Lys Ile Val Ser Ser Ile Gln Ala Ile Ser Ser Ala Glu Gly Lys  
                                  165                      170                      175  
 Tyr Lys Ala Phe Ser Thr Cys Val Ser His Leu Ser Val Val Ser Leu  
                                  180                      185                      190  
 Phe Tyr Cys Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Val Thr Gln  
                                  195                      200                      205  
 Asn Ser His Ser Thr Ala Ala Thr Ser Leu Met Tyr Thr Val Val Thr  
                                  210                      215                      220  
 Pro Met Leu Asn Pro Phe Ile Tyr Phe Phe  
 225                                   230

&lt;210&gt; 2711

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Unknown (PTE58 (544454) Abe-K 93)

&lt;400&gt;2711

```

Leu Leu Met Cys Asn Leu Cys Phe Ala Asp Ile Cys Phe Thr Ser Ala
 1           5           10           15
Ser Ile Pro Thr Asn Leu Val Asn Ile Gln Thr Lys Asn Lys Val Ile
      20           25           30
Thr Tyr Glu Gly Cys Ile Ser Gln Val Tyr Phe Phe Ile Leu Phe Gly
      35           40           45
Val Leu Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val
      50           55           60
Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Asn Arg Arg Leu
      65           70           75           80
Cys Gly Leu Leu Val Leu Gly Ser Trp Val Thr Thr Ala Leu Asn Ser
      85           90           95
Leu Leu Gln Ser Ser Met Ala Leu Arg Leu Ser Phe Cys Thr Asp Leu
      100          105          110
Lys Ile Pro His Phe Val Cys Glu Leu Asn Gln Leu Val Leu Leu Ala
      115          120          125
Cys Asn Asp Thr Phe Pro Asn Asp Met Val Met Tyr Phe Ala Ala Val
      130          135          140
Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys
      145          150          155          160
Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ser Gln Gly Lys Tyr Lys
      165          170          175
Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr
      180          185          190
Ser Thr Leu Leu Gly Val Tyr Leu Ser Ser Ser Phe Thr Gln Asn Ser
      195          200          205
His Ser Thr Ala Arg Ala Ser Val Met Tyr Ser Val Val Thr Pro Met
      210          215          220
Leu Asn Pro Phe Ile Tyr Phe Phe
      225          230

```

&lt;210&gt; 2712

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (RATGUST27 (D12820 P34987 A46750) Abe-K 93)

&lt;400&gt;2712

```

Met Ile Leu Asn Cys Asn Pro Phe Ser Gly Leu Phe Leu Ser Met Tyr
 1           5           10           15
Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Val Ser Ser
      20           25           30
Asn Ser His Leu His Asn Leu Met Tyr Phe Phe Leu Ser Asn Leu Ser
      35           40           45
Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
      50           55           60
Asn Ile His Ser Gln Thr Lys Asp Ile Ser Tyr Ile Glu Cys Leu Ser
      65           70           75           80
Gln Val Tyr Phe Leu Thr Thr Phe Gly Gly Met Asp Asn Phe Leu Leu
      85           90           95
Thr Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys His Pro Leu Asn
      100          105          110
Tyr Thr Val Ile Met Asn Leu Gln Leu Cys Ala Leu Leu Ile Leu Met
      115          120          125
Phe Trp Leu Ile Met Phe Cys Val Ser Leu Ile His Val Leu Leu Met
      130          135          140
Asn Glu Leu Asn Phe Ser Arg Gly Thr Glu Ile Pro His Phe Phe Cys
      145          150          155          160

```



Glu Leu Ala Gln Val Leu Lys Val Ala Asn Ser Asp Thr His Ile Asn  
                             165                            170                            175  
 Asn Val Phe Met Tyr Val Val Thr Ser Leu Leu Gly Leu Ile Pro Met  
                             180                            185                            190  
 Thr Gly Ile Leu Met Ser Tyr Ser Gln Ile Ala Ser Ser Leu Leu Lys  
                             195                            200                            205  
 Met Ser Ser Ser Val Ser Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser  
                             210                            215                            220  
 His Leu Cys Val Val Ser Leu Phe Tyr Gly Ser Ala Thr Ile Val Tyr  
 225                            230                            235                            240  
 Phe Cys Ser Ser Val Leu His Ser Thr His Lys Lys Met Ile Ala Ser  
                             245                            250                            255  
 Leu Met Tyr Thr Val Ile Ser Pro Met Leu Asn Pro Phe Ile Tyr Ser  
                             260                            265                            270  
 Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Lys Leu Phe Ile Arg  
                             275                            280                            285  
 Val Ala Ser Cys Pro Leu Trp Ser Lys Asp Phe Arg Pro Lys Phe Ile  
                             290                            295                            300  
 Leu Lys Pro Glu Arg Gln Ser Leu  
 305                            310

&lt;210&gt; 2713

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (K7 (MUSODORECA L14566 293754 464305 C40745) Ressler-KJ 93)

&lt;400&gt;2713

Phe Phe Leu Ser His Leu Ala Ile Val Asp Ile Ala Tyr Ala Cys Asn  
   1                            5                            10                            15  
 Thr Val Pro Gln Met Leu Val Asn Leu Leu Asp Pro Val Lys Pro Ile  
                             20                            25                            30  
 Ser Tyr Ala Gly Cys Met Thr Gln Thr Phe Leu Phe Leu Thr Phe Ala  
                             35                            40                            45  
 Ile Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val  
                             50                            55                            60  
 Ala Ile Cys His Pro Leu Arg Tyr Ser Ala Ile Met Ser Trp Arg Val  
 65                            70                            75                            80  
 Cys Ser Thr Met Ala Val Thr Ser Trp Ile Ile Gly Val Leu Leu Ser  
                             85                            90                            95  
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Val Ser Gln  
                             100                            105                            110  
 Lys Val Asn His Phe Phe Cys Glu Ile Thr Ala Ile Leu Lys Leu Ala  
                             115                            120                            125  
 Cys Ala Asp Thr His Leu Asn Glu Thr Met Val Leu Ala Gly Ala Val  
                             130                            135                            140  
 Ser Val Leu Val Gly Pro Phe Ser Ser Ile Val Val Ser Tyr Ala Cys  
 145                            150                            155                            160  
 Ile Leu Gly Ala Ile Leu Lys Ile Gln Ser Glu Glu Gly Gln Arg Lys  
                             165                            170                            175  
 Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Tyr  
                             180                            185                            190  
 Gly Thr Ala Ile Val Met Tyr Val Gly Pro Arg His Gly Ser Pro Lys  
                             195                            200                            205  
 Glu Gln Lys Lys Tyr Leu Leu Phe His Ser Leu Phe Asn  
                             210                            215                            220

&lt;210&gt; 2714

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (M50 (MUSODORECB L14567 293756 P34986 OLF5) Buck 93)

&lt;400&gt;2714

```

Tyr Phe Leu Ser Thr Met Ser Phe Leu Glu Ala Trp Tyr Ile Ser Val
 1           5           10           15
Thr Val Pro Lys Met Leu Ala Gly Phe Leu Phe His Pro Asn Thr Ile
      20           25           30
Ser Phe Leu Gly Cys Met Thr Gln Leu Tyr Phe Phe Met Ser Leu Ala
      35           40           45
Cys Thr Glu Cys Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      50           55           60
Ala Ile Cys Trp Pro Leu Arg Tyr Pro Val Met Met Thr Thr Gly Phe
      65           70           75           80
Cys Val Gln Leu Thr Ile Ser Ser Trp Val Ser Gly Phe Thr Ile Ser
      85           90           95
Met Ala Lys Val Tyr Phe Leu Ser Arg Val Ala Phe Cys Gly Asn Asn
      100          105          110
Val Leu Asn His Phe Phe Cys Asp Val Ser Pro Ile Leu Lys Leu Ala
      115          120          125
Cys Met Asn Leu Ser Met Ala Glu Thr Val Asp Phe Ala Leu Ala Ile
      130          135          140
Val Ile Leu Ile Phe Pro Leu Ser Ala Thr Val Leu Ser Tyr Gly Phe
      145          150          155          160
Ile Val Ser Thr Val Leu Gln Ile Pro Ser Ala Thr Gly Gln Arg Lys
      165          170          175
Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Val Ile Phe Tyr
      180          185          190
Thr Ala Val Ile Phe Met Tyr Val Arg Pro Arg Ala Ile Ala Ser Phe
      195          200          205
Asn Ser Asn Lys Leu Ile Ser Ala Ile Tyr Ala Val Phe Thr
      210          215          220

```

&lt;210&gt; 2715

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Unknown (K18 (MUSODORECC L14568 293758 B40745) Buck 93)

&lt;400&gt;2715

```

Arg Tyr Val Ala Ile Cys Lys Pro Leu Thr Tyr Lys Val Ile Met Ser
 1           5           10           15
Pro Lys Ile Cys Cys Leu Leu Ile Phe Ser Ser Tyr Leu Met Gly Phe
      20           25           30
Ala Ser Ala Met Ala His Thr Gly Cys Met Ile Arg Leu Ser Phe Cys
      35           40           45
Asp Ser Asn Ile Ile Asn His Tyr Met Cys Asp Ile Phe Pro Leu Leu
      50           55           60
Pro Leu Ser Cys Ser Ser Thr Tyr Val Asn Glu Leu Met Ser Ser Val
      65           70           75           80
Val Val Gly Ser Ala Ile Ile Leu Cys Cys Leu Ile Ile Leu Ile Ser
      85           90           95
Tyr Ala Met Ile Leu Phe Asn Ile Ile His Met Ser Ser Gly Lys Gly
      100          105          110
Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser
      115          120          125
Leu Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala
      130          135          140
Lys Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu
      145          150          155          160
Val

```

&lt;210&gt; 2716

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (K4 (MUSODORECD L14569 293760 464303 OLF4 P34983) Ressler-KJ 93)

&lt;400&gt;2716

```

Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys Gln Ser Thr Val
 1          5          10          15
Val Ile Pro Lys Met Leu Val Ser Phe Leu Thr Glu Met Asn Ile Ile
      20          25          30
Ser Tyr Ser Glu Cys Met Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly
      35          40          45
Ile Ala Gly Cys Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      50          55          60
Ala Ile Cys Asn Pro Leu Leu Tyr Asn Val Thr Met Ser Tyr Gln Ile
      65          70          75          80
Tyr Ser Ser Leu Ile Ser Gly Val Tyr Ile Phe Ala Val Ile Cys Ser
      85          90          95
Ser Phe Asn Thr Gly Phe Met Leu Arg Thr Gln Phe Cys Asn Leu Asp
      100          105          110
Val Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Leu Leu Asn Leu Ala
      115          120          125
Ser Ser Asn Thr Tyr Ile Asn Glu Ile Leu Ile Leu Phe Phe Ala Thr
      130          135          140
Leu Asn Ser Phe Val Pro Val Leu Thr Ile Ile Thr Ser Tyr Ile Phe
      145          150          155          160
Ile Ile Val Thr Ile Leu Ser Ile His Ser Arg Glu Gly Lys Phe Lys
      165          170          175
Ala Phe Ser Thr Cys Ser Thr His Ile Ser Ala Val Ala Ile Phe Tyr
      180          185          190
Gly Ser Gly Ala Phe Thr Tyr Leu Gln Pro Ser Ser Leu Asn Ser Met
      195          200          205
Gly Gln Ala Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val
      210          215          220

```

&lt;210&gt; 2717

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (olf3 (MUSOR3X OR3 M84005 200154 P23275 A46247) Nef 92)

&lt;400&gt;2717

```

Met Glu Val Asp Ser Asn Ser Ser Ser Gly Thr Phe Ile Leu Met Gly
 1          5          10          15
Val Ser Asp His Pro His Leu Glu Ile Ile Phe Phe Ala Val Ile Leu
      20          25          30
Ala Ser Tyr Leu Leu Thr Leu Val Gly Asn Leu Thr Ile Ile Leu Leu
      35          40          45
Ser Arg Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50          55          60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Thr Thr Ser Ser Val Pro Gln
      65          70          75          80
Met Leu Lys Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Gly Gly
      85          90          95
Cys Val Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100          105          110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115          120          125
Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys Trp Gly Leu
      130          135          140
Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
      145          150          155          160
Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys Val Asp Asn

```

165 170 175  
 Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr  
 180 185 190  
 Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Val  
 195 200 205  
 Val Pro Val Ser Val Ile Leu Val Ser Tyr Cys Phe Ile Ala Gln Ala  
 210 215 220  
 Val Met Lys Ile Arg Ser Val Glu Gly Arg Arg Lys Ala Phe Asn Thr  
 225 230 235 240  
 Cys Val Ser His Leu Val Val Val Phe Leu Phe Tyr Gly Ser Ala Ile  
 245 250 255  
 Tyr Gly Tyr Leu Leu Pro Ala Lys Ser Ser Asn Gln Ser Gln Gly Lys  
 260 265 270  
 Phe Ile Ser Leu Phe Tyr Ser Val Thr Pro Met Val Asn Pro Leu  
 275 280 285  
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Leu  
 290 295 300  
 Leu Gly Lys Gly Arg Gly Ala Ser  
 305 310

&lt;210&gt; 2718

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Unknown (MMOR23 (X92969))

&lt;400&gt;2718

Met Gln Arg Asn Asn Phe Thr Glu Val Ile Glu Phe Val Phe Leu Gly  
 1 5 10 15  
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu  
 20 25 30  
 Thr Ile Tyr Ile Leu Thr Leu Ala Gly Asn Ile Ile Ile Val Thr Ile  
 35 40 45  
 Thr His Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60  
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg  
 65 70 75 80  
 Met Leu Ser Ser Leu Ile Phe Tyr Asn Leu Pro Ile Ser Leu Ala Gly  
 85 90 95  
 Cys Ala Thr Gln Met Phe Phe Phe Val Thr Leu Ala Thr Asn Asn Cys  
 100 105 110  
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Arg Tyr Thr Ile Ile Met Ser Lys Gly Met Cys Ala Leu Leu  
 130 135 140  
 Val Cys Gly Ser Leu Gly Thr Gly Leu Val Met Ala Val Leu His Val  
 145 150 155 160  
 Pro Ala Met Phe His Leu Pro Phe Cys Gly Thr Val Val Glu His Phe  
 165 170 175  
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Val Asp Thr Thr  
 180 185 190  
 Val Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Leu Val  
 195 200 205  
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Ile Val Ser Ser Ile  
 210 215 220  
 Leu Lys Ile Val Ser Thr Glu Gly Gln Lys Lys Ala Phe Ala Thr Cys  
 225 230 235 240  
 Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile  
 245 250 255  
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Val Glu Lys Asp Leu Leu  
 260 265 270  
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val

275                      280                      285  
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val  
 290                      295                      300  
 Gly Arg Asn Thr Ser  
 305

&lt;210&gt; 2719

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR2GEN)

&lt;400&gt;2719

Met Leu Val Leu Cys Phe Ser Ala Ser Leu Leu Ser Asn Cys Asn Cys  
 1                      5                      10                      15  
 Val Val Met Met Ala Lys Gly Asn His Ser Ser Ile Thr Glu Phe Val  
 20                      25                      30  
 Leu Leu Gly Phe Ser Glu Lys Arg Ala Ile Gln Ala Val Leu Phe Met  
 35                      40                      45  
 Gly Phe Leu Leu Ile Tyr Leu Ile Thr Leu Leu Gly Asn Val Gly Met  
 50                      55                      60  
 Ile Thr Leu Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe  
 65                      70                      75                      80  
 Phe Leu Ser Ser Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Thr Ile  
 85                      90                      95  
 Thr Pro Arg Val Leu Ser Asp Leu Pro Ala Ser Gln Lys Val Ile Ser  
 100                      105                      110  
 His Ser Ala Cys Leu Ala Gln Phe Tyr Phe Tyr Ala Val Phe Ala Thr  
 115                      120                      125  
 Thr Glu Cys Tyr Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala  
 130                      135                      140  
 Ile Cys Ser Pro Leu Leu Tyr Val Phe Ser Met Ser Ser Arg Val Cys  
 145                      150                      155                      160  
 Val Leu Leu Val Ala Gly Ser Tyr Leu Val Gly Val Val Asn Ala Thr  
 165                      170                      175  
 Ile His Thr Gly Leu Ala Leu Gln Leu Ser Phe Cys Gly Pro Asn Ile  
 180                      185                      190  
 Ile Asn His Phe Tyr Cys Asp Gly Pro Pro Leu Tyr Ala Ile Ser Cys  
 195                      200                      205  
 Thr Asp Pro Thr Thr Asn Glu Ile Ala Ile Phe Leu Val Val Gly Phe  
 210                      215                      220  
 Asn Met Leu Ile Thr Ser Val Thr Ile Phe Ile Ser Tyr Thr Tyr Ile  
 225                      230                      235                      240  
 Leu Phe Ala Val Leu Arg Met His Thr Ala Ala Gly Lys Arg Lys Thr  
 245                      250                      255  
 Phe Ser Thr Cys Ala Ser His Leu Ala Thr Val Thr Leu Phe Tyr Ala  
 260                      265                      270  
 Ser Ala Gly Ser Met Tyr Ser Arg Pro Ser Ser Arg His Ser Gln Asp  
 275                      280                      285  
 Leu Asp Lys Val Ala Ser Val Phe Tyr Thr Met Val Thr Pro Met Leu  
 290                      295                      300  
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asp Val Leu  
 305                      310                      315                      320  
 Gly Lys Val Met Gly Arg Lys Ser Val Ser Asp Lys  
 325                      330

&lt;210&gt; 2720

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR3GEN)

&lt;400&gt;2720

```

Met Ala Leu Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1          5          10          15
Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
          20          25          30
Val Ile Tyr Thr Thr Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
          35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
          50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
          85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Cys
          100          105          110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
          130          135          140
Val Lys Gly Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
          145          150          155          160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
          165          170          175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
          180          185          190
Thr Leu Asn Glu Leu Leu Val Ile Ile Phe Gly Ser Leu Phe Val Met
          195          200          205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
          210          215          220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
          245          250          255
Phe Met Tyr Leu Arg Ser Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
          260          265          270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
          290          295          300
Thr Ala Thr Ser Ile Trp Leu His
305          310

```

&lt;210&gt; 2721

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR4GEN)

&lt;400&gt;2721

```

Met Ala Glu Gly Asn His Thr Leu Ala Ser Glu Phe Ile Leu Val Gly
 1          5          10          15
Leu Ser Asp His Pro Lys Met Lys Ala Ala Leu Phe Val Val Phe Leu
          20          25          30
Leu Ile Tyr Val Ile Thr Phe Gln Gly Asn Leu Gly Ile Ile Ile Leu
          35          40          45
Ile Gln Gly Asp Pro Arg Leu His Thr Ser Met Tyr Phe Phe Leu Ser
          50          55          60
Ser Leu Ser Val Val Asp Ile Cys Phe Ser Ser Val Ile Ala Pro Arg
65          70          75          80
Thr Leu Val Asn Phe Leu Ser Glu Arg Arg Thr Ile Ser Phe Thr Gly
          85          90          95
Cys Thr Gly Gln Thr Phe Phe Tyr Ile Val Phe Val Thr Thr Glu Cys
          100          105          110

```

Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn  
 115 120 125  
 Pro Leu Leu Tyr Ser Thr Ile Met Thr Arg Arg Gln Cys Met Gln Leu  
 130 135 140  
 Val Val Gly Ser Tyr Ile Gly Gly Ile Leu Asn Ala Ile Il Gln Thr  
 145 150 155 160  
 Thr Phe Ile Ile Arg Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His  
 165 170 175  
 Phe Phe Cys Asp Val Pro Pro Leu Leu Ala Leu Ser Leu Ala Ser Thr  
 180 185 190  
 Tyr Ile Ser Glu Met Ile Leu Phe Ser Leu Ala Gly Ile Ile Glu Leu  
 195 200 205  
 Ser Thr Val Thr Ser Ile Leu Val Ser Tyr Ile Phe Ile Ser Cys Ala  
 210 215 220  
 Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr  
 225 230 235 240  
 Cys Ala Ser His Leu Thr Ala Val Thr Leu Leu Tyr Gly Thr Thr Ile  
 245 250 255  
 Phe Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Thr Asp Lys  
 260 265 270  
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Gly Ala Leu Ser Arg Val  
 290 295 300  
 Val Glu Arg Ile Thr Val Arg Val  
 305 310

&lt;210&gt; 2722

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR1)

&lt;400&gt;2722

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly  
 1 5 10 15  
 Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu  
 20 25 30  
 Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu  
 35 40 45  
 Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly  
 85 90 95  
 Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Thr Glu Ser  
 100 105 110  
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu  
 130 135 140  
 Val Glu Ser Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr  
 145 150 155 160  
 Ser Gly Leu Leu Lys Leu Ser Phe Cys Tyr Ser Asn Val Val Asn His  
 165 170 175  
 Phe Phe Cys Asp Ile Ser Pro Leu Phe Gln Ile Ser Ser Ser Ile  
 180 185 190  
 Ala Ile Ser Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met  
 195 200 205  
 Ser Ser Ile Ile Ile Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr  
 210 215 220

Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile  
 245 250 255  
 Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys  
 260 265 270  
 Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu  
 290 295 300  
 Thr Ala Thr Thr Phe Gly Phe Ile Asp Ser Lys Ala Val Gln  
 305 310 315

&lt;210&gt; 2723

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR2)

&lt;400&gt;2723

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly  
 1 5 10 15  
 Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu  
 20 25 30  
 Val Ile Tyr Thr Thr Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu  
 35 40 45  
 Ile Gly Met Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln  
 50 55 60  
 Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys  
 65 70 75 80  
 Met Leu Ala Thr Phe Leu Glu Glu Arg Arg Thr Ile Ser Tyr Val Gly  
 85 90 95  
 Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Trp  
 100 105 110  
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys  
 115 120 125  
 Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu  
 130 135 140  
 Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr  
 145 150 155 160  
 Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His  
 165 170 175  
 Phe Phe Cys Asp Asn Arg Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr  
 180 185 190  
 Thr Leu Asn Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met  
 195 200 205  
 Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr  
 210 215 220  
 Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr  
 225 230 235 240  
 Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile  
 245 250 255  
 Phe Met Tyr Leu Arg Ser Val Lys Leu Phe Ser Leu Asp Thr Asp Lys  
 260 265 270  
 Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu  
 290 295 300  
 Thr Ala Thr Ser Val Trp Leu His  
 305 310

&lt;210&gt; 2724



<211> 318  
 <212> PRT  
 <213> Unknown (GGCOR3)

<400>2724

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
1          5          10          15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
20          25          30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Arg Leu
35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Cys
100         105         110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115         120         125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
130         135         140
Val Glu Ser Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
145         150         155         160
Cys Gly Leu Leu Lys Leu Ser Phe Cys Tyr Ser Asn Val Val Asn His
165         170         175
Phe Phe Cys Asp Ile Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Ile
180         185         190
Ala Ile Ser Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met
195         200         205
Ser Ser Ile Ile Ile Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
210         215         220
Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225         230         235         240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
245         250         255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
260         265         270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
275         280         285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
290         295         300
Thr Ala Thr Thr Phe Gly Phe Ile Asp Ser Lys Ala Val Gln
305         310         315

```

<210> 2725  
 <211> 312  
 <212> PRT  
 <213> Unknown (GGCOR4)

<400>2725

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
1          5          10          15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
20          25          30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys

```

```

65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Ile Gly
      85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Thr Glu Ser
      100        105        110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115        120        125
Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
      130        135        140
Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr
145      150      155      160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
      165        170        175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
      180        185        190
Thr Leu Asn Glu Leu Leu Val Phe Ile Phe Gly Ser Leu Phe Ala Met
      195        200        205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
      210        215        220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225      230      235      240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
      245        250        255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
      260        265        270
Ile Ala Ser Leu Phe Tyr Thr Val Ile Pro Met Leu Asn Pro Leu
      275        280        285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Val
      290        295        300
Ile Ala Thr Asn Val Trp Ile His
305          310

```

&lt;210&gt; 2726

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR5)

&lt;400&gt;2726

```

Met Ala Leu Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
1      5      10      15
Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
      20      25      30
Ala Ile Tyr Thr Ile Thr Leu Leu Ala Asn Leu Gly Leu Ile Ala Leu
      35      40      45
Ile Ser Val Asp Phe His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
      50      55      60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65      70      75      80
Met Leu Ala Thr Phe Leu Glu Glu Arg Arg Thr Ile Ser Tyr Val Gly
      85      90      95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Ser Ser Glu Cys
      100      105      110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115      120      125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
      130      135      140
Val Glu Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr
145      150      155      160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
      165      170      175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr

```

```

      180      185      190
Thr Leu Asn Glu Leu Leu Val Phe Ile Phe Gly Ser Trp Phe Ala Met
      195      200      205
Ser Ser Ile Ile Thr Thr Pro Ile Ser Tyr Val Phe Ile Ile Leu Thr
      210      215      220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
      245      250      255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
      260      265      270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Val
      290      295      300
Ile Ala Thr Asn Val Trp Ile His
      305      310

```

&lt;210&gt; 2727

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Unknown (GGCOR6)

&lt;400&gt;2727

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
  1      5      10      15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
      20      25      30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
      35      40      45
Ile Ser Ile Asp Leu Gln Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
      50      55      60
Asn Leu Ser Phe Thr Asp Ala Val Tyr Ser Thr Val Ile Thr Pro Lys
      65      70      75      80
Met Leu Ala Thr Phe Leu Glu Glu Thr Lys Thr Ile Ser Tyr Val Gly
      85      90      95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Arg Glu Cys
      100      105      110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Lys
      115      120      125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
      130      135      140
Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Phe Leu Val His Thr
      145      150      155      160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
      165      170      175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
      180      185      190
Ala Leu Asn Glu Leu Leu Val Phe Ile Phe Gly Ser Leu Phe Val Met
      195      200      205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
      210      215      220
Val Val Arg Ile Arg Ser Lys Glu Arg Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Ile Val
      245      250      255
Phe Met Tyr Phe Gln Pro Ala Asn Asn Phe Ser Leu Asp Lys Asp Lys
      260      265      270
Ile Met Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala

```

290 295 300  
 Ile Ala Thr Ala Val Leu Phe His  
 305 310

<210> 2728  
 <211> 162  
 <212> PRT  
 <213> Unknown (XLORXR1)

<400>2728  
 Val Ala Val Cys His Pro Leu Leu Tyr Val Phe His Met Ser Gln Lys  
 1 5 10 15  
 His Cys Thr Phe Phe Val Ser Ala Ala Trp Ile Ile Gly Phe Leu Asp  
 20 25 30  
 Pro Thr Ser Tyr Val Val Leu Ile Ser Lys Phe Ser Phe Cys Thr Ser  
 35 40 45  
 Asn Ile Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Lys Leu  
 50 55 60  
 Ser Cys Ser Asp Thr Phe Gln Ile Glu Val Leu Asn Tyr Val Glu Ser  
 65 70 75 80  
 Ala Leu Val Thr Leu Asn Ser Phe Val Leu Thr Val Ile Ser Tyr Ile  
 85 90 95  
 Phe Thr Ile Ser Ala Ile Leu Asn Ile Lys Ser Ala Glu Gly Arg His  
 100 105 110  
 Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe  
 115 120 125  
 Tyr Ser Thr Ile Ile Ser Leu Tyr Ile Arg Pro Ile Ser Thr Tyr Ala  
 130 135 140  
 Pro Lys Gln Asp Gln Phe Phe Ala Leu Leu Tyr Ile Val Leu Ile Pro  
 145 150 155 160  
 Leu Leu

<210> 2729  
 <211> 161  
 <212> PRT  
 <213> Unknown (XLORXR2)

<400>2729  
 Val Ala Ile Cys Tyr Pro Leu His Tyr Ala Leu Arg Met Ser Leu Lys  
 1 5 10 15  
 His Cys Ala Lys Ile Ile Val Gly Val Trp Val Ala Gly Phe Leu Ala  
 20 25 30  
 Pro Val Ile His Thr Val Leu Met Thr Asn Leu Ser Phe Cys Ser Ser  
 35 40 45  
 Asn His Ile Asn His Phe Leu Cys Asp Leu Thr Pro Val Leu Lys Ile  
 50 55 60  
 Ser Cys Ser Asp Thr Ser Leu Ile Glu Met Ile Thr Tyr Ile Asp Gly  
 65 70 75 80  
 Val Ile Val Ala Phe Ser Thr Phe Thr Ile Thr Ser Val Ser Tyr Val  
 85 90 95  
 Phe Ile Leu Phe Lys Ile Leu Lys Ile His Ser Ser Gln Gly Lys Lys  
 100 105 110  
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe  
 115 120 125  
 Tyr Gly Ser Ile Ile Cys Leu Tyr Met Arg Pro Thr Lys Ser Ile Ser  
 130 135 140  
 Pro Asn Gln Asp Val Phe Ala Leu Leu Tyr Ala Val Leu Val Pro Met  
 145 150 155 160  
 Leu

<210> 2730  
 <211> 155  
 <212> PRT  
 <213> Unknown (XLORXR3)

<400>2730  
 Val Ala Ile Cys Met Pro Met Leu Tyr Ser Leu Ile Met Lys Lys Ser  
 1 5 10 15  
 Ile Cys Ala Leu Leu Ala Ser Val Ser Trp Phe Met Gly Ala Met Asp  
 20 25 30  
 Ser Phe Met Phe Trp Tyr Leu Val Ser Asn Ser Ser Phe Cys Asp His  
 35 40 45  
 Gln Glu Ile Asn His Phe Phe Cys Asp Leu Lys Thr Leu Met Lys Leu  
 50 55 60  
 Ser Cys Arg Gly Ala Glu Thr Ile Lys Ile Val Ile Ile Val Ala Ser  
 65 70 75 80  
 Ala Val Leu Gly Phe Leu Pro Phe Cys Leu Ile Leu Ile Ser Tyr Ala  
 85 90 95  
 Asn Ile Ile Ser Ser Val Ser Lys Ile Arg Thr Ala Ala Gly Lys Leu  
 100 105 110  
 Lys Ile Phe Ser Ser Cys Gly Ser His Leu Thr Val Val Leu Leu Phe  
 115 120 125  
 Cys Gly Thr Cys Leu Ser Leu Tyr Met Lys Pro Asp Ser Gly Asn Ser  
 130 135 140  
 Gln Glu Asn Glu Glu Leu Leu Ser Leu Leu Tyr  
 145 150 155

<210> 2731  
 <211> 162  
 <212> PRT  
 <213> Unknown (XLORXR5)

<400>2731  
 Val Ala Ile Cys Gln Pro Leu Leu Tyr Ala Val Ile Met Asn Arg Lys  
 1 5 10 15  
 Val Val Ile Ile Phe Val Val Gly Val Tyr Leu Ser Gly Ile Phe Thr  
 20 25 30  
 Ala Ser Ile His Thr Ala Cys Thr Leu Thr Leu Ser Phe Cys Gly Pro  
 35 40 45  
 Asn Thr Ile Asn His Phe Tyr Cys Asp Ile Pro Pro Leu Met Glu Leu  
 50 55 60  
 Ser Cys Ser Asp Thr Tyr Ile His Lys Thr Val Ile Phe Val Val Val  
 65 70 75 80  
 Phe Cys Leu Gly Leu Phe Asn Val Ala Val Ile Leu Ala Ser Tyr Ser  
 85 90 95  
 Tyr Ile Phe Phe Thr Ile Ile His Ile Gln Ser Ser Cys Gly Arg His  
 100 105 110  
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Cys Val Ser Leu Phe  
 115 120 125  
 Tyr Gly Thr Val Phe Phe Met Tyr Leu Arg Pro Ala Ser Lys Tyr Ser  
 130 135 140  
 Val Ser Gln Asp Lys Val Val Ser Val Phe Tyr Thr Met Val Ile Pro  
 145 150 155 160  
 Met Met

<210> 2732  
 <211> 163  
 <212> PRT  
 <213> Unknown (XLORXR9)

&lt;400&gt;2732

```

Leu Ala Ile Cys Phe Pro Leu Asn Tyr Cys Leu Ile Met Ser Gln Ser
 1           5           10           15
Leu Arg Cys Arg Leu Val Val Val Cys Trp Ala Cys Gly Leu Val Asn
 20           25           30
Ser Leu Val Gln Ala Phe Ser Ile Ser His Leu Asp Phe Cys Gly Pro
 35           40           45
Asn Val Val Asp His Phe Phe Cys Asp Val Thr Pro Leu Phe Lys Leu
 50           55           60
Ser Cys Ser Asp Thr Arg Val Ser Glu Thr Ile Phe Leu Leu Val Val
 65           70           75           80
Ala Val Ala Gly Met Gly Pro Leu Thr Phe Ile Leu Val Thr Tyr Gly
 85           90           95
His Ile Ile Leu Ala Ile Thr Arg Ile Thr Ser Ser His Gly Arg Tyr
 100          105          110
Lys Thr Phe Ser Thr Cys Ala Ser His Phe Thr Val Val Ala Leu Tyr
 115          120          125
Tyr Gly Ser Gly Ile Phe Ser Tyr Ile Trp Pro Thr Ser Thr Tyr Ala
 130          135          140
Met Asn Lys Asp Val Lys Val Val Ala Val Leu Tyr Thr Val Met Thr
 145          150          155          160
Pro Met Leu

```

&lt;210&gt; 2733

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR13)

&lt;400&gt;2733

```

Val Ala Ile Ser Lys Pro Leu Arg Tyr Met Thr Ile Met Asn Trp Lys
 1           5           10           15
Val Cys Ala Val Leu Gly Val Ala Met Trp Thr Ala Gly Thr Val His
 20           25           30
Ser Ile Ser Phe Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro
 35           40           45
Asp Glu Ile Asp Asn Phe Phe Cys Asp Val Pro Gln Val Ile Glu Leu
 50           55           60
Ala Cys Thr Asp Thr Arg Ile Thr Glu Ile Leu Val Val Ser Asn Ser
 65           70           75           80
Gly Met Ile Ser Met Val Cys Phe Val Ile Ile Val Val Ser Tyr Ala
 85           90           95
Val Ile Leu Val Ser Leu Arg Gln Gln Ile Ser Asp Gly Lys Arg Lys
 100          105          110
Ala Leu Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu
 115          120          125
Gly His Cys Ile Phe Ile Tyr Ser Arg Pro Ser Ile Ser Leu Pro Glu
 130          135          140
Asp Lys Ile Val Ser Ala Phe Phe Thr Ala Val Thr Pro Leu Leu
 145          150          155

```

&lt;210&gt; 2734

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR17)

&lt;400&gt;2734

```

Asn Ala Ile Cys Asn Pro Leu Leu Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Thr Cys Val Ile Leu Ile Val Gly Ser Trp Leu Ile Ala Ser Ile Asn

```

```

      20      25      30
Ser Leu Ile His Thr Ile Leu Thr Phe Met Leu Pro Phe Cys Gly Ser
      35      40      45
Asn Ala Ile Asp Ser Phe Phe Cys Asp Met Pro Pro Leu Leu Lys Leu
      50      55      60
Ala Cys Thr Asp Thr Leu Val Asn Gln Ile Val Ile Phe Val Thr Gly
      65      70      75      80
Ser Cys Ile Ile Ala Gly Pro Phe Met Leu Thr Val Phe Ser Tyr Val
      85      90      95
Gln Ile Ile Ser Thr Ile Val Ser Ile Arg Ser Ser Ser Arg Lys Lys
      100      105      110
Lys Ala Phe Ser Thr Cys Thr Ser His Ile Thr Ala Val Val Ile Phe
      115      120      125
Tyr Val Pro Ser Ile Cys Ile Tyr Phe Arg Pro Lys Ser Asn Gln Ala
      130      135      140
Met Ile Gln Asp Lys Met Ala Thr Val Ile Cys Ala Val Ile Thr Pro
      145      150      155      160
Leu Leu

```

<210> 2735  
 <211> 223  
 <212> PRT  
 <213> Unknown (XLORXR42)

```

<400>2735
Cys Asn Leu Ser Ser Leu Asp Ile Ala Tyr Thr Ser Val Thr Ala Pro
 1      5      10      15
Lys Leu Ile His Ile Phe Ala Val Asn Asn His Arg Ile Ser Phe Trp
      20      25      30
Gln Cys Ile Ala Gln Leu Tyr Phe Phe Ile Ala Phe Gly Ser Thr Glu
      35      40      45
Tyr Leu Leu Leu Thr Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys
      50      55      60
Lys Pro Leu His Tyr Arg Val Val Met Ser Pro Met Leu Cys Arg Ala
      65      70      75      80
Gly Ala Ala Gly Thr Trp Ile Gly Gly Leu Leu Ala Ser Ile Pro Thr
      85      90      95
Ala Thr Ala Ala Ala Asn Ile Tyr Tyr Cys Ser Asn Asn Ile Ile Ile
      100      105      110
Asn His Phe Cys Asp Met Met Ala Leu Val Lys Leu Ala Cys Ser
      115      120      125
Asp Thr Thr Met Thr Arg Ala Val Ile Phe Val Glu Gly Met Leu Ile
      130      135      140
Leu Met Thr Cys Phe Leu Leu Thr Val Ile Ser Tyr Ile Cys Ile Leu
      145      150      155      160
Ser Thr Ile Val Arg Ile His Ser Ser Gly Gly Lys Phe Lys Ala Phe
      165      170      175
Ser Thr Cys Ala Ser His Leu Ser Val Val Ser Ile Phe Tyr Val Leu
      180      185      190
Ile Phe Tyr Leu Tyr Leu Lys Pro Lys Ser Glu Ile Ser Leu Ser Gln
      195      200      205
Gly Lys Leu Leu Thr Val Leu Tyr Val Tyr Phe Ile Pro Met Phe
      210      215      220

```

<210> 2736  
 <211> 217  
 <212> PRT  
 <213> Unknown (XLORXR46)

<400>2736

```

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1           5           10           15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
 20           25           30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
 35           40           45
Ala Ala Asp Arg Tyr Val Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
 50           55           60
Ile Ile Thr Lys Lys Leu Thr Ala Ile Phe Cys Ser Cys Phe Trp Val
 65           70           75           80
Leu Ser Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
 85           90           95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
 100          105          110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
 115          120          125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile
 130          135          140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
 145          150          155          160
Ser Asp Asn Trp Gln Lys Leu Phe Tyr Thr Cys Thr Thr His Leu Leu
 165          170          175
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Val Tyr Leu Ala Asn
 180          185          190
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
 195          200          205
Met Tyr Thr Phe Leu Pro His Leu Ala
 210          215

```

&lt;210&gt; 2737

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR106)

&lt;400&gt;2737

```

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1           5           10           15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
 20           25           30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
 35           40           45
Ala Ala Asp Arg Tyr Ile Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
 50           55           60
Ile Ile Thr Lys Lys Leu Thr Thr Ile Phe Cys Ser Cys Phe Trp Val
 65           70           75           80
Leu Ser Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
 85           90           95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
 100          105          110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
 115          120          125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile
 130          135          140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
 145          150          155          160
Ser Asp Asn Trp Gln Lys Leu Phe Tyr Thr Cys Thr Thr His Leu Leu
 165          170          175
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Met Tyr Leu Ala Asn
 180          185          190
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
 195          200          205

```



Met Tyr Thr Phe Leu Pro His Leu Ala  
 210 215

<210> 2738

<211> 217

<212> PRT

<213> Unknown (XLORXR116)

<400>2738

Leu Leu Phe Asp Thr Ile Thr Leu Pro Lys Ile Ile Ala Lys Tyr Trp  
 1 5 10 15  
 Phe Gly Ala Arg Ser Ile Ser Phe Tyr Gly Cys Ile Phe Gln Leu Phe  
 20 25 30  
 Cys Val His Ser Leu Gly Ser Leu Asp Ser Phe Ile Ile Met Leu Met  
 35 40 45  
 Ala Ile Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Arg Tyr His Ser  
 50 55 60  
 Ile Ile Ser Asn Lys Leu Val Thr Leu Leu Cys Tyr Phe Phe Trp Val  
 65 70 75 80  
 Leu Ala Ala Leu Ile Gly Ser Ile Val Ala Val Ile Ala Gly Gln Leu  
 85 90 95  
 Pro Tyr Cys Gly Pro Asn Arg Val Arg Asn Cys Phe Cys Val Asn Ser  
 100 105 110  
 Ala Val Thr Val Leu Ala Cys Val Asp Val Thr Leu Ala Arg Arg Thr  
 115 120 125  
 Val Phe Thr Leu Ala Met Cys Val Leu Leu Leu Pro Leu Ala Phe Ile  
 130 135 140  
 Ile Leu Ser Tyr Ile Leu Ile Ile Arg Val Ile His Ser Ser Thr Asn  
 145 150 155 160  
 Asn Glu Asn Ser Trp Lys Ala Phe Tyr Thr Cys Thr Thr His Leu Met  
 165 170 175  
 Val Ile Gly Leu Tyr Tyr Ile Pro Arg Val Phe Val Tyr Ser Thr Ser  
 180 185 190  
 Gln Ile Pro Leu Ile Leu Asp Val Asp Ile Asn Val Leu Leu Leu Cys  
 195 200 205  
 Leu Tyr Thr Phe Val Pro His Leu Ala  
 210 215

<210> 2739

<211> 217

<212> PRT

<213> Unknown (XLORXR117)

<400>2739

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp  
 1 5 10 15  
 Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe  
 20 25 30  
 Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met  
 35 40 45  
 Ala Ala Asp Arg Tyr Ile Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala  
 50 55 60  
 Ile Ile Thr Lys Lys Leu Thr Thr Ile Phe Cys Ser Cys Phe Trp Val  
 65 70 75 80  
 Leu Gly Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu  
 85 90 95  
 Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser  
 100 105 110  
 Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val  
 115 120 125  
 Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile

130 135 140  
 Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His  
 145 150 155 160  
 Ser Asp Asn Trp Gln Lys Pro Phe Tyr Thr Cys Thr Thr His Leu Leu  
 165 170 175  
 Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Met Tyr Leu Ala Asn  
 180 185 190  
 Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr  
 195 200 205  
 Met Tyr Thr Phe Leu Pro His Leu Ala  
 210 215

&lt;210&gt; 2740

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR171)

&lt;400&gt;2740

Gln Gln Leu Ser Val Cys Asp Leu Leu Gln Thr Ala Cys Thr Val Pro  
 1 5 10 15  
 Leu Leu Leu Trp Thr Ile Ile Asn Asp Gly Thr Thr Ile Ser Val Gly  
 20 25 30  
 Gly Cys Ile Thr Gln Phe Tyr Phe Phe Asn Ala Ser Glu Ser Val Glu  
 35 40 45  
 Cys Leu Leu Leu Thr Val Met Ser Phe Asp Arg Tyr Leu Ala Ile Cys  
 50 55 60  
 Asn Pro Leu Arg Tyr Thr Ser Leu Met Asn Pro Lys Leu Cys Val Lys  
 65 70 75 80  
 Leu Thr Leu Ile Pro Trp Leu Leu Gly Phe Ser Ile Ile Leu Ile Thr  
 85 90 95  
 Ala Asn Ala Ile Ala Thr Leu Gln Phe Cys Asn Gln Asn Thr Ile Asn  
 100 105 110  
 His Tyr Phe Cys Asp Tyr Phe Pro Leu Leu Glu Leu Ser Cys Met Asp  
 115 120 125  
 Thr Phe Phe Val Gln Thr Glu Ala Ile Leu Gln Ala Val Pro Val Val  
 130 135 140  
 Phe Ile Pro Ile Ile Leu Ile Ile Ile Ser Tyr Val Phe Ile Ile His  
 145 150 155 160  
 Thr Leu Leu Lys Ile Val Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser  
 165 170 175  
 Thr Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Ser Leu  
 180 185 190  
 Ile Gly Ile Tyr Val Val Pro Ser Arg Lys Gln Ser Pro Thr Ile Ser  
 195 200 205  
 Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Leu  
 210 215 220

&lt;210&gt; 2741

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR181)

&lt;400&gt;2741

Gln Gln Leu Ser Leu Ser Asp Leu Leu Gly Ser Thr Asn Ile Val Pro  
 1 5 10 15  
 Thr Leu Leu Glu Thr Ile Ile Leu Gly Arg Ala Ser Ile Ser Leu Val  
 20 25 30  
 Asp Cys Ile Thr Gln Phe Asn Val Phe Gly Gly Ser Glu Thr Phe Val  
 35 40 45  
 Gly Phe Leu Leu Ala Val Met Ser Asn Asp Arg Tyr Val Ala Ile Cys  
 50 55 60

```

Ile Pro Leu Arg Tyr Thr Ser Ile Thr Ser Tyr Asn Ile Cys Asn Lys
65              70              75              80
Leu Ile Leu Val Ser Trp Leu Leu Gly Leu Gly Ala Ile Leu Ile Thr
            85              90              95
Ala Asn Leu Ile*Ala Thr Leu Tyr Phe Cys Asp Gln Asn Ile Ile Asn
            100             105             110
His Phe Phe Cys Asp Phe Phe Pro Leu Leu Gln Leu Ser Cys Ser Asp
            115             120             125
Thr Phe Ile Val Gln Leu Glu Val Ile Leu Leu Ser Ile Pro Val Ile
            130             135             140
Ile Tyr Pro Phe Ile Leu Ile Ile Val Ser Tyr Ile Cys Ile Ala His
145             150             155             160
Ala Ile Leu Lys Ile Val Ser Asn Thr Gly Arg Gln Lys Ala Phe Ser
            165             170             175
Thr Cys Ser Ser His Leu Ala Val Val Ser Ile Phe Tyr Gly Ala Leu
            180             185             190
Thr Ala Val Tyr Val Ala Pro Pro Arg Lys Glu Ser Gln Thr Leu Ser
            195             200             205
Lys Val Phe Ser Leu Leu Tyr Thr Val Met Ile Pro
            210             215             220

```

&lt;210&gt; 2742

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLOR185)

&lt;400&gt;2742

```

Ser Gln Leu Ser Thr Ser Asp Ile Val Ile Ser Thr Thr Val Cys Pro
1              5              10              15
Asn Leu Leu Tyr Ile Thr Trp Asn Glu Gly Ala Tyr Ile Ser Ile Thr
            20              25              30
Gly Cys Ile Trp Gln Phe Asn Met Phe Ser Val Ser Ser Val Thr Glu
            35              40              45
Cys Phe Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Cys
            50              55              60
Lys Pro Leu His Tyr Ala Ser Ile Met Thr Trp Arg Ser Cys Ile Phe
65              70              75              80
Leu Val Met Ser Cys Trp Ser Leu Gly Phe Leu Leu Ser Met Ile Val
            85              90              95
Thr Val Met Ile His Tyr Leu His Phe Cys Gly Pro Tyr Thr Ile Asp
            100             105             110
His Leu Phe Cys Asp Tyr Thr Pro Leu Met Gln Leu Ser Cys Ser Asp
            115             120             125
Thr Thr Ile Leu Lys Met Thr Val Phe Leu Ile Ala Thr Pro Gly Thr
            130             135             140
Val Leu Gln Pro Phe Phe Ile Ile Ala Thr Tyr Ile Asn Ile Ile Leu
145             150             155             160
Asn Ile Leu Arg Ile Ser Ser Ser Ser Lys Arg Gln Lys Ala Phe Ser
            165             170             175
Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Tyr Tyr Gly Thr Leu
            180             185             190
Ile Ala Thr Tyr Ala Thr Pro Thr Asp Gly Arg Leu Ser Thr Arg Asn
            195             200             205
Lys Leu Leu Ser Leu Ile Tyr Thr Val Gly Thr Pro
            210             215             220

```

&lt;210&gt; 2743

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR206)

&lt;400&gt;2743

Gly Asn Leu Ser Phe Val Asp Ile Ser Phe Ile Ser Val Thr Val Pro  
 1 5 10 15  
 Leu Met Val Ala His Leu Leu Thr Asp Lys Lys Ser Ile Ser Phe Thr  
 20 25 30  
 Gly Cys Met Thr Gln Leu Phe Phe Ile Trp Ile Ala Val Leu Glu  
 35 40 45  
 Cys Leu Ile Leu Thr Ile Met Ala Tyr Asp Arg Leu Val Ala Ile Thr  
 50 55 60  
 Asn Pro Leu Arg Tyr Leu Ser Ile Leu Asp Arg Lys Thr Cys Trp Ser  
 65 70 75 80  
 Leu Ile Thr Phe Ser Trp Ile Leu Ser Phe Leu His Ser Leu Leu Tyr  
 85 90 95  
 Ala Ser Thr Ile Ser Ser Leu Asp Tyr Cys Gly Leu Asn Lys Val Asn  
 100 105 110  
 Glu His Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asn  
 115 120 125  
 Pro Ala Ser Leu Glu Leu Leu Val Tyr Thr Glu Gly Ser Val Met Ala  
 130 135 140  
 Met Ser Pro Phe Val Leu Ile Met Val Ser Tyr Leu Arg Ile Ile Lys  
 145 150 155 160  
 Thr Ile Leu Ser Ile His Ser Ser Ser Gly Arg Tyr Arg Ala Phe Ser  
 165 170 175  
 Thr Cys Ser Ser His Leu Ile Ser Val Gly Leu Phe Phe Val Thr Ile  
 180 185 190  
 Phe Val Ser Tyr Leu Gln Pro Ala Ser Ala Gly Ala Val Glu Thr Asn  
 195 200 205  
 Arg Pro Ile Ala Leu Val Tyr Ser Ile Leu Thr Pro Leu Pro  
 210 215 220

&lt;210&gt; 2744

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Unknown (XLORXR214)

&lt;400&gt;2744

Ser Asn Met Ser Phe Leu Glu Ile Arg Tyr Ile Ser Val Thr Leu Pro  
 1 5 10 15  
 Asn Leu Leu Val Asn Thr Leu Ser Lys Asp Met Ser Ile Ser Leu Ala  
 20 25 30  
 Gly Cys Met Ala Gln Leu Tyr Phe Phe Ile Ser Leu Met Cys Thr Glu  
 35 40 45  
 Cys Val Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Ile Ala Val Cys  
 50 55 60  
 His Pro Leu His Tyr Val Thr Ile Val Ser Asn Lys Leu Cys Ile Gln  
 65 70 75 80  
 Leu Ala Ala Ala Ser Trp Ile Ala Gly Phe Thr Val Ser Val Ile Lys  
 85 90 95  
 Val Tyr Phe Ile Ser Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Asn  
 100 105 110  
 His Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ala Cys Val Asp  
 115 120 125  
 Met Ser Leu Ala Glu Phe Val Asp Phe Val Leu Ala Leu Val Ile Leu  
 130 135 140  
 Leu Thr Pro Leu Phe Val Thr Val Ala Ser Tyr Leu Cys Ile Ile Phe  
 145 150 155 160  
 Thr Ile Leu Lys Ile Pro Thr Asn Thr Gly Arg Gln Lys Ala Phe Ser  
 165 170 175  
 Thr Cys Ala Ser His Leu Thr Val Val Thr Ile Phe Phe Ser Thr Thr  
 180 185 190  
 Leu Phe Met Tyr Ala Arg Pro Lys Lys Ala Lys Ser Leu Asp Tyr Phe

195 200 205  
 Lys Ile Leu Ser Leu Leu Tyr Ala Val Phe Thr Pro Met Leu  
 210 215 220

<210> 2745  
 <211> 312  
 <212> PRT  
 <213> Unknown (HOR5beta3)

<400>2745  
 Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro  
 1 5 10 15  
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val  
 20 25 30  
 Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys  
 35 40 45  
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu  
 50 55 60  
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met  
 65 70 75 80  
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe  
 85 90 95  
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser  
 100 105 110  
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu  
 115 120 125  
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val  
 130 135 140  
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg  
 145 150 155 160  
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe  
 165 170 175  
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe  
 180 185 190  
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp  
 195 200 205  
 Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile  
 210 215 220  
 Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile  
 225 230 235 240  
 Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu  
 245 250 255  
 Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile  
 260 265 270  
 Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val  
 275 280 285  
 Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu  
 290 295 300  
 Leu Ser Lys His Arg Phe Ser Arg  
 305 310

<210> 2746  
 <211> 310  
 <212> PRT  
 <213> Unknown (HOR5beta2 (translated via ORDEAL))

<220>  
 <221> VARIANT  
 <222> (1)...(310)  
 <223> Xaa = Any Amino Acid

&lt;400&gt;2746

```

Thr His Asn Ala Ala Pro Phe Leu Leu Pro Gly Phe Ser Val Leu Glu
 1          5          10          15
Ala Thr Tyr His Ser Ile Ser Ile Pro Phe Phe Ala Val Tyr Val Cys
          20          25          30
Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr Leu Ile Lys His Asp His
          35          40          45
Ser Leu His Glu Pro Met Tyr Cys Phe Leu Ala Thr Leu Arg Gln Asp
          50          55          60
Leu Met Val Lys Leu Thr Met Met Pro Thr Val Met Gly Val Leu Trp
65          70          75          80
Met Asn His Lys Glu Val Ile His Gly Ala Cys Phe Leu Gln Val Tyr
          85          90          95
Ile Ile His Ser His Tyr Pro Leu Ala Glu Ser Gly Ile Leu Leu Ser
          100          105          110
Met Ala Tyr Asp Arg Phe Ile Ile Ile His Met Leu Leu Arg Tyr Asn
          115          120          125
Ser Ile Ser Thr Lys Ser Trp Val Lys Ile Glu Leu Trp Leu Phe Met
          130          135          140
Arg Asp Phe Leu Ser Leu Val Pro Pro Ile Leu Pro Leu His Cys Phe
          145          150          155          160
Pro Tyr Cys His Ser His Val Leu Phe His Thr Phe Phe Leu His Gln
          165          170          175
Asp Val Leu Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn His Leu Tyr
          180          185          190
Pro Ala Ile Leu Val Ala Leu Ile Phe Phe Leu Asp Ala Leu Ile Ile
          195          200          205
Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Ile Gly Ile Ala Ser
          210          215          220
Arg Lys Glu Gln Ala Lys Ala Leu Asn Met Cys Val Ser His Ile Ser
          225          230          235          240
Cys Val Leu Val Phe His Ile Thr Val Ile Ser Glu Thr Phe Ile His
          245          250          255
Arg Phe Gly Lys His Ala Pro His Val Val His Ile Thr Val Ser Xaa
          260          265          270
Xaa Leu Ile Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr Ser Ile
          275          280          285
Lys Pro Ser Arg Ser Lys Glu Ala Leu Xaa Arg Leu Phe Ser Gly His
          290          295          300
Arg Met Ala Xaa Ala Leu
          305          310

```

&lt;210&gt; 2747

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Unknown (HOR5beta1)

&lt;400&gt;2747

```

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
 1          5          10          15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
          20          25          30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
          35          40          45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
          50          55          60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
65          70          75          80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
          85          90          95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu

```

	100		105		110
Leu Val	Leu Ala Tyr Asp Cys Phe	Ile Ala Ile Arg Thr Pro	Leu Arg		
	115	120	125		
Tyr Asn Cys	Ile Leu Thr Asn Ser Arg Val Met	Asn Ile Gly Leu Gly			
	130	135	140		
Val Leu Met Arg Gly	Phe Met Ser Ile Leu Pro Ile	Ile Leu Ser Leu			
145	150	155	160		
Tyr Cys Tyr Pro Tyr Cys Gly	Ser Arg Ala Leu Leu His Thr	Phe Cys			
	165	170	175		
Leu His Gln Asp Val Ile Lys Leu Ala Cys	Ala Asp Ile Thr Phe Asn				
	180	185	190		
His Ile Tyr Pro Ile Ile Gln Thr Ser	Leu Thr Val Phe Leu Asp Ala				
	195	200	205		
Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu	Lys Thr Val Met Gly				
	210	215	220		
Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser	Leu Asn Thr Cys Val Ser				
225	230	235	240		
His Ile Ser Cys Val Leu Val Phe His Ile Thr	Val Met Gly Leu Ser				
	245	250	255		
Phe Ile His Arg Phe Gly Lys His Ala Pro	His Val Val Pro Ile Thr				
	260	265	270		
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe	Val Asn Pro Ile Ile				
	275	280	285		
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser	Ile Ile Arg Leu Phe				
	290	295	300		
Ser Gly Gln Ser Arg Ala					
305	310				

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
19 April 2001 (19.04.2001)

PCT

(10) International Publication Number  
**WO 01/027158 A3**

(51) International Patent Classification<sup>7</sup>: **C12N 15/12**,  
C07K 14/705, C12N 5/10, G01N 33/50, C12Q 1/68

Street, 75751 Rishon LeZion (IL); YANAI, Itai [US/US];  
55 Leicester Street, Brookline, MA 02146 (US).

(21) International Application Number: **PCT/US00/27582**

(74) Agents: **CERPA, Robert, K. et al.**; Morrison & Foerster  
LLP, 755 Page Mill Road, Palo Alto, CA 94304-1018 (US).

(22) International Filing Date: **6 October 2000 (06.10.2000)**

(25) Filing Language: **English**

(26) Publication Language: **English**

(30) Priority Data:  
60/158,615 8 October 1999 (08.10.1999) US  
60/184,809 24 February 2000 (24.02.2000) US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,  
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,  
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,  
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,  
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicants (*for all designated States except US*): **DIGIS-  
CENTS** [US/US]; Suite 720, 1814 Franklin Street, Oak-  
land, CA 94612 (US). **YEDA RESEARCH AND DE-  
VELOPMENT CO., LTD.** [IL/IL]; Weizmann Institute of  
Science, P.O. Box 95, 76100 Rehovot (IL).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **BELLENSON, Joel**  
[US/US]; 244 Lakeside Drive, Apartment 15, Oakland,  
CA 94612 (US). **SMITH, Dexter** [US/US]; 868 Trestle  
Glen Road, Oakland, CA 94610 (US). **LANCET, Doron**  
[IL/IL]; 15 Weizmann Street, 76280 Rehovot (IL). **GLUS-  
MAN, Gustavo** [IL/IL]; 33/37 Ha'Alon Street, 79845  
Bnei Ayish (IL). **FUCHS, Tania** [IL/IL]; 12 Harav neria

Published:

— with international search report

(88) Date of publication of the international search report:  
26 September 2002

*For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.*

WO 01/027158 A3

(54) Title: **OLFACTORY RECEPTOR SEQUENCES**

(57) Abstract: The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensation. The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these polynucleotide sequences and host cells transfected with these polynucleotide sequences. The present invention further provides for functional variants and homologues of these polynucleotide sequences and the polypeptides encoded by these polynucleotides. Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of polypeptides in screening odorant molecules to determine the correspondence (scent representation, scent fingerprint or scent profile) between individual odorant receptors (the polypeptides) and particular odorant molecules. Also encompassed by the present invention is the use of the scent representation, scent fingerprint or scent profile to re-create and edit scents.



## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27582

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 C12N5/10 G01N33/50 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, SEQUENCE SEARCH, WPI Data, PAJ

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WETZEL CHRISTIAN H ET AL: "Specificity and sensitivity of a human olfactory receptor functionally expressed in human embryonic kidney 293 cells and Xenopus laevis oocytes." JOURNAL OF NEUROSCIENCE, vol. 19, no. 17, pages 7426-7433, XP002178954 ISSN: 0270-6474 cited in the application the whole document	
A	WO 95 18140 A (YEDA RES & DEV ;RYCUS AVIGAIL (IL); BEN ARIE NISSIM (IL); LANCET D) 6 July 1995 (1995-07-06) pages 3,4,6; Figs 3 + 4 --- -/--	

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document relating to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "A" document member of the same patent family

Date of the actual completion of the international search

2 October 2001

Date of mailing of the international search report

15. 01. 02

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

Holtorf, S

## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 00/27582

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>GLUSMAN GUSTAVO ET AL: "Sequence analysis in the olfactory receptor gene cluster on human chromosome 17: Recombinatorial events affecting receptor diversity." GENOMICS, vol. 37, no. 2, 1996, pages 147-160, XP002178955 ISSN: 0888-7543 the whole document</p>	
A	<p>&amp; DATABASE EMBL SEQUENCE LIBRARY [Online] 22 July 1994 (1994-07-22) CROWE M.L., PERRY B.N., CONNERTON I.F.: "olfactory receptor; OR17-40 gene" abstract</p>	
A	<p>--- BUETTNER JILL A ET AL: "Organization and evolution of olfactory receptor genes on human chromosome 11." GENOMICS, vol. 53, no. 1, 1 October 1998 (1998-10-01), pages 56-68, XP002178956 ISSN: 0888-7543 the whole document</p>	
A	<p>--- TRASK B J ET AL: "Members of the olfactory receptor gene family are contained in large blocks of DNA duplicated polymorphically near the ends of human chromosomes" HUMAN MOLECULAR GENETICS, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 7, no. 1, January 1998 (1998-01), pages 13-26, XP002135641 ISSN: 0964-6906 the whole document</p>	
A	<p>&amp; DATABASE EMBL SEQUENCE LIBRARY [Online] 9 June 1996 (1996-06-09) TRASK, B.J., ET AL.: "Homo sapiens chromosome-19 36.3-kbp cosmid F7501, with 3 regions of similarity to olfactory receptor protein genes" accession no. L78442</p>	
A	<p>--- KRAUTWURST D ET AL: "Identification of ligands for olfactory receptors by functional expression of a receptor library" CELL, CELL PRESS, CAMBRIDGE, MA, US, vol. 95, 25 June 1998 (1998-06-25), pages 917-926, XP002153217 ISSN: 0092-8674 cited in the application</p> <p>---</p> <p style="text-align: center;">-/--</p>	

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27582

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 98 50081 A (ZHAO HAIQING ; FIRESTEIN STUART J (US)) 12 November 1998 (1998-11-12) cited in the application ---	
P,X	DATABASE EMBL SEQUENCE LIBRARY [Online] 14 June 2000 (2000-06-14) HEILIG R., ET AL.: "Human chromosome 14 DNA sequence BAC R-55G7 of library RPCI-11 from chromosome 14 of Homo sapiens (Human)" XP002178959 accession no. AL359218 ---	1,4
T	GLUSMAN GUSTAVO ET AL: "Sequence, structure, and evolution of a complete human olfactory receptor gene cluster." GENOMICS., vol. 63, no. 2, 15 January 2000 (2000-01-15), pages 227-245, XP002178957 ISSN: 0888-7543 the whole document ---	
T	FUCHS TANIA ET AL: "The human olfactory subgenome: From sequence to structure and evolution." HUMAN GENETICS, vol. 108, no. 1, January 2001 (2001-01), pages 1-13, XP002178958 ISSN: 0340-6717 -----	

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/27582

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-7, 15-19 partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim : 1

Invention 1:

claims 1-7, 15-19 partially

Isolated nucleotide sequence encoding an olfactory receptor as characterized by SEQID1; the recombinant expression of the same in host cells; the translated polypeptide sequence of SEQID1 and a host cell and phage expressing said polypeptide; furthermore, a library of olfactory receptors suitable of determining the interaction pattern of a composition with said receptors comprising the translated expression products of at least two, 50, 100, 200 or 500 polynucleotides encoding olfactory receptors, one of which is characterized by SEQID1.

2. Claim : 2

Invention 2-115:

claims 1-7, 15-19 partially

As invention one but as characterized by SEQIDs 2-73 and 111-152.

3. Claim : 3

Invention 116-1047:

claims 8-10 and 15-19 partially, 31,32,33 completely

Isolated nucleotide sequence encoding an olfactory receptor as characterized by one of the SEQIDs from the group of SEQID153 to SEQID1084; the recombinant expression of the same in a host cell; furthermore, a library of olfactory receptors suitable of determining the interaction pattern of a composition with said receptors comprising the translated expression products of at least two, 50, 100, 200 or 500 polynucleotides encoding olfactory receptors, one of which is characterized by one of the SEQIDs from the group of SEQID153 to SEQID1084; furthermore, a DNA array or a DNA chip comprising a DNA segment derived from one SEQID of the group of SEID153 to SEQID1084, a method determining the differences among individuals with respect to their olfactory faculties,

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

comprising comparing the olfactory DNA of the individual against said DNA array or chip; method to determine a single nucleotide polymorphism in olfactory receptors based on primers designed according to the first and last 25 bases of one of the SEQIDs of the group of SEQID153 to SEQID1084.

4. Claim : 4

Invention 1048-1971:

claims 11-14,20-24,25-30 partially

Isolated olfactory receptor polypeptide  
as characterized by one of the SEQIDs from the group of  
SEQID1085 to SEQID2008; a recombinant host cell or phage  
expressing said polypeptide;  
furthermore, a library of olfactory receptors suitable of  
determining the interaction pattern of a composition with  
said receptors comprising at least two, 50, 100, 200 or 500  
olfactory receptor polypeptides, one of which is  
characterized by one of the SEQIDs from the group of  
SEQID1085 to SEQID2008;  
furthermore, a method for determining the binding pattern of  
a composition with olfactory receptors, comprising exposing  
said library to a composition, further determining whether  
the receptor is activated.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/27582

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9518140	A	06-07-1995	WO	9518140 A1	06-07-1995
-----					
WO 9850081	A	12-11-1998	US	5993778 A	30-11-1999
			AU	7372898 A	27-11-1998
			EP	0983506 A2	08-03-2000
			US	6218358 B1	17-04-2001
			WO	9850081 A2	12-11-1998
-----					